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<b>(54) Title:</b> NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS																											
<b>(57) Abstract</b> <p>The invention provides proteins from Neisseria meningitidis, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.</p>																											
<div style="text-align: right;"><b>919 (46 kDa)</b></div> <div style="text-align: right;"><b>A) PURIFICATION</b></div> <div style="text-align: right;"><p>M1 919</p></div>																											

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## NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

This application is a continuation-in-part of the following U.S. Provisional Patent applications, from each of which priority is claimed, and each of which is incorporated by reference in its entirety: 60/083,758 (filed May 1, 1998); 60/094,869 (filed July 31, 1998); 60/098,994 (filed September 2, 1998); 60/099,062 (filed September 2, 1998); 60/103,749 (filed October 9, 1998); 60/103,794 (filed October 9, 1998); 60/103,796 (filed October 9, 1998); and 60/121,528 (filed February 25, 1999).

This invention relates to antigens from the bacterial species: *Neisseria meningitidis* and *Neisseria gonorrhoeae*.

### BACKGROUND

*Neisseria meningitidis* is a non-motile, gram negative diplococcus human pathogen. It colonizes the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoea*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

*N. meningitidis* causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks. (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al.* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al.* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the

United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [*eg.* Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease". In: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B (menB) remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of  $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (*eg.* Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28).

Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (e.g. EP-A-0467714, WO96/29412), but this is by no means complete. Other men B proteins may include those listed in WO 97/28273, WO 96/29412, WO 95/03413, US 5,439,808, and US 5,879,686.

The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae* including *Neisseria meningitidis* or *Neisseria gonorrhoeae*. Those sequences specific to *N. meningitidis* or *N. gonorrhoeae* that are more highly conserved are further preferred sequences.

It is thus an object of the invention is to provide Neisserial DNA sequences which encode proteins that are antigenic or immunogenic.

## BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates the products of protein expression and purification of the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 2 illustrates the products of protein expression and purification of the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 3 illustrates the products of protein expression and purification of the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 4 illustrates the products of protein expression and purification of the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 5 illustrates the products of protein expression and purification of the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 6 illustrates the products of protein expression and purification of the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 7 illustrates the products of protein expression and purification of the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 8 illustrates the products of protein expression and purification of the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 9 illustrates the products of protein expression and purification of the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 10 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 11 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 12 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 13 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 14 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 15 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 16 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 17 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 18 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 19 shows an alignment comparison of amino acid sequences for ORF 225 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 20 shows an alignment comparison of amino acid sequences for ORF 235 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 21 shows an alignment comparison of amino acid sequences for ORF 287 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 22 shows an alignment comparison of amino acid sequences for ORF 519 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 23 shows an alignment comparison of amino acid sequences for ORF 919 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

## THE INVENTION

The invention provides proteins comprising the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (i.e., those having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of homology (sequence identity) is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman

homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with parameters: gap penalty 12, gap extension penalty 1.

The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least  $n$  consecutive amino acids from the sequences and, depending on the particular sequence,  $n$  is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (eg. native, fusions *etc.*). They are preferably prepared in substantially pure or isolated form (*ie.* substantially free from other *N. meningitidis* or *N. gonorrhoeae* host cell proteins)

According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences and *N. gonorrhoeae* nucleotide sequences disclosed in the examples.

According to a further aspect, the invention comprises nucleic acids having sequence identity of greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) to the nucleic acid sequences herein. Sequence identity is determined as above-discussed.

According to a further aspect, the invention comprises nucleic acid that hybridizes to the sequences provided herein. Conditions for hybridization are set forth herein.

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least  $n$  consecutive nucleotides from the *N. meningitidis* sequences or *N. gonorrhoeae* sequences and depending on the particular sequence,  $n$  is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, in part or in whole, from genomic or cDNA libraries, from the

organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also protein nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (*eg.* as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of (I) a medicament for treating or preventing infection due to Neisserial bacteria (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria or (iii) for raising antibodies. Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Methodology - Summary of standard procedures and techniques.

General

This invention provides *Neisseria meningitidis* menB nucleotide sequences, amino acid sequences encoded therein. With these disclosed sequences, nucleic acid probe assays and expression cassettes and vectors can be produced. The expression vectors can be transformed into host cells to produce proteins. The purified or isolated polypeptides (which may also be chemically synthesized) can be used to produce antibodies to detect menB proteins. Also, the host cells or extracts can be utilized for biological assays to isolate agonists or antagonists. In addition, with these sequences one can search to identify open reading frames and identify amino acid sequences. The proteins may also be used in immunogenic compositions, antigenic compositions and as vaccine components.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature e.g., Sambrook *Molecular Cloning: A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C.C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.



All publications, patents, and patent applications cited herein are incorporated in full by reference.

#### Expression systems

The *Neisseria menB* nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, plant cells, baculoviruses, bacteria, and yeast.

##### i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation (Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual*, 2nd ed.).

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible). Depending on the promoter selected, many promoters may be inducible using known substrates, such as the use of the mouse mammary tumor virus (MMTV) promoter with the glucocorticoid responsive element (GRE) that is induced by glucocorticoid in hormone-responsive transformed cells (see for example, U.S. Patent 5,783,681).

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a

regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.). Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer (Dijkema et al (1985) *EMBO J.* 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777) and from human cytomegalovirus (Boshart et al. (1985) *Cell* 41:521). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237).

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation (Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M.

Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105). These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 (Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*).

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 (Gluzman (1981) *Cell* 23:175) or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 (Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946) and pHEBO (Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines.

## ii. Plant Cellular Expression Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, Gibberellins: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Repr.* 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet.*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension.

These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

### iii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to

those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO



Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human ( $\alpha$ ) interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See

Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15  $\mu\text{m}$  in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. *Current Protocols in Microbiology* Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (PCT Pub. No. WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, e.g., Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g., HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g., proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

#### iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps

initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) (Chang *et al.* (1977) *Nature* 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) (Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; U.S. Patent 4,738,921; EPO Publ. Nos. 036 776 and 121 775). The beta-lactamase (*bla*) promoter system (Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)), bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128) and T5 (U.S. Patent 4,689,406) promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent 4,551,433). For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074). In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publ. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon

(Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA (Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberg)). To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site, it is often necessary to optimize the distance between the SD sequence and the ATG of the eukaryotic gene (Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*).

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO Publ. No. 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene (Nagai *et al.* (1984) *Nature* 309:810). Fusion proteins can also be made with sequences from the *lacZ* (Jia *et al.* (1987) *Gene* 60:197), *trpE* (Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11), and *Chey* (EPO Publ. No. 324 647) genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated (Miller *et al.* (1989) *Bio/Technology* 7:698).

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria (U.S. Patent 4,336,336). The

signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghrayeb *et al.* (1984) *EMBO J.* 3:2437) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. No. 244 042).

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number

vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EPO Publ. No. 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541), *Escherichia coli* (Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EPO Publ. Nos. 036 776, 136 829 and 136 907), *Streptococcus cremoris* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655); *Streptococcus lividans* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655), *Streptomyces lividans* (U.S. Patent 4,745,056).

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with  $\text{CaCl}_2$  or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by

electroporation. Transformation procedures usually vary with the bacterial species to be transformed. (See e.g., use of *Bacillus*: Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541; use of *Campylobacter*: Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; and Wang *et al.* (1990) *J. Bacteriol.* 172:949; use of *Escherichia coli*: Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; use of *Lactobacillus*: Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173; use of *Pseudomonas*: Fiedler *et al.* (1988) *Anal. Biochem* 170:38; use of *Staphylococcus*: Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203; use of *Streptococcus*: Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Eur. Cong. Biotechnology* 1:412.

#### v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences.



Examples include alcohol dehydrogenase (ADH) (EPO Publ. No. 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO Publ. No. 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1).

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EPO Publ. No. 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, (Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;).

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, plant, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human

superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See e.g., EPO Publ. No. 196056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (e.g., WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EPO Publ. No. 012 873; JPO Publ. No. 62:096,086) and the A-factor gene (U.S. Patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EPO Publ. No. 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Patent Nos. 4,546,083 and 4,870,008; EPO Publ. No. 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (See e.g., PCT Publ. No. WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.* (1979) *Gene* 8:17-24), pCI/1 (Brake *et al.* (1984) *Proc. Natl. Acad. Sci. USA* 81:4642-4646), and YRp17 (Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See e.g., Brake *et al.*, *supra*.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750). The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions (Butt *et al.* (1987) *Microbiol. Rev.* 51:351).

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors and methods of introducing exogenous DNA into yeast hosts have been developed for, *inter alia*, the following yeasts: *Candida albicans* (Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142); *Candida maltosa* (Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141); *Hansenula polymorpha* (Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302); *Kluyveromyces fragilis* (Das, *et al.* (1984) *J. Bacteriol.* 158:1165); *Kluyveromyces lactis* (De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135); *Pichia guilliermondii* (Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141); *Pichia pastoris* (Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555); *Saccharomyces cerevisiae* (Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163); *Schizosaccharomyces pombe* (Beach and Nurse (1981) *Nature* 300:706); and *Yarrowia lipolytica* (Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49).

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See e.g., [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J.*

*Bacteriol.* 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; U.S. Patent Nos. 4,837,148 and 4,929,555; *Pichia*]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

### Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

A "conserved" *Neisseria* amino acid fragment or protein is one that is present in a particular *Neisserial* protein in at least x% of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an amino acid is "conserved" in a particular *Neisserial* protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria* strains.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a *Neisserial* sequence is heterologous to a mouse host cell.

"Epitope" means antigenic determinant, and may elicit a cellular and/or humoral response.

Conditions for "high stringency" are 65 degrees C in 0.1 xSSC 0.5% SDS solution.

An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as a DNA, RNA or amino acid sequence differing from but having homology with the native or disclosed sequence. Depending on the particular sequence, the degree of homology (sequence identity) between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) which is calculated as described above. As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs at essentially the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions. (see, for example, U.S. Patent 5,753,235).

#### Antibodies

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanized antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria menB* proteins.

Antibodies elicited against the proteins of the present invention bind to antigenic polypeptides or proteins or protein fragments that are present and specifically associated with strains of *Neisseria meningitidis* menB. In some instances, these antigens may be associated with specific strains, such as those antigens specific for the menB strains. The antibodies of the invention may be immobilized to a matrix and utilized in an immunoassay or on an affinity chromatography column, to enable the detection and/or separation of polypeptides, proteins or protein fragments or cells comprising such polypeptides, proteins or protein fragments. Alternatively, such polypeptides, proteins or protein fragments may be immobilized so as to detect antibodies bindably specific thereto.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein (*Nature* (1975) 256:495-96), or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells that express membrane-bound immunoglobulin specific for the antigen bind to the plate, and

are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly  $^{32}\text{P}$  and  $^{125}\text{I}$ ), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example,  $^{125}\text{I}$  may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with  $^{125}\text{I}$ , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Antigens, immunogens, polypeptides, proteins or protein fragments of the present invention elicit formation of specific binding partner antibodies. These antigens, immunogens, polypeptides, proteins or protein fragments of the present invention comprise immunogenic compositions of the present invention. Such immunogenic compositions may further comprise or include adjuvants, carriers, or other compositions that promote or enhance



or stabilize the antigens, polypeptides, proteins or protein fragments of the present invention. Such adjuvants and carriers will be readily apparent to those of ordinary skill in the art.

#### Pharmaceutical Compositions

Pharmaceutical compositions can comprise (include) either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature, when given to a patient that is febrile. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of

organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

#### Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal and transcutaneous applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

#### Vaccines

Vaccines according to the invention may either be prophylactic (i.e., to prevent infection) or therapeutic (i.e., to treat disease after infection).

Such vaccines comprise immunizing antigen(s) or immunogen(s), immunogenic polypeptide, protein(s) or protein fragments, or nucleic acids (e.g., ribonucleic acid or deoxyribonucleic acid), usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or

liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the immunogen or antigen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (PCT Publ. No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi<sup>TM</sup> adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox<sup>TM</sup>); (3) saponin adjuvants, such as Stimulon<sup>TM</sup> (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g., IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g., gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63, LT-R72, CT-S109, PT-K9/G129; see, e.g., WO 93/13302 and WO 92/19265; and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59 are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

The vaccine compositions comprising immunogenic compositions (e.g., which may include the antigen, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Alternatively, vaccine compositions comprising immunogenic compositions may comprise an antigen, polypeptide, protein, protein fragment or nucleic acid in a pharmaceutically acceptable carrier.

More specifically, vaccines comprising immunogenic compositions comprise an immunologically effective amount of the immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g., nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Typically, the vaccine compositions or immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

The immunogenic compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal and transcutaneous applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed (e.g., Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648).

### Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs, including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence in vivo can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses e.g., MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (e.g., HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102,

WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (i.e., there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors comprising sequences of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ

described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human



immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinita virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu &

Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed to transform a host cell. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in U.S. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. 5,206,152 and WO92/11033.

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP- 0524968; and in Stryer, *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

### **Delivery Methods**

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *eg.* WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

### **Polynucleotide and polypeptide pharmaceutical compositions**

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

#### **A. Polypeptides**

One example are polypeptides which include, without limitation: asioloorosomuroid (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF),

granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

#### B.Hormones, Vitamins, Etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

#### C.Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides or polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

#### D.Lipids, and Liposomes

The desired polynucleotide or polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide or polypeptide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and

DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, *eg.* Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See *eg.* Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

#### E. Lipoproteins

In addition, lipoproteins can be included with the polynucleotide or polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been

isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (*supra*); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750.

Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443.

Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA.

Further description of lipoproteins can be found in Zuckermann et al., PCT. Appln. No. US97/14465.

#### F. Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide or polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

#### Synthetic Polycationic Agents

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin<sup>®</sup>, and lipofectAMINE<sup>®</sup> are monomers that form polycationic complexes when combined with polynucleotides or polypeptides.

#### Immunodiagnostic Assays

Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are

assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

### **Nucleic Acid Hybridisation**

"Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated  $T_m$  of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to  $10^{-9}$  to  $10^{-8}$  g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy



yeast gene can be detected with an exposure time of only 1 hour starting with 1 µg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of  $10^8$  cpm/µg. For a single-copy mammalian gene a conservative approach would start with 10 µg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than  $10^8$  cpm/µg, resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature ( $T_m$ ) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4[\%(G + C)] - 0.6(\%\text{formamide}) - 600/n - 1.5(\%\text{mismatch}).$$

where  $C_i$  is the salt concentration (monovalent ions) and  $n$  is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe which is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be

washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

### **Nucleic Acid Probe Assays**

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

One example of a nucleotide hybridization assay is described by Urdea *et al.* in international patent application WO92/02526 [see also US patent 5,124,246].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patent 4,683,195; and US patent 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al.* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes

containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

## EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, and *N. gonorrhoeae* along with their respective and putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N. meningitidis*
- the putative translation product of said *N. meningitidis* sequence
- a computer analysis of said translation product based on database comparisons
- a corresponding nucleotide sequence identified from *N. gonorrhoeae*
- the putative translation product of said *N. gonorrhoeae* sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a corresponding nucleotide sequence identified from strain A of *N. meningitidis*
- the putative translation product of said *N. meningitidis* strain A sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a description of the characteristics of the protein which indicates that it might be suitably antigenic or immunogenic.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [*eg.* see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters represent ambiguities which arose during

alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

For each of the following examples: based on the presence of a putative leader sequence and/or several putative transmembrane domains (single-underlined) in the gonococcal protein, it is predicted that the proteins from *N. meningitidis* and *N. gonorrhoeae*, and their respective epitopes, could be useful antigens or immunogenic compositions for vaccines or diagnostics.

The standard techniques and procedures which may be employed in order to perform the invention (*e.g.* to utilize the disclosed sequences for vaccination or diagnostic purposes) were summarized above. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

In particular, the following methods were used to express, purify and biochemically characterize the proteins of the invention.

#### **Chromosomal DNA Preparation**

*N.meningitidis* strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20%(w/v) Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml of lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension incubated at 37°C for 2 hours. Two phenol extractions (equilibrated to pH 8) and one CHCl<sub>3</sub>/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes of ethanol, and collected by centrifugation.

The pellet was washed once with 70%(v/v) ethanol and redissolved in 4.0ml TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0). The DNA concentration was measured by reading the OD at 260 nm.

### Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by designing the 5' primers to sequence immediately downstream from the predicted leader sequence.

For most ORFs, the 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, *Eco*RI-*Nde*I or *Eco*RI-*Nhe*I), depending on the restriction pattern of the gene of interest. The 3' primers included a *Xho*I or a *Hind*III restriction site (table 1). This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using *Bam*HI-*Xho*I, *Bam*HI-*Hind*III, *Eco*RI-*Xho*I or *Eco*RI-*Hind*III), and pET21b+ (using *Nde*I-*Xho*I, *Nhe*I-*Xho*I, *Nde*I-*Hind*III or *Nhe*I-*Hind*III).

5'-end primer tail:	<u>CGCGGATCCCATATG</u>	( <i>Bam</i> HI- <i>Nde</i> I)
	<u>CGCGGATCCGCTAGC</u>	( <i>Bam</i> HI- <i>Nhe</i> I)
	<u>CCGGAATTCTACATATG</u>	( <i>Eco</i> RI- <i>Nde</i> I)
	<u>CCGGAATTCTAGCTAGC</u>	( <i>Eco</i> RI- <i>Nhe</i> I)
3'-end primer tail:	<u>CCCGCTCGAG</u>	( <i>Xho</i> I)
	<u>CCCGCTCGAG</u>	( <i>Hind</i> III)

For cloning ORFs into the pGEX-His vector, the 5' and 3' primers contained only one restriction enzyme site (*Eco*RI, *Kpn*I or *Sal*I for the 5' primers and *Pst*I, *Xba*I, *Sph*I or *Sal*I for the 3' primers). Again restriction sites were chosen according to the particular restriction pattern of the gene (table 1).

5'-end primer tail:	(AAA) <u>AAAGAATTC</u>	( <i>Eco</i> RI)
	(AAA) <u>AAAGGTACC</u>	( <i>Kpn</i> I)
3'-end primer tail:	(AAA) <u>AAACTGCAG</u>	( <i>Pst</i> I)
	(AAA) <u>AAATCTAGA</u>	( <i>Xba</i> I)

AAAGCATGC

(*SphI*)

AAAAAAGTCGAC

(SaII)

As well as containing the restriction enzyme recognition sequences, the primers

(tail excluded)

(whole primer)

The melting temperatures of the selected oligonucleotides were usually 65-70°C for

Table 1 shows the forward and reverse primers used for each amplification. In certain

Oligonucleotides were synthesized using a Perkin Elmer 394 DNA/RNA Synthesizer.

## Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA was used as a

Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase). In some cases, PCR was optimised by the addition of 10µl DMSO or 50µl 2M Betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a two-step amplification. The first 5 cycles were performed using the hybridization temperature that excluded the restriction enzyme tail of the primer (see above). This was followed by 30 cycles using the hybridization temperature calculated for the whole length oligos. The cycles were completed with a 10 minute extension step at 72°C. The standard cycles were as follows:

	<b>Denaturation</b>	<b>Hybridisation</b>	<b>Elongation</b>
First 5 cycles	30 seconds 95°C	30 seconds 50-55°C	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds 65-70°C	30-60 seconds 72°C

Elongation times varied according to the length of the ORF to be amplified. Amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% (w/v) agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a volume suitable to be loaded on a 1.0% agarose gel. The DNA fragment corresponding to the band of correct size was purified using the Qiagen Gel Extraction Kit, following the manufacturer's protocol. DNA fragments were eluted in a volume of 30µl or 50µl with either H<sub>2</sub>O or 10mM Tris, pH 8.5.

#### **Digestion of PCR fragments**

The purified DNA corresponding to the amplified fragment was doubly-digested with the appropriate restriction enzymes for; cloning into pET-21b+ and expressing the protein as a C-terminus His-tagged fusion, for cloning into pGEX-KG and expressing the protein as a N-



terminus GST-fusion, and for cloning into pGEX-His and expressing the protein as a N-terminus GST-His tagged fusion.

Each purified DNA fragment was incubated at 37°C for 3 hours to overnight with 20 units of appropriate restriction enzyme (New England Biolabs) in a volume of either 30 or 40 µl in the presence of suitable digestion buffer. Digested fragments were purified using the QIAquick PCR purification kit (following the manufacturer's instructions) and eluted in a volume of 30 µl or 50 µl with either H<sub>2</sub>O or 10 mM Tris, pH 8.5. The DNA concentration was determined by quantitative agarose gel electrophoresis (1.0% gel) in the presence of a titrated molecular weight marker.

#### **Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, pET21b+, pGEX-KG, and pGEX-His)**

The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream of the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia). 10 µg plasmid was double-digested with 50 units of each restriction enzyme in 200 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD<sub>260</sub> of the sample, and adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

10 µg of plasmid vector was doubly-digested with 50 units of each restriction enzyme in a volume of 200 µl with the appropriate buffer overnight at 37°C. The digest was loaded onto a 1.0% agarose gel and the band corresponding to the digested vector purified using the Qiagen QIAquick Gel Extraction Kit. DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD<sub>260nm</sub> and the concentration adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

#### **Cloning**

For some ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 µl, a molar

ratio of 3:1 fragment/vector was ligated using 0.5  $\mu$ l of NEB T4 DNA ligase (400 units/ $\mu$ l), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boheringer "Rapid Ligation Kit", following the manufacturer's instructions.

In order to introduce the recombinant plasmid in a suitable strain, 100  $\mu$ l *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800  $\mu$ l LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200  $\mu$ l of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml).

The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37 °C in either 2 ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100  $\mu$ g/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30  $\mu$ l. 5  $\mu$ l of each individual miniprep (approximately 1g) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

For other ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated into both pET21b+ and pGEX-KG. A molar ratio of of 3:1 fragment/vector was used in a final volume of 20 $\mu$ l, that included 0.5 $\mu$ l T4 DNA ligase (400 units/ $\mu$ l, NEB) and ligation buffer supplied by the manufacturer. The reaction was performed at room temperature for 3 hours. In some experiments, ligation was performed using the Boheringer "Rapid Ligation Kit" and the manufacturer's protocol.

Recombinant plasmid was transformed into 100 $\mu$ l of competent *E. coli* DH5 or HB101 by incubating the ligase reaction solution and bacteria for 40 minutes on ice then at 37°C for 3 minutes. This was followed by the addition of 800 $\mu$ l LB broth and incubation at 37°C for 20 minutes. The cells were centrifuged at maximum speed in an Eppendorf microfuge, resuspended in approximately 200 $\mu$ l of the supernatant and plated onto LB ampicillin (100mg/ml) agar.

Screening for recombinant clones was performed by growing 5 randomly selected colonies overnight at 37°C in either 2.0ml (pGEX-KG clones) or 5.0ml (pET clones) LB broth + 100µg/ml ampicillin. Cells were pelleted and plasmid DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions. Approximately 1µg of each individual miniprep was digested with the appropriate restriction enzymes and the digest loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1kb DNA Ladder, GIBCO). Positive clones were selected on the basis of the size of insert.

ORFs were cloned into PGEX-His, by doubly-digesting the PCR product and ligating into similarly digested vector. After cloning, recombinant plasmids were transformed into the *E.coli* host W3110. Individual clones were grown overnight at 37°C in LB broth with 50µg/ml ampicillin.

Certain ORFs may be cloned into the pGEX-HIS vector using *EcoRI-PstI* cloning sites, or *EcoRI-SalI*, or *SalI-PstI*. After cloning, the recombinant plasmids may be introduced in the *E.coli* host W3110.

### Expression

Each ORF cloned into the expression vector may then be transformed into the strain suitable for expression of the recombinant protein product. 1 µl of each construct was used to transform 30 µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100 µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20 ml of LB+Amp (100 µg/ml) in 100 ml flasks, making sure that the OD<sub>600</sub> ranged between 0.1 and 0.15. The flasks were incubated at 30°C into gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge, the pellet

resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

#### **GST-fusion proteins large-scale purification.**

For some ORFs, a single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD<sub>550</sub> 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000 rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD<sub>280</sub> of 0.02-0.06. The GST-fusion protein was eluted by addition of 700µl cold Glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl) and fractions collected until the OD<sub>280</sub> was 0.1. 21µl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M") (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

For other ORFs, for each clone to be purified as a GST-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp. (100µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD<sub>550nm</sub> reached 0.6-0.8. Recombinant protein expression was induced by addition of IPTG (final concentration 0.2mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml cold PBS. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia), previously equilibrated with PBS, and incubated at room temperature with gentle agitation for 30 min. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batchwise) with 10ml cold PBS for 10 min, resuspended in 1ml cold PBS, and loaded onto a disposable column. The resin continued to be washed with cold PBS, until the OD<sub>280nm</sub> of the flow-through reached 0.02-0.01. The GST-fusion protein was eluted by addition of 700µl cold glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl pH 8.0) and fractions collected, until the OD<sub>280nm</sub> of the eluate indicated all the recombinant protein was obtained. 20µl aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. The molecular mass of the purified proteins was determined using either the Bio-Rad broad range molecular weight standard (M1) (200, 116, 97.4, 66.2, 45.0, 31.0, 21.5, 14.4, 6.5 kDa) or the Amersham Rainbow Marker (M2) (220, 66.2, 46.0, 30.0, 21.5, 14.3 kDa). The molecular weights of GST-fusion proteins are a combination of the 26 kDa GST protein and its fusion partner. Protein concentrations were estimated using the Bradford assay.

#### **His-fusion soluble proteins large-scale purification.**

For some ORFs, a single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD<sub>550</sub> 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold 10mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Ni<sup>2+</sup>-resin (Pharmacia) (previously washed with 10mM imidazole buffer) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold 10mM imidazole buffer for 10 minutes,

resuspended in 1ml cold 10mM imidazole buffer and loaded on a disposable column. The resin was washed at 4°C with 2ml cold 10mM imidazole buffer until the flow-through reached the O.D<sub>280</sub> of 0.02-0.06. The resin was washed with 2ml cold 20mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) until the flow-through reached the O.D<sub>280</sub> of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl cold 250mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) and fractions collected until the O.D<sub>280</sub> was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

#### **His-fusion insoluble proteins large-scale purification.**

A single colony was grown overnight at 37 °C on a LB + Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600ml fresh medium and let to grow at the optimal temperature (37°C) to O.D<sub>550</sub> 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was stored at -20°C, while the pellets were resuspended in 2 ml guanidine buffer (6M guanidine hydrochloride, 100mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes. The supernatant was mixed with 150µl Ni<sup>2+</sup>-resin (Pharmacia) (previously washed with buffer B) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4°C. The resin was washed twice with 10 ml buffer B for 10 minutes, resuspended in 1ml buffer B, and loaded on a disposable column. The resin was washed at room temperature with 2ml buffer B until the flow-through reached the OD<sub>280</sub> of 0.02-0.06. The resin was washed with 2ml buffer C (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D<sub>280</sub> of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl elution buffer (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions collected until the OD<sub>280</sub> was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

**Purification of His-fusion proteins.**

For each clone to be purified as a His-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp (100 µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100 µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD<sub>550nm</sub> reached 0.6-0.8. Expression of recombinant protein was induced by addition of IPTG (final concentration 1.0mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8.0) for soluble proteins or (ii) buffer B (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. For insoluble proteins, pellets were resuspended in 2.0 ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated with a Dounce homogenizer for 10 cycles. The homogenate was centrifuged at 13 000xg for 40 min and the supernatant retained.

Supernatants for both soluble and insoluble preparations were mixed with 150µl Ni<sup>2+</sup>-resin (previously equilibrated with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 min. The resin was Chelating Sepharose Fast Flow (Pharmacia), prepared according to manufacturers protocol. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batch-wise) with 10ml buffer A or B for 10 min, resuspended in 1.0 ml buffer A or B and loaded onto a disposable column. The resin continued to be washed with either (i) buffer A at 4°C or (ii) buffer B at room temperature, until the OD<sub>280nm</sub> of the flow-through reached 0.02-0.01. The resin was further washed with either (i) cold buffer C (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8.0) or (ii) buffer D (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the the OD<sub>280nm</sub> of the flow-through reached 0.02-0.01. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8.0) or (ii) elution buffer B (8 M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions

collected until the  $O.D_{280nm}$  indicated all the recombinant protein was obtained. 20 $\mu$ l aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. Protein concentrations were estimated using the Bradford assay.

### **His-fusion proteins renaturation**

In the cases where denaturation was required to solubilize proteins, a renaturation step was employed prior to immunization. Glycerol was added to the denatured fractions obtained above to give a final concentration of 10%(v/v). The proteins were diluted to 200 $\mu$ g/ml using dialysis buffer I (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, 2.0M urea, pH 8.8) and dialysed against the same buffer for 12-14 hours at 4°C. Further dialysis was performed with buffer II (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Alternatively, 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 $\mu$ g/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

### **Purification of proteins**

To analyse the solubility, pellets obtained from 3.0ml cultures were resuspended in 500 $\mu$ l buffer M1 (PBS pH 7.2). 25 $\mu$ l of lysozyme (10mg/ml) was added and the bacteria incubated for 15 min at 4°C. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and the pellet resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M  $NaH_2PO_4$ ] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M  $NaH_2PO_4$ ] overnight at 4°C. The



supernatants from all steps were analysed by SDS-PAGE. Some proteins were found to be soluble in PBS, others need urea or guanidium-HCl for solubilization.

For preparative scale purifications, 500ml cultures were induced and fusion proteins solubilized in either buffer M1, M2 or M3 using the procedure described above. Crude extracts were loaded onto a Ni-NTA superflow column (Quiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer employed. Unbound material was eluted by washing the column with the same buffer. The recombinant fusion protein was eluted with the corresponding buffer containing 500mM imidazole then dialysed against the same buffer in the absence of imidazole.

### **Mice immunisations**

20µg of each purified protein are used to immunise mice intraperitoneally. In the case of some ORFs, Balb-C mice were immunised with Al(OH)<sub>3</sub> as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For other ORFs, CD1 mice could be immunised using the same protocol. For ORFs 25 and 40, CD1 mice were immunised using Freund's adjuvant, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for still other ORFs, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49. Alternatively, 20µg of each purified protein was mixed with Freund's adjuvant and used to immunise CD1 mice intraperitoneally. For many of the proteins, the immunization was performed on days 1, 21 and 35, and immune response was monitored in samples taken on days 34 and 49. For some proteins, the third immunization was performed on day 28, rather than 35, and the immune response was measured on days 20 and 42, rather than 34 and 49.

### **ELISA assay (sera analysis)**

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD<sub>620</sub>. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated

for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200 µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN<sub>3</sub> in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100 µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100 µl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 µl of H<sub>2</sub>O) were added to each well and the plates were left at room temperature for 20 minutes. 100 µl H<sub>2</sub>SO<sub>4</sub> was added to each well and OD<sub>490</sub> was followed. The ELISA was considered positive when OD<sub>490</sub> was 2.5 times the respective pre-immune sera.

Alternatively, The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD<sub>620</sub>. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10 000rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 1 hour at 37°C and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN<sub>3</sub> in PBS) were added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-

phenildiamine and 10 $\mu$ l of H<sub>2</sub>O<sub>2</sub>) were added to each well and the plates were left at room temperature for 20 minutes. 100 $\mu$ l of 12.5% H<sub>2</sub>SO<sub>4</sub> was added to each well and OD<sub>490</sub> was followed. The ELISA titers were calculated arbitrarily as the dilution of sera which gave an OD<sub>490</sub> value of 0.4 above the level of preimmune sera. The ELISA was considered positive when the dilution of sera with OD<sub>490</sub> of 0.4 was higher than 1:400.

#### **FACScan bacteria Binding Assay procedure.**

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD<sub>620</sub>. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA in PBS, 0.4% NaN<sub>3</sub>) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD<sub>620</sub> of 0.07. 100 $\mu$ l bacterial cells were added to each well of a Costar 96 well plate. 100 $\mu$ l of diluted (1:100, 1:200, 1:400) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200 $\mu$ l/well of blocking buffer in each well. 100 $\mu$ l of R-Phicoerytrin conjugated F(ab)<sub>2</sub> goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200 $\mu$ l/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 $\mu$ l/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan (Laser Power 15mW) setting were: FL2 on; FSC-H threshold:92; FSC PMT Voltage: E 01; SSC PMT: 474; Amp. Gains 6.1; FL-2 PMT: 586; compensation values: 0.

#### **OMV preparations**

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10' on ice ( 50% duty cycle, 50% output ). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope

fraction recovered by centrifugation at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

#### **Whole Extracts preparation**

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30' minutes.

#### **Western blotting**

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded onto a 12% SDS-polyacrylamide gel and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, using transfer buffer (0.3 % Tris base, 1.44 % glycine, 20% (v/v) methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

#### **Bactericidal assay**

MC58 and 2996 strains were grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD<sub>620</sub> was in between 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD<sub>620</sub> of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted (1:100) mice sera (dilution buffer: Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1h were counted.

### Gene Variability

The *ORF4* and *919* genes were amplified by PCR on chromosomal DNA extracted from various *Neisseria* strains (see list of strains). The following oligonucleotides used as PCR primers were designed in the upstream and downstream regions of the genes:

orf 4.1	(forward)	CGAATCCGGACGGCAGGACTC
orf 4.3	(reverse)	GGCAGGGAATGGCGGATTAAAG
919.1	(forward)	AAAATGCCTCTCCACGGCTG or CTGCGCCCTGTGTTAAAATCCCCCT
919.6	(reverse)	CAAATAAGAAAGGAATTTTG or GGTATCGCAAAACTTCGCCTTAATGCG

The PCR cycling conditions were:

1 cycle	2 min. at 94°
30 cycles	30 sec. at 94°
	30 sec. at ~ 54° or ~ 60° ( in according to Tm of the primers)
	40 sec. at 72°
1 cycle	7 min. at 72°

The PCR products were purified from 1 % agarose gel and sequenced using the following primers:

orf 4.1 (forward)	CGAATCCGGACGGCAGGACTC
orf 4.2 (forward)	CGACCGCGCCTTTGGGACTG
orf 4.3 (reverse)	GGCAGGGAATGGCGGATTAAAG
orf 4.4 (reverse)	TCTTTGAGTTTGATCCAACC

- 919.1 (forward) AAAATGCCTCTCCACGGCTG or  
CTGCGCCCTGTGTAAATCCCCT
- 919.2 (forward) ATCCTTCCGCTCGGCTGCG
- 919.3 (forward) AAAACAGCGGCACAATCGAC
- 919.4 (forward) ATAAGGGCTACCTCAAATC
- 919.5 (forward) GCGCGTGGATTATTTTGGG
- 919.6 (reverse) CAAATAAGAAAGGAATTTTG or  
GGTATCGCAAACTTCGCCTTAATGCG
- 919.7 (reverse) CCCAAGGTAATGTAGTGCCG
- 919.8 (reverse) TAAAAAAAGTTTCGACAGGG
- 919.9 (reverse) CCGTCCGCTGTCTCGCCC
- 919.10 (reverse) TCGTCCGGCGGGTCGGGG

All documents cited herein are incorporated by reference in their entireties.

The following Examples are presented to illustrate, not limit, the invention

#### EXAMPLE 1

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

**Table 1: Oligonucleotides used for PCR for Examples 2-10**

ORF	Primer	Sequence	Restriction sites
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT <SEQ ID 3021>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTAGAAGCGGGCGGCAA <SEQ ID 3022>	XhoI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA <SEQ ID 3023>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC <SEQ ID 3024>	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT <SEQ ID 3025>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTGATGTCGAC <SEQ ID 3026>	XhoI
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC <SEQ ID 3027>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG <SEQ ID 3028>	XhoI
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT <SEQ ID 3029>	BamHI-NdeI

128	Reverse	CCCGCTCGAG-ATAATAATATCCGCGCCC <SEQ ID 3030>	XhoI
	Forward	CGCGGATCCCATATG-ACTGACAACGCACT <SEQ ID 3031>	BamHI-NdeI
	Reverse	CCCGCTCGAG-GACCGCGTTGTGCGAAA <SEQ ID 3032>	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA <SEQ ID 3033>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAGTATGTGC <SEQ ID 3034>	XhoI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG <SEQ ID 3035>	EcoRI-NheI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC <SEQ ID 3036>	XhoI
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG <SEQ ID 3037>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG <SEQ ID 3038>	XhoI

### Localization of the ORFs

The following DNA and amino acid sequences are identified by titles of the following form: [g, m, or a] [#].[seq or pep], where "g" means a sequence from *N. gonorrhoeae*, "m" means a sequence from *N. meningitidis B*, and "a" means a sequence from *N. meningitidis A*; "#" means the number of the sequence; "seq" means a DNA sequence, and "pep" means an amino acid sequence. For example, "g001.seq" refers to an *N. gonorrhoeae* DNA sequence, number 1. The presence of the suffix "-1" to these sequences indicates an additional sequence found for the same ORF, thus, data for an ORF having both an unsuffixed and a suffixed sequence designation applies to both such designated sequences. Further, open reading frames are identified as ORF #, where "#" means the number of the ORF, corresponding to the number of the sequence which encodes the ORF, and the ORF designations may be suffixed with ".ng" or ".a", indicating that the ORF corresponds to a *N. gonorrhoeae* sequence or a *N. meningitidis A* sequence, respectively. The word "partial" before a sequence indicates that the sequence may be a partial or a complete ORF. Computer analysis was performed for the comparisons that follow between "g", "m", and "a" peptide sequences; and therein the "pep" suffix is implied where not expressly stated. Further, in the event of a conflict between the text immediately preceding and describing which sequences are being compared, and the

designated sequences being compared, the designated sequence controls and is the actual sequence being compared.

ORF: contig:

279 gnm4.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3039>:  
m279.seq

```

1   ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTCG GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGGCGCGT TTGGCACCGG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCCCTGCA ATCACGATTT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 3040; ORF 279>:  
m279.pep

```

1   ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCS SKPRIAATAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPA
151 SK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3041>:  
g279.seq

```

1   atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgtcg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgcggt ttggctccgg cttctttggc ggcagccatg
151 gtgcttcgga cggcggcggc gttgcctgca atcacgactt gtccgggcga
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcattt tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcggcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 3042; ORF 279.ng>:  
g279.pep

```

1   MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCS SKPKMAATAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:     : :     :     :     :     :     :					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60



	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
	:       :					
g279	ITTCPGELKLTASTTSPCADSAQICLTCSKPKMAAIAPTPCGTADCISSARRRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPASKX					
	:					
g279	SAKSNASAATSAVYSPRLCPATAAGVLPPTSKX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3043>:

```
a279.seq
1   ATGACNCNGA TTTGCGGCTG CTTGATTCA ACGGTTTNA GGGCTTCGC
51  GAGTTTGTG GCGGCGGGT TCATGAGGCT GCAATGGGA GGTACNGACA
101 CNGGCAGCG CAGGCGCGT TTGGCGCCG CTTCTTTGG GCAAGCATA
151 GCGCGCTCGA CGGCGCGGC ATTGCCTGCA ATCACGACT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAA
251 TTTGTTTAC CTGTTCATCT TCCAAGCCGA GAATCGCCG CATTGCGCC
301 ACGCCTTGCG GTACGCGGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGC GTGT
401 ATTCGCGGAN GCTGTGTCCG GCAACGGCG CAGCGGTTT GCCGCCGCT
451 TCCGAATAG
```

This corresponds to the amino acid sequence <SEQ ID 3044; ORF 279.a>:

```
a279.pep
1   MTXICGLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
51  ARSTAAALPA ITTCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAAT SAVYSPXLCP ATAAGVLP
151 SE*
```

m279/a279 ORFs 279 and 279.a showed a 88.2% identity in 152 aa overlap

	10	20	30	40	50	60
m279.pep	ITRICGLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAMARPTAAALPA					
	:                     :       :					
a279	MTXICGLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
	:       :					
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPASKX					
	:					
a279	SAKSNAPAATSAVYSPXLCPATAAGVLPASEX					
	130	140	150			

519 and 519-1 gnm7.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3045>:

```
m519.seq (partial)
1   ..TCCGTTATCG GCGTATGGA GTTGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAT CGAACAAATC AACCTTGCCA
```

```

251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTGTC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
551 TGATTTCTGC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3046; ORF 519>:

```

m519.pep (partial)
1  .SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLLISAGMK IIDSSSKTAK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3047>:

```

g519.seq
1  atggaatddd tcatatctt gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatttt gattcccttt
151 atcgaccgag tcgcctaccg ccattcgctg aaagaaatcc cttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgctc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgctgctctc gccctcgatg aagccgccgg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgag tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgccgccct tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaagg ttgccgaaat cgggaaccct
901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaaata
951 a

```

This corresponds to the amino acid sequence <SEQ ID 3048; ORF 519.ng>:

```

g519.pep
1  MEFFIILLAA VAVFGKFSV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEK RKIEQINLAS
201 GQREAEIQQS EGQAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAAN
251 RQIAAALQTO SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
301 NFRHEKFSF EAKTAK*

```

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

```

m519/g519

m519.pep                               10      20      30
                                      SVIGRMELDKTFEERDEINSTVVAALDEAA
g519      YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
           90      100      110      120      130      140

m519.pep           40      50      60      70      80      90
GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE

```

```

a519.seq
  1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTTGT GTCATCCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGCTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCGTTTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAACG GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCGGG AGCTTGGGGT
451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGGTCCGCG CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGTG CTAATAATCG AACAAATCAA CCTTGGCCAT
601 GGTGACCGCG AAGCCGAAAT CGAACATCC GAAGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGC GC TTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAACCCCAA GCGGTTGCGG ATGCGGTCAA
801 TCTGAAGATT CGGGAACAAT ACGTCGCGCG GTTCAACAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGGCCAATG TTGCCGACAT CCGGACCGCT
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

```
a519.pep
  1  MEFFFIILLAA VVVFGKSFV VIPQQEVHVV ERLGRFHRL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTILRSVIG RMELDKTFEE REIDNSTVVS ALDEAAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAAQAVNA SNAEKIARIN RAKEAESLR LVAEANAEAI
251 RQIAAALQTS GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKLIDS SKTAK*
```

[illegible]

```

m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAFAIRQIAAALQTQGGADAV
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAFAIRQIAAALQTQGGADAV
                210      220      230      240      250      260

                160      170      180      190      200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                270      280      290      300      310

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3051>:

```

m519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
51  ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
101 GCGGTTTCCA TCGCGCCCTG ACGGcCGGTT TGAATATTTT GATTCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCGAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TGTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3052; ORF 519-1>:

```

m519-1.
1  MEFFIILLVA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHS L KEIPLDVPSQ VCITRDNTQ L TVDGIIYFQV TDPKLASYGS
101 SNYIMAITQ L AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAFAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3053>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCGAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGT AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 CGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG

```

851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG  
 901 ATTTCTGCCG GCATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 3054; ORF 519-1.ng>:

g519-1.pep  
 1 MEFFIILLAA VAVFGFKSFV VIPQOEHVHV ERLGRFHRAL TAGLNILIPF  
 51 IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLSYGS  
 101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG  
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS  
 201 GQREAEIQQS EGEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAIAI  
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL  
 301 ISAGMKIIDS SKTAK\*

m519-1/g519-1 ORFs 519-1 and 519-1.ng showed a 99.0% identity in 315 aa overlap

g519-1.pep	10	20	30	40	50	60
m519-1	10	20	30	40	50	60
g519-1.pep	70	80	90	100	110	120
m519-1	70	80	90	100	110	120
g519-1.pep	130	140	150	160	170	180
m519-1	130	140	150	160	170	180
g519-1.pep	190	200	210	220	230	240
m519-1	190	200	210	220	230	240
g519-1.pep	250	260	270	280	290	300
m519-1	250	260	270	280	290	300
g519-1.pep	310					
m519-1	310					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3055>:

a519-1.seq  
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA  
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG  
 101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT  
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT  
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG  
 251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGTTTCG  
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGTCGCTTC  
 351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA

```
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAATAA
```

This corresponds to the amino acid sequence <SEQ ID 3056; ORF 519-1.a>:

a519-1.pep.

```
1 MEFFIILLAA VVVFQFKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51 IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLSYGS
101 SNYIMAITQL AQTTLSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*
```

m519-1/a519-1 ORFs 519-1 and 519-1.a showed a 99.0% identity in 315 aa overlap

a519-1.pep	10	20	30	40	50	60
m519-1	10	20	30	40	50	60
a519-1.pep	70	80	90	100	110	120
m519-1	70	80	90	100	110	120
a519-1.pep	130	140	150	160	170	180
m519-1	130	140	150	160	170	180
a519-1.pep	190	200	210	220	230	240
m519-1	190	200	210	220	230	240
a519-1.pep	250	260	270	280	290	300
m519-1	250	260	270	280	290	300
a519-1.pep	310					
m519-1	310					

576 and 576-1 gnm22.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3057>:

```
m576.seq.. (partial)
1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
51  GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCGGC
301 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451 GTGATTCCGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
501 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGC GG
551 GCGACAAAT CCGTCCGAAC GCCACTTTGG TATTGATGT GAAACTGGTC
601 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTAAGTCGA
651 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 3058; ORF 576>:

```
m576.pep.. (partial)
1  ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFVDKLV
201 KIGAPENAPA KQPAQVDIKK VN*
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3059>:

```
g576.seq.. (partial)
1  ..atgggcggtgg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttcttcgagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccc
251 aagacggcgt gaagaccact gcttcgggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgtaa ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccgcc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtcggg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcggcgc acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa
```

This corresponds to the amino acid sequence <SEQ ID 3060; ORF 576.ng>:

```
g576.pep.. (partial)
1  ..MGVDIGRSLK QMKEQGAIED LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KERGEAFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*
```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 ORFs 576 and 576.ng showed a 97.2% identity in 215 aa overlap

```
m576.pep      10      20      30      40      50      60
MQQASYAMGVDIGRSLKQMKEQGAEIDLKVTEAMQAVYDGKEIKMTEEQAQEVMMKFLQ
|||||
```

```

g576          MGVDIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLO
                10      20      30      40      50

                70      80      90      100     110     120
m576.pep      EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQEGKQPTKDDIV
                |||||
g576          EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTTASGLQYKITKQEGKQPTKDDIV
                60      70      80      90      100     110

                130     140     150     160     170     180
m576.pep      TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
                |||||
g576          TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE
                120     130     140     150     160     170

                190     200     210     220
m576.pep      QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN
                |||||
g576          QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN
                180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3061>:

```

a576.seq
1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51 ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCG TCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAA CCGGCGCCCG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGC GG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3062; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLKENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

m576/a576 ORFs 576 and 576.a showed a 99.5% identity in 222 aa overlap

```

                10      20      30
m576.pep      MQQASYAMGV DIGRSLQMK EQGAEIDLKV
                |||||
a576          CGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV DIGRSLQMK EQGAEIDLKV
                30      40      50      60      70      80

                40      50      60      70      80      90
m576.pep      FTEAMQAVYDGKEIKMTEEQAQEVMMKFLOEQQAKAVEKHKADAKANKEKGEAFLKENAA
                |||||
a576          FTEAMQAVYDGKEIKMTEEQAQEVMMKFLOEQQAKAVEKHKADAKANKEKGEAFLKENAA
                90      100     110     120     130     140

```



	100	110	120	130	140	150
m576.pep	KDGVKTTASGLQYKITKQEGEKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
a576	KDGVKTTASGLQYKITKQEGEKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
	150	160	170	180	190	200
m576.pep	VIPGWTEGVQLLEKGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
a576	VILGWTEGVQLLEKGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
	210	220	230	240	250	260
m576.pep	KQPAQVDIKKVN					
a576	KQPAQVDIKKVN					
	270					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3063>:

m576-1.seq

1	ATGAACACCA	TTTTCAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTTCCGCG	CAGGGCGACA	CCTCTTCGAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC	GATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	GCAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGAAG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	GCTCAGGAAG	TCATGATGAA	ATTCCTTCAG	GAACAACAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGACG	CGAAGGCCAA	TAAAGAAAAA	GGCGAAGCCT
401	TTCTGAAAGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGC
451	CTGCAATACA	AAATCACCAA	ACAGGGCGAA	GGCAAACAGC	CGACAAAAGA
501	CGACATCGTT	ACCGTGGAAT	ACGAAGGCCG	CCTGATTGAC	GGTACGGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	TCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACAG	CTTCTGAAAG	AAGGCGGCGA
651	AGCCACGTTT	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCCG
701	GCGACAAAAT	CGGTCCGAAC	GCCACTTTGG	TATTTGATGT	GAAACTGGTC
751	AAAATCGGCG	CACCCGAAAA	CGCGCCCGCC	AAGCAGCCGG	CTCAAGTCGA
801	CATCAAAAAA	GTAATTAA			

This corresponds to the amino acid sequence <SEQ ID 3064; ORF 576-1>:

m576-1.pep

1	MNTIFKISAL	TLAALALSA	CGKKEAPAS	ASEPAAASSA	QGDTSSIGST
51	MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ
101	AQEVMMKFLQ	EQQAKAVEKH	KADAKANKEK	GEAFLKENAA	KDGVKTTASG
151	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID	GTVPDSSKAN	GGPVTFPLSQ
201	VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFDVKLV
251	KIGAPENAPA	KQPAQVDIKK	VN*		

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3065>:

g576-1.seq

1	ATGAACACCA	TTTTCAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTGCCGCG	CAGGGCGACA	CCTCTTCAAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC	AATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	ACAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGATG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	GCCCAGGAAG	TGATGATGAA	ATTCTTCGAG	GAGCAGCAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGATG	CGAAGGCCAA	CAAAGAAAAA	GGCGAAGCCT
401	TCCTGAAGGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGT
451	CTGCACTACA	AAATCACCAA	ACAGGGTGAA	GGCAAACAGC	CGACAAAAGA
501	CGACATCGTT	ACCGTGGAAT	ACGAAGGCCG	CCTGATTGAC	GGTACCGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	CCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACGG	CTTCTGAAAG	AAGGCGGCGA
651	AGCCACGTTT	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCCG

701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3066; ORF 576-1.ng>:

g576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ  
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITYKQE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ  
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGFN ATLVFDVKLV  
 251 KIGAPENAPA KQPDQVDIKK VN\*

g576-1/m576-1 ORFs 576-1 and 576-1.ng showed a 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TLSAALALSA	CGKKEAAPAS	ASEPAASAA	QGDTSSIGST	MQQASYAMGV
m576-1	MNTIFKISAL	TLSAALALSA	CGKKEAAPAS	ASEPAASAA	QGDTSSIGST	MQQASYAMGV
	10	20	30	40	50	60
	70	80	90	100	110	120
g576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
	130	140	150	160	170	180
g576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITYKQE	GKQPTKDDIV	TVEYEGRLID
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITYKQE	GKQPTKDDIV	TVEYEGRLID
	130	140	150	160	170	180
	190	200	210	220	230	240
g576-1.pep	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE	QGAGEKIGFN
m576-1	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE	QGAGEKIGFN
	190	200	210	220	230	240
	250	260	270			
g576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
	250	260	270			

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3067>:

a576-1.seq

1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTCCG CCGCTTGGC  
 51 ACTTCCGCC TGCGCAAAA AAGAAGCCG CCGCATCT GCATCCGAAC  
 101 CTGCGCCGC TTCTCCGCG CAGGCGACA CCTCTCGAT CGGCAGCAG  
 151 ATGCAGCAG CAAGCTATG GATGGCGTG GACATCGGAC GCTCCCTGAA  
 201 GCAAATGAAG GAACAGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG  
 251 CCATGCAGG AGTGTATGAC GGCAAGAAA TCAAAATGAC CGAAGAGCAG  
 301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT  
 351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT  
 401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTCCGCG  
 451 CTGCAATACA AAATCACCAA ACAGGCGGAA GGCAACAGC CGACCAAGA  
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT  
 551 TCGACAGCAG CAAAGCCAA GCGGCCCGG TCACCTTCCC TTTGAGCCAA  
 601 GTGATTCTGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGCGGCGA  
 651 AGCCACGTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG

701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGGCCCGCC AAGCAGCCGG CTCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3068; ORF 576-1.a>:

a576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ  
 101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVTKTASG  
 151 LQYKITQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ  
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPAQVDIKK VN\*

a576-1/m576-1 ORFs 576-1 and 576-1.a showed a 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLAALALSACGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLAALALSACGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVTKTASGLQYKITQGEKGKOPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVTKTASGLQYKITQGEKGKOPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

919 gnm43.seq

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3069>:

m919.seq

1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CCGCCGCCAT  
 51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA  
 101 CATCCGTCAT CAACGCCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC  
 151 GGAACGACGG TCGGCGGCGG CGGGGCCGTC TATACCGTTG TACCGCACCT  
 201 GTCCCTGCCC CACTGGGCGG CGCAGGATTG CGCCAAAAGC CTGCAATCCT  
 251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG  
 301 TGCGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCTTTCAGG CAAAACAGTT  
 351 TTTTGAACGC TATTTCACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG  
 401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG

```

451 CGGACGGCAC AAGCCCGCTT CCCGATTTC GGTATTCCCG ACGATTTTAT
501 CTCGTGCCCC CTGCCTGCGG GTTTCGCGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCcG ATTCCCCATC ACCGCGCGCA CAACAGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCGATACT CGGTTCAGCC
751 GAAGACCCTG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCyTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC
901 AAATCGGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TGCGGCAAAA
951 TCCGCAACGC CTGCGCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGTGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG
1301 GTATGAAGCC CGAATACCGc CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3070; ORF 919>:

m919.pep

```

1  MKKYLFRAL YGIAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51  GTTVGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMOGI KSYMQRNPQR LAEVLGQNP S YIFFRELAYS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

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The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3071>:

g919.seq

```

1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAGC CTGCAATCCT
251 TCCGCCCTCG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCCTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGCG cgtGGCaggT tgcaggcaAC GGAAGcCTTG
401 CaggTaccgt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCTGCGG GTTTCGCGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCCcg tccggcaaat acatCCGCAt cggATacgcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcatc aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTGCGCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGTCCG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 3072; ORF 919.ng>:

```

g919.pep
  1  MKKHLLRSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
 51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101  CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151  RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201  HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251  EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301  KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGVPVVALG
351  TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401  AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

```

m919/g919

      10      20      30      40      50      60
m919.pep  MKKYLFRALYGIAAAILAACQSKSIQTFPQDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g919       MKKHLLRSALYGIAAAILAACQSRSIQTFPQDTSVINGPDRPAGIPDPAGTTVAGGGAV
          10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep  YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g919       YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
          70      80      90     100     110     120

     130     140     150     160     170     180
m919.pep  YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGIIPDDFISVPLPAGLRSGKA
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g919       YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRTERARFPIYGIIPDDFISVPLPAGLRGGKN
          130     140     150     160     170     180

     190     200     210     220     230     240
m919.pep  LVRIRQTGKNSGTIDNTGGTHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g919       LVRIRQTGKNSGTIDNAGGTHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL
          190     200     210     220     230     240

     250     260     270     280     290     300
m919.pep  DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g919       DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          250     260     270     280     290     300

     310     320     330     340     350     360
m919.pep  KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIIFRELAYSNDGPVVALGTPLMGEYAGA
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g919       KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIIFRELAYSNEGVPVVALGTPLMGEYAGA
          310     320     330     340     350     360

     370     380     390     400     410     420
m919.pep  VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g919       IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          370     380     390     400     410     420

```

```

              430      440
m919.pep      QKTTGYVWQLLPNGMKPEYRPX
              |||||
g919           QKTTGYVWQLLPNGMKPEYRPX
              430      440

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3073>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCGGCCCTG TCGGCATCG CCGCGCCCAT
51 CCTCGCGGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT CGCCAAAAGC CTGCAATCCT
251 TCCGCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGGCCAAG CCTTCAAAC CCCCGTCCAT TCCGTTCAAG CAAAACAGTT
351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCTGCGG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCCCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTGAAGGAA GCCGTTCTT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTACGCC
751 GAAGACCCCG TCGAACTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTGCG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTATTG TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCTCAACCG CCGTATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGCAGGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3074; ORF 919.a>:

```

a919.pep
1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

m919/a919 ORFs 919 and 919.a showed a 98.6% identity in 441 aa overlap

```

              10      20      30      40      50      60
m919.pep      MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
              |||||
a919           MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m919.pep      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
              |||||
a919           YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
              70      80      90      100     110     120

```

m919.pep	130	140	150	160	170	180
	YFTPWQVAGNSLAGTVTGYE	PVLKGD	DRRTAQA	RFPIYG	IPDDFIS	VPLPAGLRSGKA
a919	YFTPWQVAGNSLAGTVTGYE	PVLKGD	DRRTAQA	RFPIYG	IPDDFIS	VPLPAGLRSGKA
m919.pep	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGT	HTADLSR	FPITART	TAIKGR	FEFSRFL	PHYTRNQINGGAL
a919	LVRIRQTGKNSGTIDNTGGT	HTADLSQ	FPITART	TAIKGR	FEFSRFL	PHYTRNQINGGAL
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFM	HIQSGS	RKLT	PSGKYI	RIGYAD	KNEHPYVSIGRYMADKGYL
a919	DGKAPILGYAEDPVELFFM	HIQSGS	RKLT	PSGKYI	RIGYAD	KNEHPYVSIGRYMADKGYL
m919.pep	310	320	330	340	350	360
	KLQTS	MQGIKSYMRQNPQRLAE	VLGQNP	SYIFFR	ELAGSS	NDGPVGALGTPLMGEYAGA
a919	KLQTS	MQGIKAYMQNPQRLAE	VLGQNP	SYIFFR	ELAGSS	NDGPVGALGTPLMGEYAGA
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPLFVATAHP	VRTRKAL	NRLIMAQ	DGSAIK	GAVRVDY	FWGYGDEAGELAGK
a919	VDRHYITLGAPLFVATAHP	VRTRKAL	NRLIMAQ	DGSAIK	GAVRVDY	FWGYGDEAGELAGK
m919.pep	430	440				
	QKTTGYVWQLLPNGMKPEY	RPX				
a919	QKTTGYVWQLLPNGMKPEY	RPX				

121 and 121-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3075>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CCAATTGCTG
151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCCTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxGAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCCG TATTTGCGAC
701 AACGCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGACGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGCGAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGTTGGC GCGTGTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA

```

1051 GCAACCGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG  
1101 A

This corresponds to the amino acid sequence <SEQ ID 3076; ORF 121>:

m121.pep

1 METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL  
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ  
101 TVRHAPEHGY SIQLADLPLL Axxxxxxxxxxxx xxxxxxxxxxxxxx  
151 xxxxxxxxxxxxxx xxxxxxxxxxxxxx xxxxxxxxxxxxxx xxxxxxxxxxxxxx  
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL  
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV  
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK  
351 ATGASKPCIL XAGYYY\*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3077>:

g121.seq

1 ATGGAAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG  
51 GCGGATGCC GTGCTGGTAC GGATGGACGG CCGCAAATGG CTGGGCGCGG  
101 AAGGGCACGC CTTTACCCCT TACCCTGACC GGTGCGCCG CAAATTGCTG  
151 GATTTCAGG ACACAGGCAC AGACGAACGT CACCGCAGCA GGATGTTGTC  
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA  
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA  
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATACAGC TTGCCGATTT  
351 GCGCTGCTG GCGGAACGa cgcggatttT TACCGTCggc gacttcCGCA  
401 GCGCGACCT TGCTGCCGCG GgacaAGGTG CGCCGCTCGT CCCCGCCTTT  
451 CACGAAGCCC TGTTCGCGA TGACAGGGAA ACACGCGTGG TACTGAACAT  
501 CCGCGGGATT GCCAACATCA GCGTACTCCC CCCCggCGCA CCCGCCTTCG  
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca  
601 cacTGGcagc TGCTTTACGA CAAAacggt gcAAAGgcgg cacAAGGCAA  
651 catatTGCcg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTTCAC  
701 AACCCcacc aaAAAGCACG GGgcGCGaac TgtttgcccT AAattggctc  
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgtat tgcggacgct  
801 ttcccgattc accgcgcaaA ccgTttggga cgcggtctca CACGCAGCGG  
851 CAGATGCCCG TCAAATGTAC ATTTGCGCGG GCGGCATCCG CAATCCTGTT  
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG  
951 CACGCGCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATTtg  
1001 cgtggttgC GCGGTGTTGG ATTAACCGCA TTCCCGGTAG TCCGCACAAA  
1051 GCGACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG  
1101 A

This corresponds to the amino acid sequence <SEQ ID 3078; ORF 121.ng>:

g121.pep

1 METQLYIGIM SGTSMGADA VLVRMDGGKW LGAEGHAFTP YPDRLLRRKLL  
51 DLQDTGTDEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ  
101 TVRHAPEHGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPAF  
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPG NMLMDAWTQA  
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL  
251 ETYLDGGENR YDVLRTLSRF TAQTVWDAYS HAAADARQMY ICGGGIRNPV  
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAWLAACW INRIPGSPHK  
351 ATGASKPCIL GAGYYY\*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	:     :     :     :     :     :					
g121	METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	:     :     :     :     :     :					



```

g121      HRSRMLSQELSRLYAQTAELLCSONLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL
           70      80      90      100      110      120
           130      140      150      160      170      180
m121.pep  AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      AELTRIFTVGDFRSRDLAAGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPPGA
           130      140      150      160      170      180
           190      200      210      220      230      240
m121.pep  XXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
           190      200      210      220      230      240
           250      260      270      280      290      300
m121.pep  GRELFAINWLETYLDGGENRYDVLRTLRSRFTAQTVCDVASHAAADARQMYICDGGIRNPV
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVWDVASHAAADARQMYICGGGIRNPV
           250      260      270      280      290      300
           310      320      330      340      350      360
m121.pep  LMADLAECFGRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      LMADLAECFGRVSLHSTAE LNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
           310      320      330      340      350      360

m121.pep  XAGYYXX
           | : : : :
g121      GAGYYXX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3079>:

```

a121.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCC TACCCCGGCA GGTTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGCG GACTTCCGCA
401 GCCGCGACCT TCGCGCCGCG GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC GTTTCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCGACGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGCG AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCGG TATTTGCGAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATT ACCCGCGCAA CCGTTTTCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCC
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3080; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGADA VLIRMDGKWK LGAEGHAFTP YPGRLLRKL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPGP NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRSF TAQTVFDAVS HAAADARQMY ICGGGIRNPV

```

301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK  
 351 ATGASKPCIL GAGYYY\*

m121/a121 ORFs 121 and 121.a showed a 74.0% identity in 366 aa overlap

m121.pep	10	20	30	40	50	60
	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTYPYGRRLRQLLDLQDTGADEL					
a121	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTYPYGRRLRKLDDLQDTGADEL					
	10	20	30	40	50	60
m121.pep	70	80	90	100	110	120
	HRSRILSQELSRLYAQTAELCSQNLAPSDITALGCHGQTVRHAPHEHGYISQLADLPPL					
a121	HRSRILSQELSRLYAQTAELCSQNLAPSDITALGCHGQTVRHAPHEHSYSVQLADLPPL					
	70	80	90	100	110	120
m121.pep	130	140	150	160	170	180
	AXXX					
a121	AERTQIFTVGDFRSRDLAAGGQGAFLVPAFHEALFRDDRETRAVLNIGGIANISVLPDPA					
	130	140	150	160	170	180
m121.pep	190	200	210	220	230	240
	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121.pep	250	260	270	280	290	300
	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNPV					
a121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFDVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
m121.pep	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
a121	LMADLAECFGTRVSLHSTAE LNLDPQWVEA AAFAWMAACWVNRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYX					
a121	GAGYYYX					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3081>:

m121-1.seq

1	ATGGAACAC	AGCTTTACAT	CGGCATCATG	TCGGGAACCA	GCATGGACGG
51	GGCGGATGCC	GTACTGATAC	GGATGGACGG	CGGCAAATGG	CTGGGCGCGG
101	AAGGGCACGC	CTTTACCCCC	TACCCCGGCA	GGTTACGCGG	CCAATTGCTG
151	GATTTGCAGG	ACACAGGCGC	AGACGAACTG	CACCGCAGCA	GGATTTTGTC
201	GCAAGAACTC	AGCCGCCTAT	ATGCGCAAAC	CGCCGCCGAA	CTGCTGTGCA
251	GTCAAAACCT	CGCACCGTCC	GACATTACCG	CCCTCGGCTG	CCACGGGCAA
301	ACCGTCCGAC	ACGCGCCGGA	ACACGGTTAC	AGCATACAGC	TTGCCGATTT
351	GCCGCTGCTG	GCGGAACGGA	CGCGGATTTT	TACCGTCGGC	GACTTCCGCA
401	GCCGCGACCT	TGCGGCCGCG	GGACAAGGCG	CGCCACTCGT	CCCCGCCTTT
451	CACGAAGCCC	TGTTCCGCGA	CAACAGGAA	ACACGCGCGG	TACTGAACAT
501	CGGCGGGATT	GCCAACATCA	GCGTACTCCC	CCCCGACGCA	CCCGCCTTCG
551	GCTTCGACAC	AGGGCCGGGC	AATATGCTGA	TGGACGCGTG	GACGCAGGCA
601	CACTGGCAGC	TTCTTACGA	CAAAAACGGT	GCAAAGGCGG	CACAAGGCAA
651	CATATTGCCG	CAACTGCTCG	ACAGGCTGCT	CGCCCACCCG	TATTTGCGAC
701	AACCCACCCC	TAAAAGCACG	GGGCGCGAAC	TGTTTGCCCT	AAATTGGCTC
751	GAAACCTACC	TTGACGCGCG	CGAAAACCGA	TACGACGTAT	TGCGGACGCT
801	TTCCCGTTTT	ACCGCGCAAA	CCGTTTGCGA	CGCCGTCTCA	CACGCAGCGG

```

851 CAGATGCCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGAAGCC GCCGNATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3082; ORF 121-1>:

```

m121-1.pep
1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRQLL
51  DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 ORFs 121-1 and 121.ng showed a 95.6% identity in 366 aa overlap

m121-1.pep	10	20	30	40	50	60
	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTYPGRLLRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEGHAFTYPDRLLRKLDDLQDTGTDEL					
	10	20	30	40	50	60
m121-1.pep	70	80	90	100	110	120
	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
g121	HRSRMLSQELSRLYAQTAAELLCSONLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	70	80	90	100	110	120
m121-1.pep	130	140	150	160	170	180
	AERTRIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDNRETRAVLNIGGIANISVLPPDA					
g121	AELTRIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDDRETRVVLNIGGIANISVPPGA					
	130	140	150	160	170	180
m121-1.pep	190	200	210	220	230	240
	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
m121-1.pep	250	260	270	280	290	300
	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDAYSHAAADARQMYICGGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAYSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
m121-1.pep	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
g121	LMADLAECFGTRVSLHSTAE LNLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121-1.pep	XAGYYYYX					
g121	GAGYYYYX					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3083>:

```

a121-1.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG

```

```

51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCGG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAATG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCGCTG ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCG GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCGGCA
401 GCCGCGACCT TGCGGCCGGC GGACAAGGCG CGCCGCTCGT CCCCCTTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 CGTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACCCACCCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGATTG ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCC TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACGCGCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCGCACAAA
1051 GCAACCGCG CATCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3084; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCQNLAAPS DITALGCHGQ
101 TVRHAPESHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHTAE LNLDPQWVEA AFAFWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121-1/a121-1 ORFs 121-1 and 121-1.a showed a 96.4% identity in 366 aa overlap

m121-1.pep	10	20	30	40	50	60
	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGLRRQLDLQDTGADEL					
a121-1	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGLRRKLLDLQDTGADEL					
	10	20	30	40	50	60
m121-1.pep	70	80	90	100	110	120
	HRSRILSQELSRLYAQTAAELLCQNLAAPSDITALGCHGQTVRHAPHEHGSYIQLADLPLL					
a121-1	HRSRMLSQELSRLYAQTAAELLCQNLAAPSDITALGCHGQTVRHAPESHSYSVQLADLPLL					
	70	80	90	100	110	120
m121-1.pep	130	140	150	160	170	180
	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDNRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121-1.pep	190	200	210	220	230	240
	PAFGFDTPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121-1.pep	250	260	270	280	290	300
	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

```

          310      320      330      340      350      360
m121-1.pep  LMADLAECFGTRVSLHSTADLNLDPOQWVEAAAXFAWLAACWINRIPGSPHKATGASKPCIL
          |||||:|||||:|||||:|||||:|||||:|||||
a121        LMADLAECFGTRVSLHSTAE LNLDPOQWVEAAAFWMAACWVNRI PGSPHKATGASKPCIL
          310      320      330      340      350      360

m121-1.pep  XAGYXX
          |||||
a121        GAGYXX

```

128 and 128-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3085>:

```

m128.seq (partial)
1  ATGACTGACA ACGCACTGCT CCATTGGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTCGAC ACCCTCTCCC CCGCACAAA AACCAACTC AACCAC
1  TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51  wGTCAAAAAA TAyTTCcCyG TCGGCAAwGT ATTAACCGGA CTGTTCGCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCCGTC
151 TGGCACAAAG ACGTGCCTTA TtTGAATTG CAACAAACG GCGAaMCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTAKA ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGAAAAAT TTCGTTTGGG AATACAATGT CTTGGCACAA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCcC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAaG CGGCATGTTC yTsGTCCGCG AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTGA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTGCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCGGCCACA
901 GGCAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAAATC TTCAAAGCCT TCCGCGGCCG CGAACCGAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 3086; ORF 128&gt;:

```

m128.pep (partial)
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVEPLTGIT ERVGRIGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

//
1  YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGfTEKTPV
51  WHKDVRXYEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFSdGTL
101 QLPTAYLVCN FAPPVGGREA RLShDEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQQVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT
301 GKRFWQEILA VGXSRGAES FKAFRGREPS IDALLRHSGF DNAV*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3087>:

```

g128.seq
1  atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTTaatca
51  aatccaaacc gaagACAtca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCGGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCACGACC
401 TCGCGGATTT CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA .CGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCGCG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGccaaa cTGCTCGGCT TTA AAAATTA CGCCGAATTG TCCTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCGCGCGCG CCAAACCCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAACACCTCG GTCTCGCCGA CCCGCAGCCG TGGGACTTGA
1001 GCTACGCGCG GAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTGCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGGCGCG TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACtaca AAGGCCGCG CGGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCTAC CTGCTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AacCGGCCAC GGA CTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGCGAT CAacggcgtA GAATGGGACG CGGTCTGAAC GCCCAGCCAG
1501 TTTATGGAAA ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCGCG
1551 CCACGAAGAA AccgGCGAGC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TcgCGCCAA AAACCTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTACAGT GAAAGCGACG AATGCCGCTC
1701 GAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GtcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCCGCGAG CTATTACAGC TACGCATGGG CCGAAGTCCt
1851 cAGCACCGAT GCCTACGCCG CCTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAAACG CTTCTGGCAA GAAAtccttg ccgtcggcgg ctCCCGCAGC
1951 gcgCGCGAAT CTTTCAAAGC CTTCCGCGGA CGCGAACC GAATAGACGC
2001 ACTGCTGCGC CAaagcggtT TCGACAACGC gGcttgA

```

This corresponds to the amino acid sequence <SEQ ID 3088; ORF 128.ng>:

```

g128.pep
1  MIDNALLHLG EEPRFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTGTGA
51  NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 QQDIELYNRF KTIKNSPEFA TLSPAQTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDSL YAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFWWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDVSRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYA AFESDD VAATGKRWFQ EILAVGGSRS

```

651 AESFKAFRG REPSIDALLR QSGFDNAA\*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng)  
from *N. gonorrhoeae*:

m128/g128

g128.pep	10	20	30	40	50	60
	MIDNALLHLGEEPRFNQIQ	TEDIKPAVQTAIAEARGQIAAVKAQ	THTGWANTVERLTGIT			
m128	MTDNALLHLGEEPRFDQIK	TEDIKPAQTAIAEAREQIAAIKAQ	THTGWANTVEPLTGIT			
	10	20	30	40	50	60
g128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNSVVD	TPELRAVYNELMPEITVFFTEIGQDIELYNR	FKTIKNSPEFA			
m128	ERVGRIWGVVSHLNCVAD	TPELRAVYNELMPEITVFFTEIGQDIELYNR	FKTIKNSPEFD			
	70	80	90	100	110	120
g128.pep	130	140	150	160	170	180
	TLSPAQKTKLDHDLRDF	VLSGAELPPERQAELAKLQTEGAQLSAKFSQ	NVL DATDAFGIY			
m128	TLSPAQKTKLNH					
	130					
	//					
g128.pep			340	350	360	
			YAGEKLREAKYAFSET	EVKKYFPVGKVL	AG	
m128			YASEKLREAKYAFSET	XVKKYFPVGXVL	NG	
			10	20	30	
g128.pep	370	380	390	400	410	420
	LFAQIKKLYGIGFAEKT	VPVWHKDVRYFELQNGKTIGGVYMDLYAREG	KRGGAWMNDYK			
m128	LFAQXKKLYGIGFTEKT	VPVWHKDVRYXELQNGEXIGGVYMDLYAREG	KRGGAWMNDYK			
	40	50	60	70	80	90
g128.pep	430	440	450	460	470	480
	GRRRFADGTLQLPTAY	LVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQV	DELGV			
m128	GRRRFSGDTLQLPTAY	LVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQV	DELGV			
	100	110	120	130	140	150
g128.pep	490	500	510	520	530	540
	SGINGVEWDAVELPSQ	FMFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQ	RGMF			
m128	SGINGVXWDAVELPSQ	FMFVWEYNVLAQXSAHEETGVPLPKELXDKMLAAKNFQ	XGMF			
	160	170	180	190	200	210
g128.pep	550	560	570	580	590	600
	LVRQMEFALFDMMIY	SESDCRLKNWQQVLD	SVRKEVAVIQPEYNR	FANSFGHIFAGGY		
m128	XVRQXEFALFDMMIY	SEDDGRLKNWQQVLD	SVRKKVAVIQPEYNR	FALSFGHIFAGGY		
	220	230	240	250	260	270
g128.pep	610	620	630	640	650	660
	SAGYYSYAWAEVLST	DAYAAFEESDDVAATGKRFWQEILAVGGS	RSAAESFKAFRGREPS			
m128	SAAXYSYAWAEVLSA	DYAAFEESDDVAATGKRFWQEILAVGXS	RSRGAESFKAFRGREPS			
	280	290	300	310	320	330

```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSFGFNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3089>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTAC CGACACGCCC GAACGTGCGG
251 CGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCCAGGATC
401 TGC GCGATT T CGTCTCAGC GGCGCGGAAC TGCGGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAA CGAAGGCGCG CAACCTTTCCG CCAAATTTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCGCGCAAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCAATC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCGCGCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCCG
1101 CCAATCAAAA AAATCTACG GCATCGGATT TACCGAAAAA ACGTCCCGC
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGGG
1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CCGTTTTTTC GACGGCACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTCACCCG GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCAGCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGAAA ATTTCTTTG GGAATACAA GTCTTGGCGC AAATGTCCCG
1551 CCACGAAGAA ACCGGCGTTC CCTGCGGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTTCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CTTTGAAGA AAGCGACGAT GTCGCGGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3090; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWGA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTA LLGFKNYAEL SLATKMATDP EQVLNLFHLD
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVKG VLNLGFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDVAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAARNFQ RGMFLVRQME

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551 FALFDMMIYS EDDEGR LKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF  
 601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS  
 651 AAESFKAFRG REPSIDALLR HSGFDNAA\*

m128/a128 ORFs 128 and 128.a showed a 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
a128	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
m128.pep	70	80	90	100	110	120
	ERVGRIGVGVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	70	80	90	100	110	120
	ERVGRIGVGVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	130	140	150	160	170	180
	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128.pep	-----					
a128	190	200	210	220	230	240
	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYV					
m128.pep	-----					
a128	250	260	270	280	290	300
	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNLFHDL					
m128.pep						140
						YASEKLEAKYAFSETXVKKYFPVGX
a128	310	320	330	340	350	360
	ARRAKPYAEKDIAEVKAFARESLGLADLPWDLGYAGEKLEAKYAFSETEVKKYFPVGK					
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTPVWHKDVRYXELQQNGEXIGGVYMDLYAREGKRGGAWM					
a128	370	380	390	400	410	420
	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	430	440	450	460	470	480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDVAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	490	500	510	520	530	540
	ELGVSGINGVWDVAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGR LKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	550	560	570	580	590	600
	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					

```

400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRGAESFKAFRG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a128      AGGYSAAGYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRAAESFKAFRG
          610      620      630      640      650      660

460      470
m128.pep  REPSIDALLRHSGFDNAVX
          |||||:|||||:
a128      REPSIDALLRHSGFDNAAX
          670

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3091>:

```

ml28-1.seq
1  ATGACTGACA  ACGCACTGCT  CCATTGGGGC  GAAGAACCCC  GTTTTGATCA
51  AATCAAAACC  GAAGACATCA  AACCCCGCCCT  GCAAAACCGCC  ATCGCCGAAG
101 CGCGCGAACA  GAATCGCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
151 AACACTGTCT  AACCCCTGAC  CGGCATCACC  GAACGCGTCG  CGAGGATTGT
201 GGGCGTGGTG  TCGCACTCTA  ACTCGTCTCG  CGACACGCCC  GAACTGCGCG
251 CCGTCTATAA  CGAACTGATG  CCCGAAATCA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAGCTGTA  CAACCGCTTC  AAAACCATCA  AAAATCTCCC
351 CGAATTCGAC  ACCCTCTCCC  CCGCAAAAAA  AACCACAACT  AACCAGCATC
401 TGGCGGATT  CGTCTCAGC  GGC GCGAAC  TGCCGCCCGA  ACAGCAGGCA
451 GAACTGGCAA  AACTGCAAA  CGAAGGCGCG  CAACTTTCCG  CCAAATCTG
501 CCAAACGTC  CTAGACGCGA  CCGACGCGTT  CGGCATTTC  TTTGACGATG
551 CCGCACCCT  TGCCGCGATT  CCGGAAGACG  CGCTCGCCAT  GTTTGCGGCC
601 GCGCGCAAA  GCGAAAGCAA  AACAGGCTAC  AAAATCGGCT  TGCAGATTCC
651 ACACTACCT  GCCGTCTACC  AATACGCCGA  CAACCGCGAA  CTGCGCGAAC
701 AAATCTACCG  CGCTACGTT  ACCCGCGCCA  CGCAACTTTC  AGACGACGCG
751 AAATTCGACA  ACACCGCCAA  CATCGACCGC  AGCTTCGCAA  AGCCCTGCA
801 AACCGCCAAA  CTGCTCGGCT  TCAAAAATA  CGCCGAATTG  TCGTGGCAA
851 CCAAATGGC  GGCACGCCC  GAACAAGTTT  TAAACTTCT  GCACGACCTC
901 CCGCGCCGCG  CCAAACCTA  CGCCGAAAAA  GAACCTCGCG  AAGTCAAAGC
951 CTTGCGCCG  AAAAGCTGA  ACCTCGCCGA  TTTGCAACCG  TGGGACTTGG
1001 GCTACGCCAG  CGAAAACTG  CGCGAAGCCA  AATACGCGT  GACGAGAAAC
1051 GAAGTCAAAA  AATACTTCCC  CGTCGGCAA  GTATTAAACG  GACTGTTCTG
1101 CCAATCAAAA  AAATCTACG  GCATCGGATT  TACCGAAAAA  ACCGTCCCCG
1151 TCTGGCACA  AGACGTGCGC  TATTTGAAT  TGCACAAAAA  CGCGGAAACC
1201 ATAGGCGGCG  TTTATATGGA  TTTGTACGCA  CGCGAAGGCA  AAGCGGCGCG
1251 CGCGTGGATG  AACGCTACA  AAGCGCGCG  CCGTTTTTCA  GACGGCACGC
1301 TGCACCTGCC  CACCGCTAC  CTCGTCTGCA  ACTTCGCCCC  ACCCGTCGG
1351 GGCAGGGAAG  CCGCGCTGAG  CACGACGAA  ATCTCATCC  TCTTCCACG
1401 AACCGGACAC  GGGCTGCACC  ACCTGCTTAC  CCAAGTGGAC  GAACTGGGCG
1451 TATCGGCAT  CAACGGCGTA  GAATGGGACG  CGTTCGAAC  GCCAGCCAG
1501 TTTATGGAAA  ATTTCTGTTG  GGAATACAAT  GTCTTGGCAC  AAATGTCAGC
1551 CCACGAAGAA  AC CGGCTTC  CCTTGCGAA  AGAATCTTC  GACAAAAATG
1601 TCGCCGCCAA  AAATTCCAA  CGCGCATGT  TCCTCGTCCG  GCAATGGAG
1651 TTCGCCCTCT  TTGATAGTAT  GATTACAGC  GAAGACGACG  AAGGCCGTCT
1701 GAAAACTGG  CAACAGGTTT  TAGACAGCGT  GCGCAAAAAA  GTCGCCGTCA
1751 TCCAGCCGCA  CGAATACAA  CGTTGCGCT  TGAGCTTCGG  CCACATCTC
1801 GCAGGCGGCT  ATTCCGCAGG  CTATTACAG  TAGCGTGGG  CGGAAGTATT
1851 GAGCGCGGAC  GCATACGCG  CCTTGAAGA  AAGCGACGAT  GTCGCCGCCA
1901 CAGGCAAAAC  CTTTGGGAC  GAAATCCTG  CCGTCGGCGG  ATCGCGCAGC
1951 CGGCGAGAAT  CTTCAAAGC  CTTCCGCGCG  CGCGAACCGA  GCATAGACGC
2001 ACTCTTGCGC  CACAGCGGTT  TCGACAACG  GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 3092; ORF 128-1>:

m128-1.pep.  
1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHGTWA  
51 NTVEPLTGIT ERVGRIWGVV SHLSNVADTP ELRAVYNELM PEITVFETEI

```

101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKSTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLANALQTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLNLGFAQIK KLYGIGFTEK TVPVWHKDVR YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLLKNW QQVLDVSRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
651 AESFKAFRG REPSIDALLR HSGFDNAV*

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The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3093>:

g128-1.seq (partial)

```

1 ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51 AATCAAAACC GAAGACATCA AACC CGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCTGT TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCACGACC
401 TCGCGGATTT CGTATTGAGC GGC GCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAA CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCG
601 GCCGCGCAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGCCAAA CTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CAAAATGGC GGACACGCCC GAACAGGTTT TAACTTCCT GCACGACCTC
901 GCGCGCGCG CCAAACCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAACACCTCG GTCTCGCCGA CCGCAGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTCGC
1101 CCAAATCAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGGCGCGC TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAA GACGACGAA ATCTCACCC TCTTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 3094; ORF 128-1.ng>:

g128-1.pep (partial)

```

1 MIDNALLHLG EEPFRNQIKT EDIKPAVQTA IAEARGQIAA VKAQTHTGWA
51 NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL NHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKSTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV K

```

m128-1/g128-1 ORFs 128-1 and 128-1.ng showed a 94.5% identity in 491 aa overlap

10 20 30 40 50 60

g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGTWANTVERLTGIT
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
	10 20 30 40 50 60
g128-1.pep	ERVGRIWGVVSHLSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
m128-1	ERVGRIWGVVSHLSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
	70 80 90 100 110 120
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAQSESKTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
g128-1.pep	TRASELSNDGKFDNTANIDRTLENALKTAKLLGFKNYAELSLATKMADTPEQVLNLFHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNLFHDL
	250 260 270 280 290 300
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPWDLSYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWM
m128-1	VNLGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVD
	430 440 450 460 470 480
g128-1.pep	ELGVSGINGVK
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3095>:

a128-1.seq

1	ATGACTGACA	ACGCACTGCT	CCATTGGGC	GAAGAACCCC	GTTTTGATCA
51	AATCAAAACC	GAAGACATCA	AACCCGCCCT	GCAAACCGCC	ATTGCCGAAG
101	CGCGCGAACA	AATCGCCGCC	ATCAAAGCCC	AAACGCACAC	CGGCTGGGCA
151	AACACTGTCTG	AACCCCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGGCGTGGTG	TCGCACCTCA	ACTCCGTCAC	CGACACGCC	GAACGCGCG
251	CCGCCTACAA	TGAATTAATG	CCCAGAAATTA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TCGAGCTGTA	CAACCGCTTC	AAAACCATCA	AAAACCTCCC
351	CGAGTTCGAC	ACCCCTCTCC	ACGCGCAAAA	AACCAAATC	AACCACGATC
401	TGCGCGATT	CGTCCTCAGC	GGCGCGGAAC	TGCCGCCCGA	ACAGCAGGCA
451	GAATTGGCAA	AACTGCAAAC	CGAAGGCGCG	CAACTTTCG	CCAAATTCTC

```

501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTC AGACGACGCG
751 AAATTGACA ACACCGCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCCCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCG CGAAAACTG CGGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCCG
1101 CCAAATCAAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGCGGCG TTTATATGGA TTGTACGCA CGGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAAC GCCCAGTCAG
1501 TTTATGAAA ATTTCTGTTT GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AACTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGCGGCGT ATTCCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCC CTTTGAAGA AAGCGACGAT GTCGCGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGA CGCAACCGA GCATAGACGC
2001 ACTCTTGGC CACAGCGCT TCGACAACG GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3096; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51 NTVEPLTGIT ERVGRIVGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVEFPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKREWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*

```

m128-1/a128-1 ORFs 128-1 and 128-1.a showed a 97.8% identity in 677 aa overlap

```

          10      20      30      40      50      60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWTVEPLTGIT
|||||
m128-1 MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWTVEPLTGIT
          10      20      30      40      50      60

          70      80      90     100     110     120
a128-1.pep ERVGRIVGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
|||||:|||||:|||||
m128-1 ERVGRIVGVVSHLNSVADTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90     100     110     120

        130      140      150      160      170      180

```

a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
a128-1.pep	190 200 210 220 230 240
	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAAQSESKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYV
	190 200 210 220 230 240
a128-1.pep	250 260 270 280 290 300
	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMDTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMDTPEQVLNFLHDL
	250 260 270 280 290 300
a128-1.pep	310 320 330 340 350 360
	ARRAKPYAEKDLAEVKAFARESGLADLQPWDLGYAGEKLEAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESGLADLQPWDLGYAGEKLEAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	370 380 390 400 410 420
	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	430 440 450 460 470 480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	490 500 510 520 530 540
	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540
a128-1.pep	550 560 570 580 590 600
	RGMFLVRQMEFALFDMMIYSEDDGRLKNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
m128-1	RGMFLVRQMEFALFDMMIYSEDDGRLKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIF
	550 560 570 580 590 600
a128-1.pep	610 620 630 640 650 660
	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
m128-1	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
	610 620 630 640 650 660
a128-1.pep	670 679
	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAVX
	670

206

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3097>:

m206.seq

1	ATGTTTCCCC	CGACAAAAAC	CCTTTTCCTC	TGCTCAGCG	CACTGCTCCT
51	CGCCTCATGC	GGCAGGACCT	CCGGCAAACA	CCGCCAACCG	AAACCCAAAC
101	AGACAGTCCG	GCAAATCCAA	GCCGTCGCGA	TCAGCCACAT	CGACCGCACA
151	CAAGGCTCGC	AGGAACCTCAT	GTCCACAGC	CTCGGACTCA	TCGGCAGCGC
201	CTACAAATGG	GGCGGCGAGCA	GCACCGCAAC	CGGCTTCGAT	TGCAGCGGCA
251	TGATTCAATT	CGTTTACAAT	AACGCCCTCA	ACGTCAAGCT	GCCGCGCACC
301	GCCCGCGACA	TGGCGGCGGC	AAGCCGAAA	ATCCCCGACa	GCCGcyTCAA
351	GGCCGGCGAC	CTCGTATTCT	TCAACACCGG	CGGCGCACAC	CGCTACTCAC
401	ACGTCGGACT	CTACATCGGC	AAAGGCGAAT	TCATCCATGC	CCCCAGCAGC
451	GGCAAAACCA	TCAAAACCGA	AAAACCTCTC	ACACCGTTTT	ACGCCAAAAA
501	CTACCTCGGC	GCACATACTT	TTTTTACAGA	ATGA	

This corresponds to the amino acid sequence <SEQ ID 3098; ORF 206>:

m206.pap..

```

1  MFPPDKTLFL  CLSALLLASC  GTTSGKHRQP  KPQQTVRQIQ  AVRISHIDRT
51  QGSQELMLHS  LGLIGTPYKW  GGSSTATGFD  CSGMIQFVYK  NALNVKLPRT
101  ARDMAAASRK  IPDSRXKAGD  LVFFNTGGAH  RYSHVGLYIG  NGEFIHAPSS
151  GKTIKTEKLS  TPFYAKNYLG  AHTPFTE*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 3099>:

g206.seq

1	atgttttccc	ccgacaaaac	ccttttctct	tgtctcggcg	cactgtctct
51	cgcctcatgc	ggcacgacct	ccggcaaaaca	ccgccaaccg	aaacccaaac
101	agacagtcgc	gcaaatccaa	gccgtccgca	tcagccacat	cggccgcaca
151	caaggctcgc	aggaactcat	gctccacagc	ctcggactca	tcggcacgccc
201	ctacaaatgg	ggcggcgagca	gcaccgcagc	cggctctcag	tgcagcggca
251	tgattcaatt	ggtttacaaa	aacgccttca	acgtcaagct	gccgcgcacc
301	gccgcgcgaca	tggcggcggc	aagccgcaaa	atccccgaca	gccgcctcaa
351	ggccggcgac	atcgtattct	tcaacaccgg	cggcgcacac	cgctactcac
401	acgtcggact	ctacatccgc	aaacgtcgaat	tcattcatgc	ccccggcagc
451	ggcaaaacca	tcaaaaccca	aaaactctcc	acaccgtttt	acgccaaaaa
501	ctaccttgga	gcgcatacgt	tttttacaga	atga	

This corresponds to the amino acid sequence <SEQ ID 3100; ORF 206.ng>:

g206.pep

```

1 MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT
51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPDPKTLFLCLLSALLASCGETTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS	:				
g206	MFSPDKTLFLCLGALLASCGETTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS	:				
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSSTATGFDCSGMIQFVYKNALNVKLPRRTARDMAAASRKIPDSRXKAGD	:				
g206	LGLIGTPYKWGGSSSTATGFDCSGMILVYKNALNVKLPRRTARDMAAASRKIPDSRLKAGD	:				
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX	:				
g206	IVFFNTGGAHRYSHVGLYIGNGEFIHAPSGKTIKTEKLSTPFYAKNYLGAHTFFE	:				

130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3101>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCCGACA GCCGCTTAA
351 GGCCGCGCAG CTCTGATTCT TCAACACCGG CGGCGCACAC CGTACTCAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 3102; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 ORFs 206 and 206.a showed a 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT QGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT QGSQELMLHS					
	10	20	30	40	50	60
m206.pep	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT ARDMAAASRK IPDSRLKAGD					
a206	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT ARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLG AHTFFTE*					
a206	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLG AHTFFTE*					
	130	140	150	160	170	
m206.pep	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLG AHTFFTE*					
a206	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLG AHTFFTE*					
	130	140	150	160	170	

287

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3103>:

```
m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  CTGCGGGGGC GCGCGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTGTTTCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GGCGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGTT
551 CTTGAGATCC CATCCCGCG TCAAACCTG CACCTGCGAA TGGCGGTAGC
```



```

601 AATTTTGGAA GGGTTGATTT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGA TGAAGAAGTA CAGCTAAAT CAGAATTGA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GGCGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCGAG
1201 TTTGCCGCAA AAGTCGATTT CGGCAGCAA TCTGTGGACG GCATTATCGA
1251 CAGCGCGGAT GATTTGCATA TGGGTACGCA AAAATTCAAA GCCGCCATCG
1301 ATGGAACCGG CTTTAAGGGG ACTTGACGCG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCC ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTTGCCGCGA
1451 AAAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 3104; ORF 287>:

```

m287.pep
1  MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAQ
51  EDAPQAGSQG QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGGDDPSA GGQNAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRVLDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRRLPAE MPLIPVQAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTKFKF AAIDGNGFKG TWTENGSGDV
451 SGKFYGPAGE EVAGKYSYRP TDAEKGFGV FAGKKEQD*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3105>:

```

g287.seq
1  atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51  ctgtgggggc ggcggtggcg gatcgccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggccgcccc gttgttgcg aaaatgcgg ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgcgcgaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 tttcggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgccgcga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 ccccgcgctc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 gttgaccac tgtaaaaggc attcttgtaa tgggtgataa ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaaagcat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttcgggcc
751 gagattccgc tgattccgt caatcaggcc gatacgtga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcatccgg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcggtatc
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttgg
951 cacggcggcg tacaacggcg aagtgtgtga tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccc caaaagtcca ttcggcagc
1051 aaatctgtgg acggcattat cgacacgggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatggaaa cggctttaag gggacttgga
1151 cggaaaatgg cggcggggat gtttcgggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattcggc gtgtttgccc gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 3106; ORF 287.ng>:

```

g287.pep
1  MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV

```

		10	20	30	40	49	
m287.pep		MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSKPAAPVVSE-----KETE				A	
						:	
g287		MFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA					
		10	20	30	40	50	60
m287.pep	50	60	70	80	90	100	109
	KEDAPQAGSQGGAPS	AQSQSDMAAVSEENTGNGGAVTADNPKNEDEVAQN	DMPQNAAGT				
	:	: :					
g287	AGGAPQADTD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQN	DMPQNAA--					
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDPNMLAGNMENQATDAGES SQPANQPDMANAADGMQGDDPSAGGQNA	GNTA					
g287	-----						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIASNPAPANGGSNFGRVDLANGVLIDGPSQNI	TLTHCKGDS					
	: :     :						
g287	-ESANQTGNNOQAGSSDSAPASNPAPANGGSDFGRTNVGN SVVIDGPSQNI	TLTHCKGDS					
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSDADKISNYKKDGKNDKFVGLVADSVMKGINQYI	IIFYKP					
	: :   :						
g287	CNGDNLLEDEEAPSKSEFEKLSDDEEKIKRYKKDEQRENFVGLVADR VKKDGTNKYI	IIFYTD					
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNFI	FAPEGNYRILT					
	:						
g287	KPPT-----RSARSRRSLPAEIPLIPVNQADTLIVDGEAVSLTGHSNFI	FAPEGNYRILT					
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFEHTENG RPYPTRG RF AAKVDFGS						
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGR PYP S GGR F AAKVDFGS						
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSV DGI IDSGDDLHMGTQKFKA AIDGNGFGKTWTWENGSGDVS GKFYGPAGEE VAGKY SYR						
g287	KSV DGI IDSGDDLHMGTQKFKA AIDGNGFGKTWTWENGSGDVS GRFYGPAGEE VAGKY SYR						
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKGGFGVFAGKKEODX						

g287

|||||:|  
PTDAEKGFGVFAGKKDRDX  
420 430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3107>:

a287.seq

```
1 ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC
51 CTGTGGGGGC GCGGTGGCG GATCGCCCGA TGTTAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTACTG AAGATGTCGG GGAAGAGGTG
151 CTGCCGAAAG AAAAGAAAGA TGAGGAGCGG GTGAGTGGTG CGCCGCAAGC
201 CGATACGCAG GACGCAACCG CCGGAAAAGG CGGTCAAGAT ATGGCGGCAG
251 TTTCGGCAGA AAATACAGGC AATGGCGGTG CGGCAACAAC GGATAATCCC
301 GAAAATAAAG ACGAGGGACC GCAAAATGAT ATGCCGCAAA ATGCCGCCGA
351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGAATCGGC ACAACCGGCA
451 AACCAACCGG ATATGGCAAA TGCGGCGGAC GGAATGCAGG GGGACGATCC
501 GTCGGCAGGG GAAAATGCCG GCAATACGGC AGATCAAGCT GCAATCAAG
551 CTGAAACAA TCAAGTCGGC GGCTCTCAA ATCCTGCCTC TTCAACCAAT
601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
651 TGGCATCAAG CTTGACAGCG GTTCGGAAAA TGTAACGTTG ACACATTGTA
701 AAGACAAAGT ATGCGATAGA GATTCTTAG ATGAAGAAGC ACCACCAAAA
751 TCAGAATTTG AAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA
801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CGCGATTCAG GCGTCTGCA CGGTGAGGC GGTGCTTCC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GGCGGATACG CTGATTGTCG
1001 ATGGGGAAGC GGTGAGCCTG ACGGGGCATT CCGGCAATAT CTTGCGGCC
1051 GAAGGGAATT ACCGCTATCT GACTTACGGG GCGGAAAAAT TGTCCGGCGG
1101 ATCGTATGCC CTCAGTGTGC AAGGCGAACC GGCAAAGGC GAAATGCTTG
1151 CCGGCACGGC CGTGTACAAC GCGGAAGTGC TGCATTCCA TATGGAAAC
1201 GGCGTCCGT CCCCCTCCG AGGCAGGTTT GCCGCAAG TCGATTTCGG
1251 CAGCAAATCT GTGGACGGCA TTATCGACAG CGCGGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGGAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTT ACGGCCCGGC
1401 CCGCGAAGAA GTGGCGGGA AATACAGCTA TCGCCGACA GATCGCGAAA
1451 AGGCGCGATT CCGCGTGTTC GCCGCAAAA AAGAGCAGGA TTGA
```

This corresponds to the amino acid sequence <SEQ ID 3108; ORF 287.a>:

a287.pep

```
1 MFKRSVIAMA CIVALSACGG GGGGSPDVKS ADTLSKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATTDNP
101 ENKDEGPQND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA
151 NQPDMANAAD GMDGDDPSAG ENAGNTADQA ANQAENNQVG GSQNPASSTN
201 PNATNGGSDF GRINVANGIK LDGSENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VIIYKDKSAS
301 SSSARFRRSA RSRRLPAEM PLIPVQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMEN
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGD LHMGTQKFKA VIDGNGFKGT
451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEGGFGVF AGKKEQD*
```

m287/a287 ORFs 287 and 287.a showed a 77.2% identity in 501 aa overlap

```
10 20 30 40 49
m287.pep MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSKPAAPVVSE-----KETEA
|||||:|
a287 MFKRSVIAMACIVALSACGGGGGSPDVKSADTLSKPAAPVVTEDVGEEVLPEKKDEEA
10 20 30 40 50 60

50 60 70 80 90 100 109
m287.pep KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDVAQNMPQNAAGT
||||:| |:::||||| |||||:|:|:|:| |||||
a287 VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNPNKDEGPQNDMPQNAADT
70 80 90 100 110
```

	110	120	130	140	150	160	169
m287.pep	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDDPSAGGQNAGNTA						
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGGDDPSAG-ENAGNTA						
	120	130	140	150	160	170	
	170	180	190	200	210	220	229
m287.pep	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFGRLVLANGVLIDGPSQNTLTHCKGDS						
a287	DQAAQAENNQVGGSQNPASSTPNP NATNGGSDFGRINVANGIKLDSGSENVTLTHCKDKV						
	180	190	200	210	220	230	
	230	240	250	260	270	280	289
m287.pep	CSGNNFLDEEVQLKSEFEKLSADKISNYKKDGKNDKRVGLVADSVQMKGINQYIIFYKP						
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVYIYKD						
	240	250	260	270	280	290	
	290	300	310	320	330	340	
m287.pep	KP--TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRY						
a287	KSASSSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRY						
	300	310	320	330	340	350	
	350	360	370	380	390	400	
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF						
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF						
	360	370	380	390	400	410	
	410	420	430	440	450	460	
m287.pep	GSKSV DGIIDSGDDLHMG TQKFKA AIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS						
a287	GSKSV DGIIDSGDDLHMG TQKFKA VIDGNGFKGTWTENGSGDVSGRFRYGPAGEEVAGKYS						
	420	430	440	450	460	470	
	470	480	489				
m287.pep	YRPTDAEKG GFGVFAGKKEQDX						
a287	YRPTDAEKG GFGVFAGKKEQDX						
	480	490					

406

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3109>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACAC TGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAACAA CTGAAAGCCC AAACAAAAC T GGAATATTTT GCAGTAGACA

```

```

701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3110; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPYRSETT AETTSGLTGT LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEAF
251 AYKENYALWM GPYKVSKEIK PTEGLMVDPS DIRPYGNHTG NSAPSVFADN
301 SHEGYGYSDE VVRQHRQGQP *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3111>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGTACTCCA
251 TTGATGCACT GATTCGCGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3112; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPYRSETT AETTSGLTGT LTTSLSTLNA PALSRTQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEAF
251 AYKENYALWM GPYKVSKEIK PTEGLMVDPS DIQPYGNHTG NSAPSVFADN
301 SHEGYGYSDE AVRQHRQGQP *

```

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

```

          10      20      30      40      50      60
g406.pep  MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAAVKDMDLQALHGR
          |||
m406      MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAAVKDMDLQALHGR

```

	10	20	30	40	50	60
	70	80	90	100	110	120
g406 . pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
	130	140	150	160	170	180
g406 . pep	LTTSLSTLNAPALSRTQSDGSGSRSSLGLNIGGMGDYRNETLTTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	190	200	210	220	230	240
g406 . pep	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	250	260	270	280	290	300
g406 . pep	IKPKTNAFEAAAYKENYALWMGPYKVS KG IKPTEGLMVD FSDIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVS KG IKPTEGLMVD FSDIRPYGNHTGNSAPSVEADN					
	310	320				
g406 . pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3113>:

```

a406.seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC TGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3114; ORF 406.a>:

```

a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVS ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA

```

251 AYKENYALWM GPYKVSXGKIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN  
 301 SHEGYGYSDE AVRRHRQQQP \*

m406/a406 ORFs 406 and 406.a showed a 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPIILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
a406	MQARLLIPIILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTS GGLTG					
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTS GGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m406.pep	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m406.pep	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSXGKIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSXGKIKPTEGLMVDFS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
m406.pep	SHEGYGYSDEVVRQRQQQPX					
a406	SHEGYGYSDEAVRRHRQQQPX					
	310	320				

## EXAMPLE 2

### Expression of ORF 919

The primer described in Table 1 for ORF 919 was used to locate and clone ORF 919. The predicted gene 919 was cloned in pET vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 919-His fusion protein purification. Mice were immunized with the purified 919-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; PP, purified protein, TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm

that 919 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 are provided in Figure 10. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 and the amino acid sequence encoded thereby is provided in Example 1.

### EXAMPLE 3

#### Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 11. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided in Example 1.

### EXAMPLE 4

#### Expression of ORF 576 and 576-1

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera



were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).. These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 12. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

#### EXAMPLE 5

##### Expression of ORF 519 and 519-1

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 13. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 6

Expression of ORF 121 and 121-1

The primer described in Table 1 for ORF 121 was used to locate and clone ORF 121. The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 121 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 121 are provided in Figure 14. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 121 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 7

Expression of ORF 128 and 128-1

The primer described in Table 1 for ORF 128 was used to locate and clone ORF 128. The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 128 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 128 are provided in Figure 15. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J.*

*Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 128 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 8

### Expression of ORF 206

The primer described in Table 1 for ORF 206 was used to locate and clone ORF 206. The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 206 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 16. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 206 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 9

Expression of ORF 287

The primer described in Table 1 for ORF 287 was used to locate and clone ORF 287. The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A). These experiments confirm that 287 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 287 are provided in Figure 17. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 287 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 10

Expression of ORF 406

The primer described in Table 1 for ORF 406 was used to locate and clone ORF 406. The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 406 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 406 are provided in Figure 18. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 406 and the amino acid sequence encoded thereby is provided in Example 1.

### EXAMPLE 11

Table 2 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 225 among different strains.

**Table 2**

#### **225 gene variability: List of used *Neisseria* strains**

<b>Identification Strains number</b>	<b>Source / reference</b>
<b>Group B</b>	
zo01_225 NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo02_225 BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zo03_225 NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo04_225 297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zo05_225 1000	R. Moxon / Seiler <i>et al.</i> , 1996
zo06_225 BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zo07_225 BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zo08_225 528	R. Moxon / Seiler <i>et al.</i> , 1996
zo09_225 NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zo10_225 BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zo11_225 NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zo12_225 NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zo13_225 NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zo14_225 NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zo15_225 SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zo16_225 NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zo17_225 NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zo18_225 BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zo19_225 BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zo20_225 44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zo21_225 MC58	R. Moxon
zo96_225 2996	Our collection
<b>Group A</b>	
zo22_225 205900	R. Moxon
zo23_225 F6124	R. Moxon
z2491 22491	R. Moxon / Maiden <i>et al.</i> , 1998
<b>Group C</b>	
zo24_225 90/18311	R. Moxon
zo25_225 93/4286	R. Moxon

**Others**

zo26\_225 A22 (group W) R. Moxon / Maiden *et al.*, 1998  
 zo27\_225 E26 (group X) R. Moxon / Maiden *et al.*, 1998  
 zo28\_225 860800 (group Y) R. Moxon / Maiden *et al.*, 1998  
 zo29\_225 E32 (group Z) R. Moxon / Maiden *et al.*, 1998

**Gonococcus**

zo32\_225 Ng F62 R. Moxon / Maiden *et al.*, 1998  
 zo33\_225 Ng SN4 R. Moxon  
  
 fa1090 FA1090 R. Moxon

**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
 Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

>FA1090 <SEQ ID 3115>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS  
 GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
 RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN\*

Z2491 <SEQ ID 3116>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRVPARRAGNA  
 DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF  
 MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF  
 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN\*

Z001\_225 <SEQ ID 3117>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDSRFLN\*

Z002\_225 <SEQ ID 3118>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDSRFLN\*

Z003\_225 <SEQ ID 3119>  
 MDSFFKPAVWAVLWLMFAVRLALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDSRFLN\*

Z004\_225 <SEQ ID 3120>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z005\_225 <SEQ ID 3121>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z006\_225 <SEQ ID 3122>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z007\_225 <SEQ ID 3123>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z008\_225 <SEQ ID 3124>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z009\_225 <SEQ ID 3125>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z010\_225 <SEQ ID 3126>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z011\_225 <SEQ ID 3127>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF  
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF  
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN\*

Z012\_225 <SEQ ID 3128>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z013\_225 <SEQ ID 3129>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFIQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z014\_225 <SEQ ID 3130>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z015\_225 <SEQ ID 3131>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCS  
GFMQHIKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN\*

Z016\_225 <SEQ ID 3132>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z017\_225 <SEQ ID 3133>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z018\_225 <SEQ ID 3134>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z019\_225 <SEQ ID 3135>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z020\_225 <SEQ ID 3136>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG  
NADELIGSAMGLNEQVLPINRAPARRAGNADELIGSAMGLNEQVLPVNRVPARRAGNA  
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF  
MQHIKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF  
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN\*

Z021\_225 <SEQ ID 3137>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z022\_225 <SEQ ID 3138>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR



SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

ZO23\_225 <SEQ ID 3139>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

ZO24\_225 <SEQ ID 3140>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

ZO25\_225 <SEQ ID 3141>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

ZO26\_225 <SEQ ID 3142>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

ZO27\_225 <SEQ ID 3143>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

ZO28\_225 <SEQ ID 3144>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

ZO29\_225 <SEQ ID 3145>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

ZO32\_225 <SEQ ID 3146>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG  
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS  
GFMQHIKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN\*

ZO33\_225 <SEQ ID 3147>

MDSFFKPAVWAVLWLMFAVRSALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG  
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS  
GFMQHIKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN\*

ZO96\_225 <SEQ ID 3148>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLVNVNRPARRAGNADELIGNAMGLNEQPVLVNVNRPARRAGNA  
 DELIGNAMGLLGIAYRYGGSISTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDPSRFLN\*

Figure 19 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 225, further confirming its utility as an antigen for both vaccines and diagnostics.

### EXAMPLE 12

Table 3 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 235 among different strains.

**Table 3**

235 gene variability: List of used <i>Neisseria</i> strains		
Identification Strains number		Reference
Group B		
gnmzq01	NG6/88	Seiler <i>et al.</i> , 1996
gnmzq02	BZ198	Seiler <i>et al.</i> , 1996
gnmzq03	NG3/88	Seiler <i>et al.</i> , 1996
gnmzq04	1000	Seiler <i>et al.</i> , 1996
gnmzq05	1000	Seiler <i>et al.</i> , 1996
gnmzq07	BZ169	Seiler <i>et al.</i> , 1996
gnmzq08	528	Seiler <i>et al.</i> , 1996
gnmzq09	NGP165	Seiler <i>et al.</i> , 1996
gnmzq10	BZ133	Seiler <i>et al.</i> , 1996
gnmzq11	NGE31	Seiler <i>et al.</i> , 1996
gnmzq13	NGE28	Seiler <i>et al.</i> , 1996
gnmzq14	NGH38	Seiler <i>et al.</i> , 1996
gnmzq15	SWZ107	Seiler <i>et al.</i> , 1996
gnmzq16	NGH15	Seiler <i>et al.</i> , 1996
gnmzq17	NGH36	Seiler <i>et al.</i> , 1996
gnmzq18	BZ232	Seiler <i>et al.</i> , 1996
gnmzq19	BZ83	Seiler <i>et al.</i> , 1996
gnmzq21	MC58	Virji <i>et al.</i> , 1992
Group A		
gnmzq22	205900	Our collection

gnmzq23 F6124 Our collection  
z2491 Z2491 Maiden *et al.*, 1998

#### Group C

gnmzq24 90/18311 Our collection  
gnmzq25 93/4286 Our collection

#### Others

gnmzq26 A22 (group W) Maiden *et al.*, 1998  
gnmzq27 E26 (group X) Maiden *et al.*, 1998  
gnmzq28 860800 (group Y) Maiden *et al.*, 1998  
gnmzq29 E32 (group Z) Maiden *et al.*, 1998  
gnmzq31 *N. lactamica* Our collection

#### Gonococcus

gnmzq32 Ng F62 Maiden *et al.*, 1998  
gnmzq33 Ng SN4 Our collection

fa1090 FA1090 Dempsey *et al.* 1991

#### References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.  
Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279  
Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3149>  
MKPLILGLAAVLALSACQVRKAPDLDTYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVGAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK\*

GNMZQ01 <SEQ ID 3150>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ02 <SEQ ID 3151>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ03 <SEQ ID 3152>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ04 <SEQ ID 3153>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ05 <SEQ ID 3154>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ07 <SEQ ID 3155>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ08 <SEQ ID 3156>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ09 <SEQ ID 3157>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ10 <SEQ ID 3158>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ11 <SEQ ID 3159>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ13 <SEQ ID 3160>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ14 <SEQ ID 3161>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ15 <SEQ ID 3162>  
MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ16 <SEQ ID 3163>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ17 <SEQ ID 3164>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ18 <SEQ ID 3165>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ19 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ21 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ22 <SEQ ID 3167>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ23 <SEQ ID 3168>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ24 <SEQ ID 3169>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ25 <SEQ ID 3170>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ26 <SEQ ID 3171>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ27 <SEQ ID 3172>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ28 &lt;SEQ ID 3173&gt;

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ29 &lt;SEQ ID 3174&gt;

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ31 &lt;SEQ ID 3175&gt;

MKPLILGLAAVLALSACQVQKAPDFDYTAFKESKPASILVVPPLNESPDVNGTWGMLAST  
 AEPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKAAAYDLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ32 &lt;SEQ ID 3176&gt;

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK\*

GNMZQ33 &lt;SEQ ID 3177&gt;

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK\*

22491 &lt;SEQ ID 3178&gt;

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

Figure 20 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 235, further confirming its utility as an antigen for both vaccines and diagnostics.

### EXAMPLE 13

Table 4 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 287 among different strains.

**Table 4**

#### **287 gene variability: List of used *Neisseria* strains**

<b>Identification Strains number</b>	<b>Reference</b>
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**Group B**

287_2	BZ198	Seiler <i>et al.</i> , 1996
287_9	NGP165	Seiler <i>et al.</i> , 1996
287_14	NGH38	Seiler <i>et al.</i> , 1996
287_21	MC58	Virji <i>et al.</i> , 1992

**Group A**

z2491	Z2491	Maiden <i>et al.</i> , 1998
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**Gonococcus**

fa1090	FA1090	Dempsey <i>et al.</i> 1991
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**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.  
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279  
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

287\_14 <SEQ ID 3179>

MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG  
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS  
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNO  
 TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGDCSCGNNFLDEEV  
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFKVGLVADSVQMKGINQYIIIFYKPKPTSFAF  
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTGAEKLP  
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPSRGREFAAKVDFGSKSVDGII  
 DSGDGLHMGTKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEK  
 GFGVFAGKKEQD\*

287\_2 <SEQ ID 3180>

MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG  
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS  
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNO  
 TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGDCSCGNNFLDEEV  
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFKVGLVADSVQMKGINQYIIIFYKPKPTSFAF  
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTGAEKLP  
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPSRGREFAAKVDFGSKSVDGII  
 DSGDGLHMGTKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEK  
 GFGVFAGKKEQD\*

287\_21. <SEQ ID 3181>

MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG  
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAAGTDSSTPNHTPDP  
 NMLAGNMENQATDAGESSQPANQPDMAANTADGMQGGDDPSAGGQAGNTAAQGANQAGNNQ  
 AAGSSDPIPASNPAPANGGNSFGRVLDLAVGLIDGPSQNTLTHCKGDCSCGNNFLDEEV  
 QLKSEFEKLSADAKISNYKKDGKNDKFKVGLVADSVQMKGINQYIIIFYKPKPTSFAFRRS

ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY  
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVVDGIIDSGD  
DLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGV  
FAGKKEQD\*

287\_9 <SEQ ID 3182>

MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSPKPAAPVVTEDVGEVLPKEKKDEEA  
VSGAPQADTQDATAGKGGQDMAAVSAENTGNGGAATTDNPENKDEGPQNDMPQNAADTDS  
STPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMAADGMQGGDDPSAGENAGNTADQA  
ANQAENNVQGGSONPASSTPNATNGGSDFRINVANGIKLDSGSENVTLTHCKDKVCDR  
DFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVITYKDKSAS  
SSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYG  
AEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKS  
VDGIIDSGDDLHMGTOQKFAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPT  
DAEKGFGVFAGKKEQD\*

FA1090 <SEQ ID 3183>

MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA  
AGGAPQADTQDATAGEGSDMAAVSAENTGNGGAATTDNPKNEDEGAQNDMPQNAAESAN  
QTGNNQAGSSDSAPASNAPANGGSDFRTNVGNSSVVIDGPSQNTLTHCKGDSNGDN  
LLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVEKNGTNKYVITYKDKSAS  
SARSRRSLPAEIPLIIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGS  
YALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKSVVDGIIDSG  
DDLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPTDAEKGFGV  
VFAGKKDRD\*

Z2491 <SEQ ID 3184>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVSEKETEAKEDAPQAGSQG  
QGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGTDSSTPNHTPDP  
NMLAGNMENQATDAGESSQPANQPDMAADGMQGGDDPSAGGQAGNTAAQGANQAGNNQ  
AAGSSDPIPASNPAPANGGNSFGRVDLANGVLIDGPSQNTLTHCKGDSNGNLFDEEV  
QLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMGKINQYIIFYKPKPTSFARFRS  
ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY  
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVVDGIIDSGD  
DLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGV  
FAGKKEQD\*

Figure 21 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 287, further confirming its utility as an antigen for both vaccines and diagnostics.

#### EXAMPLE 14

Table 5 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 519 among different strains.

Table 5

#### 519 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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**number****Group B**

zv01_519	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv02_519	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zv03_519ass	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv04_519	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zv05_519	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zv06_519ass	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zv07_519	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zv11_519	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zv12_519	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zv18_519	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zv19_519	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zv20_519ass	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zv21_519ass	MC58	R. Moxon
zv96_519	2996	Our collection

**Group A**

zv22_519ass	205900	R. Moxon
z2491_519	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

**Others**

zv26_519	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zv27_519	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zv28_519	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zv29_519ass	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998

**Gonococcus**

zv32_519	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
fa1090_519	FA1090	R. Moxon

**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090\_519 <SEQ ID 3185>  
MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGANGVKVLRYEIKDLVPPQEILRAMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

Z2491\_519 &lt;SEQ ID 3186&gt;

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV01\_519 &lt;SEQ ID 3187&gt;

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV02\_519 &lt;SEQ ID 3188&gt;

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV03\_519 &lt;SEQ ID 3189&gt;

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV04\_519 &lt;SEQ ID 3190&gt;

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV05\_519 &lt;SEQ ID 3191&gt;

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV06\_519ASS &lt;SEQ ID 3192&gt;

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV07\_519 &lt;SEQ ID 3193&gt;

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV11\_519 &lt;SEQ ID 3194&gt;

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV12\_519 &lt;SEQ ID 3195&gt;

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV18\_519 &lt;SEQ ID 3196&gt;

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV19\_519 &lt;SEQ ID 3197&gt;

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV20\_519ASS &lt;SEQ ID 3198&gt;

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM  
ISAGMKIIDSSKTAK\*

ZV21\_519ASS &lt;SEQ ID 3199&gt;

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV22\_519ASS &lt;SEQ ID 3200&gt;

MEFFIILLAAVVVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV26\_519 &lt;SEQ ID 3201&gt;

MEFFIILLAAVVVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV27\_519 &lt;SEQ ID 3202&gt;

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV28\_519 <SEQ ID 3203>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV29\_519ASS <SEQ ID 3204>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTIVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREPEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSNKTAK\*

ZV32\_519 <SEQ ID 3205>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV96\_519 <SEQ ID 3206>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

Figure 22 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 519, further confirming its utility as an antigen for both vaccines and diagnostics.

#### EXAMPLE 15

Table 6 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 919 among different strains.

**Table 6**

#### **919 gene variability: List of used *Neisseria* strains**

Identification Strains	Source / reference
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**number****Group B**

zm01	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm02	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zm03	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm04	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zm05	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zm06	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zm07	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zm08n	528	R. Moxon / Seiler <i>et al.</i> , 1996
zm09	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zm10	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zm11asbc	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zm12	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zm13	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zm14	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zm15	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zm16	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zm17	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zm18	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zm19	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zm20	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zm21	MC58	R. Moxon
zm96	2996	Our collection

**Group A**

zm22	205900	R. Moxon
zm23asbc	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

**Group C**

zm24	90/18311	R. Moxon
zm25	93/4286	R. Moxon

**Others**

zm26	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zm27bc	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zm28	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zm29asbc	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998
zm31asbc	<i>N. lactamica</i>	R. Moxon

**Gonococcus**

zm32asbc	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
zm33asbc	Ng SN4	R. Moxon
fa1090	FA1090	R. Moxon

**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3207>

MKKHLLRSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER  
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDGRTERARFPIYGIPTDDFISVPLPAGLRGKKN  
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNEGVPVAGLGTPLMGEYAGA  
IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

Z2491 <SEQ ID 3208>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKAYMQQNQRLAEVLGQNPSYIFFRELTSNDGVPVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM01 <SEQ ID 3209>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELTSNDGVPVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM02 <SEQ ID 3210>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELTSNDGVPVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM03 <SEQ ID 3211>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELTSNDGVPVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM04 <SEQ ID 3212>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIROQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM05 <SEQ ID 3213>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIROQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM06 <SEQ ID 3214>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIROQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM07 <SEQ ID 3215>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIROQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM08N <SEQ ID 3216>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIROQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM09 <SEQ ID 3217>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIROQTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM10 <SEQ ID 3218>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIROQTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM11ASBC <SEQ ID 3219>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM12 <SEQ ID 3220>

MKKYLFRAALYGIAAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM13 <SEQ ID 3221>

MKKYLFRAALYGIAAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAEQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM14 <SEQ ID 3222>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSRNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM15 <SEQ ID 3223>

MKKYLFRAALYGIAAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDLAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNHQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM16 <SEQ ID 3224>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPGRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM17 <SEQ ID 3225>



MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM18 <SEQ ID 3226>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM19 <SEQ ID 3227>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM20 <SEQ ID 3228>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM21 <SEQ ID 3229>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM22 <SEQ ID 3230>

MKKYLFRAALCGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM23ASBC <SEQ ID 3231>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTSKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGETAGK  
MKEPGYVWQLLPNGMKPEYRP\*

ZM24 <SEQ ID 3232>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM25 <SEQ ID 3233>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM26 <SEQ ID 3234>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM27BC <SEQ ID 3235>

MKKYLFRAALYGISAAAILAACQSKSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGETAGK  
MKEPGYVWQLLPNGMKPEYRP\*

ZM28 <SEQ ID 3236>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM29ASBC <SEQ ID 3237>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATTHPITRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM31ASBC <SEQ ID 3238>

MKKHLFRAALYGIAAAILAACQSKSIQTFFPQPDTSIIKGPDRPAGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIIPDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPYSYIFFRELAGSGNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM32ASBC <SEQ ID 3239>

MKKHLRSALYGIAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
 YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIIPDDFISVPLPAGLRGGKA  
 LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPYSYIFFRELAGSGDGPVGALGTPLMGGYAGA  
 IDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM33ASBC <SEQ ID 3240>

MKKHLRSALYGIAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
 YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIIPDDFISVPLPAGLRGGKN  
 LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPYSYIFFRELAGSGNEGPVGALGTPLMGEYAGA  
 IDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM96 <SEQ ID 3241>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIIPDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPYSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

Figure 23 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 919, further confirming its utility as an antigen for both vaccines and diagnostics.

#### EXAMPLE 16

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

**Table 7:** Oligonucleotides used for PCR to amplify complete or partial ORFs

ORF primer Sequence		Restriction sites
001	Forward CGCGGATCCCATATG-TGGATGGTGCTGGTCAT	BamHI-
	Reverse CCCGCTCGAG-TGCCGTCTTGTCAC	NdeI
003	Forward CGCGGATCCCATATG-GTCGTATTCGTGGC	XhoI
	Reverse CCCGCTCGAG-AAAATCATGAACACGCGC	BamHI-
005	Forward CGCGGATCCCATATG-GACAATATTGACATGT	NdeI
	Reverse CCCGCTCGAG-CATCACATCCGCCCC	XhoI
006	Forward CGCGGATCCCATATG-CTGCTGGTGCTGG	BamHI-
	Reverse CCCGCTCGAG-AGTTCCGGCTTTGATGT	NdeI
007	Forward CGCGGATCCCATATG-GCCGACAACAGCATCAT	XhoI
	Reverse CCCGCTCGAG-AAGGCGTTCATGATATAAG	BamHI-
008	Forward CGCGGATCCCATATG-AACAACAGACATTTTG	NdeI
	Reverse CCCGCTCGAG-CCTGTCCGGTAAAAGAC	XhoI
009	Forward CGCGGATCCCATATG-CCCCGCGCTGCT	BamHI-
	Reverse CCCGCTCGAG-TGGCTTTTGCCACGTTTT	NdeI
011	Forward CGCGGATCCCATATG-AAGACACACCGCAAG	XhoI
	Reverse CCCGCTCGAG-GGCGGTCAGTACGGT	BamHI-
012	Forward CGCGGATCCCATATG-CTCGCCCGTTGCC	NdeI
	Reverse CCCGCTCGAG-AGCGGGGAAGAGGCAC	XhoI
013	Forward CGCGGATCCCATATG-CCTTTGACCATGCT	BamHI-
	Reverse CCCGCTCGAG-CTGATTCGGCAAAAAATCT	NdeI
018	Forward CGCGGATCCCATATG-CAGCAGAGGCAGTT	XhoI
	Reverse CCCGCTCGAG-GACGAGGCGAACGCC	BamHI-
019	Forward AAAGAATTC-CTGCCAGCCGGCAAGACCCCGGC	NdeI
	Reverse AAAGTGCAG-TCAGCGGGCGGGGACAATGCCCAT	XhoI
023	Forward AAAGAATTC-AAAGAATATTCGGCATGGCAGGC	Eco RI
	Reverse AAAGTGCAG-TTACCCCCAAATCACTTTAACTGA	Pst I
025	Forward AAAGAATTC-TGCGCCACCCAACAGCCTGCTCC	Eco RI
	Reverse AAAGTGCAG-TCAGAACGCGATATAGCTGTTCCG	Pst I
031	Forward CGCGGATCCCATATG-GTCTCCCTTCGCTT	BamHI-
	Reverse CCCGCTCGAG-ATGTAAGACGGGGACAAC	NdeI
032	Forward CGCGGATCCCATATG-CGGCGAAACGTGC	XhoI
		BamHI-

	Reverse	CCCGCTCGAG-CTGGTTTTTTGATATTTGTG	NdeI
033	Forward	CGCGGATCCCATATG-GCGGCGGCAGACA	XhoI
	Reverse	CCCGCTCGAG-ATTTGCCGCATCCCGAT	BamHI-
034	Forward	CGCGGATCCCATATG-GCCGAAAACAGCTACGG	NdeI
	Reverse	CCCGCTCGAG-TTTGACGATTTGGTTCAATT	XhoI
036	Forward	CGCGGATCCCATATG-CTGAAGCCGTGCG	BamHI-
	Reverse	CCCGCTCGAG-CCGGA CTGCGTATCGG	NdeI
038	Forward	CGCGGATCCCATATG-ACCGATTTCGCCA	XhoI
	Reverse	CCCGCTCGAG-TTCTACGCCGTACTGCC	BamHI-
039	Forward	CGCGGATCCCATATG-CCGTCCGAACCGC	NdeI
	Reverse	CCCGCTCGAG-TAGGATGACGAGGTAGG	XhoI
041	Forward	CGCGGATCCCATATG-TTCGTGCGCGAACCGC	BamHI-
	Reverse	CCCGCTCGAG-GCCCAAAA ACTCTTTCAA	NdeI
042	Forward	CGCGGATCCCATATG-ACGATGATTTGCTTGC	XhoI
	Reverse	CCCGCTCGAG-TTTGCAGCCTGCATTTGAC	BamHI-
043	Forward	AAAAAAGGTACC-ATGGTTGTTCAAATCAAATATC	NdeI
	Reverse	AAACTGCAG-TTATTGCGCTTACCTTCCGCCG	XhoI
043a	Forward	AAAAAAGGTACC-GCAAAGTGCATGGCGGCTTGGACGGTGC	Kpn I
	Reverse	AAAAAACTGCAG-TTAATCCTGCAACACGAATTCGCCCCGTCCG	Pst I
044	Forward	CGCGGATCCCATATG-CCGTCCGACTAGAG	Kpn I
	Reverse	CCCGCTCGAG-ATGCGCTACGGTAGCCA	Pst I
046	Forward	AAAGAATTC-ATGTCGGCAATGCTCCCGACAAG	BamHI-
	Reverse	AAACTGCAG-TCACTCGGCGACCCACACCGTGAA	NdeI
047	Forward	CGCGGATCCCATATG-GTCATCATA CAGGCG	XhoI
	Reverse	CCCGCTCGAG-TCCGAAAAAGCCCATTTTG	Eco RI
048	Forward	AAAGAATTC-ATGCTCAACAAAGGCGAAGAATTGCC	Pst I
	Reverse	AAACTGCAG-TCAAGATTCGACGGGGATGATGCC	Eco RI
049	Forward	AAAGAATTC-ATGCGGGCGCAGGCGTTTGATCAGCC	Pst I
	Reverse	AAACTGCAG-AAGGCGTATCTGAAAAAATGGCAG	BamHI-
050	Forward	CGCGGATCCCATATG-GGCGCGGGCTGG	NdeI
	Reverse	CCCGCTCGAG-AATCGGGCCATCTTCGA	XhoI
052	Forward	AAAAAAGAATTC-ATGGCTTTGGTGGCGGAGGAAAC	Eco RI
	Reverse	AAAAAAGTCGAC-TCAGGCGGCGTTTTCACCTTCCT	Sal I
052a	Forward	AAAAAAGAATTC-GTGGCGGAGGAAACGGAAATATCCGC	Eco RI

	Reverse	AAAAAACTGCAG-TTAGCTGTTTTTGGAAACGCCGTCCAACCC	Pst I
073	Forward	CGCGGATCCCATATG-TGTATGCCATATAAGAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACCGGATTGTCCGAC	XhoI
075	Forward	CGCGGATCCCATATG-CCGTCTTACTTCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCACCAATGCCGATTATTT	XhoI
077a	Forward	AAAAAAGAATTC-GGCGGCATTTTCATCGACACCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGAACATCTGCACAAACGCAAT	Pst I
080	Forward	AAAGAATTC-GCGTCCGGGCTGGTTTGGTTTACAATTC	Eco RI
	Reverse	AAACTGCAG-CTATTCTTCGGATTCTTTTTCGGG	Pst I
081	Forward	AAAGAATTC-ATGAAACCACTGGACCTAAATTTTCATCTG	Eco RI
	Reverse	AAACTGCAG-TCACTTATCCTCCAATGCCTC	Pst I
082	Forward	AAAGAATTC-ATGTGGTTGTTGAAGTTGCCTGC	Eco RI
	Reverse	AAACTGCAG-TTACGCGGATTCGGCAGTTGG	Pst I
084	Forward	AAAGAATTC-TATCACCCAGAATATGAATACGGCTACCG	Eco RI
	Reverse	AAACTGCAG-TTATACTTGGGCGCAACATGA	Pst I
085	Forward	CGCGGATCCCATATG-GGTAAAGGGCAGGACT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAAGCCTTAAACGCTTCG	XhoI
086	Forward	AAAAAAGGTACC-TATTTGGCATCAAAAGAAGGCGG	Kpn I
	Reverse	AAACTGCAG-TTACTCCACCCGATAACCGCG	Pst I
087	Forward	AAAGAATTC-ATGGGCGGTAAAACCTTTATGC	Eco RI
	Reverse	AAACTGCAG-TTACGCCGCACACGCAATCGC	Pst I
087a	Forward	AAAAAAGAATTC-AAGCTATTAGGCGTGCCGATTGTGATTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCTGCAAGATGCCAGCTTGCC	Pst I
088	Forward	AAAAAAGAATTC-ATGTTTTTATGGCTCGCACATTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGATTTTGAGGGTACTCAAACC	Pst I
089	Forward	CGCGGATCCCATATG-CCGCCAAAATCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCGCATACCAAAGCCA	XhoI
090	Forward	CGCGGATCCCATATG-CGCATAGTCGAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAAAACGGCGGTACG	XhoI
091	Forward	AAAGAATTC-ATGGAAATACCCGTACCGCCGAGTCC	Eco RI
	Reverse	AAACTGCAG-TCAGCGCAGGGGGTAGCCCAAGCC	Pst I
092	Forward	AAAGAATTC-ATGTTTTTTATTTCAATCCG	Eco RI
	Reverse	AAACTGCAG-TCAAATCTGTTTCGACAATGC	Pst I
093	Forward	AAAGAATTC-ATGCAGAATTTTGGCAAAGTGGC	Eco RI
	Reverse	AAACTGCAG-CTATGGCTCGTCATACCGGGC	Pst I
094	Forward	AAAGAATTC-ATGCCGTCACGGAAGCGCATCAACTC	Eco RI
	Reverse	AAACTGCAG-TTATCCCGGCCATACCGCCGAACA	Pst I
095	Forward	AAAGAATTC-ATGTCCTTTTCATTTGAACATGGACGG	Eco RI
	Reverse	AAACTGCAG-TCAACGCCGCAGGCACTAACGCC	Pst I
096	Forward	AAAGAATTC-ATGGCTCGTCATACCGGGCAGGG	Eco RI

	Reverse	AAACTGCAG-TCAAAGGAAAAGGCCGTCTGAAAAGCG	Pst I
097	Forward	AAAGAATTC-ATGGACACTTCAAAACAAACACTGTTG	Eco RI
	Reverse	AAACTGCAG-TCAGCCCAAATACCAGAATTTTCAG	Pst I
098	Forward	AAAGAATTC-GATGAACGCAGCCCAGCATGGATACG	Eco RI
	Reverse	AAACTGCAG-TTACGACATTCTGATTTGGCA	Pst I
102	Forward	AAAAAAGAATTC-GGCCTGATGATTTTGGAAGTCAACAC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
105	Forward	CGCGGATCCCATATG-TCCGCAAACGAATACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGTTCTGCCAGTTTCAG	XhoI
107	Forward	AAAAAAGAATTC- CTGATGATTTTGGAAGTCAACACCCATTATCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
107b	Forward	AAAAAAGAATTC- GATACCCAAGCCCCCGCCGGCACAACACTACTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCGTCGCCTTTAAAGTATTTGAGCAGGCTGGAGAC	Pst I
108	Forward	AAAGAATTC-ATGTTGCCGGGCTTCAACCG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
108a	Forward	AAAAAAGAATTC-GGTAACACATTCGGCAGCTTAGACGGTGG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
109	Forward	AAAGAATTC-ATGTATTATCGCCGGGTATGGG	Eco RI
	Reverse	AAACTGCAG-CTAGCCCAAAGATTTGAAGTGTTT	Pst I
111	Forward	CGCGGATCCCATATG-TGTTCGGAACAAACCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGAGCAGTTTTTCAAA	XhoI
114	Forward	CGCGGATCCCATATG-GCTTCCATCACTTCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCCGCGAAATCGTC	XhoI
117	Forward	AAAAAAGGTACC-ATGGTCGAAGAACTGGAAGTCTG	Kpn I
	Reverse	AAACTGCAG-TTAAAGCCGGGTAACGCTCAATAC	Pst I
118	Forward	AAAGTCGACATGTGTGAGTTCAAGGATATTATAAG	Sal I
	Reverse	AAAGCATGC-CTATTTTTTGTGTAATAATCAAATC	Sph I
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC	XhoI
122	Forward	CGCGGATCCCATATG-GTCATGATTAAATCCGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATCTTGGTAGATTGGATT	XhoI
125	Forward	AAAGAATTC-ATGTCGGGCAATGCCTCCTCTCC	Eco RI
	Reverse	AAACTGCAG-TCACGCCGTTTCAAGACG	Pst I
125a	Forward	AAAAAAGAATTC-ACGGCAGGCAGCACCGCCGCACAGGTTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTATTTTGCCACGTCGGTTTCTCCGGTGAACAACGC	Pst I
126	Forward	CGCGGATCCCATATG-CCGTCTGAAACCC	BamHI-

	Reverse	CCCGCTCGAG-ATATTCCGCCGAATGCC	NdeI
127	Forward	AAAGAATTC-ATGGAAATATGGAATATGTTGGACACTTG	XhoI
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Eco RI
127a	Forward	AAAAAAGAATTC-AAGGAACTGATTATGTGTCTGTCGGG	Pst I
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Eco RI
128	Forward	CGCGGATCCCATATG-ACTGACAACGCACT	Pst I
	Reverse	CCCGCTCGAG-GACCGCGTTGTCTGAAA	BamHI-
130	Forward	CGCGGATCCCATATG-AAACAACCTCCGCGA	NdeI
	Reverse	CCCGCTCGAG-GAATTTTGCACCGGATTG	XhoI
132	Forward	AAAGAATTC-ATGGAACCTTCAAAACCTTAATTTG	Eco RI
	Reverse	AAAAAACTGCAG-TCACCATGTCCGCATTTGAAAAAC	Pst I
134	Forward	CGCGGATCCCATATG-TCCCAAGAAATCCTC	BamHI-
	Reverse	CCCGCTCGAG-CAGTTTGACCGAATGTTC	NdeI
135	Forward	CGCGGATCCCATATG-AAATACAAAAGAATCGTATT	XhoI
	Reverse	CCCGCTCGAG-AAATTCGGTCAGAAGCAGG	BamHI-
137	Forward	AAAAAAGGTACC-ATGATTACCCATCCCCAATTCGATCC	NdeI
	Reverse	AAAAAACTGCAG-TCAGTGCTGTTTTTTCATGCCGAA	XhoI
137a	Forward	AAAAAAGAATTC-GGCCGCAAAACACGGCATCGGCTTCCT	Kpn I
	Reverse	AAAAAACTGCAG-TTAAGCGGGATGACGCGGCAGCATACC	Pst I
138	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Pst I
141	Forward	AAAGAATTC-ATGAGCTTCAAAACCGATGCCGAAATCGC	Xba I
	Reverse	AAACTGCAG-TCAGAACAAGCCGTGAATCACGCC	Eco RI
142	Forward	CGCGGATCCCATATG-CGTGCCGATTTTCATG	Pst I
	Reverse	CCCGCTCGAG-AAACTGCTGCACATGGG	BamHI-
143	Forward	AAAAAAGAATTC- ATGCTCAGTTTCGGCTTTCTCGGCGTTCAGAC	NdeI
	Reverse	AAAAAACTGCAG-TCAAACCCCGCCGTGTGTTTCTTTAAT	XhoI
144	Forward	AAAAAAGAATTC-GGTCTGATCGACGGGCGTGCCGTAAC	Eco RI
	Reverse	AAAAAATCTAGA-TCGGCATCGGCCGGCATATGTCCG	Pst I
146	Forward	AAAAAAGAATTC- CGCCAAGTCGTCATTGACCACGACAAAGTC	Xba I
	Reverse	AAAAAACTGCAG-TTAGGCATCGGCAAATAGGAACTGGG	Eco RI
147	Forward	AAAAAAGAATTC-ACTGAGCAATCGGTGGATTTGGAAAC	Pst I
	Reverse	AAAAAATCTAGA-TTAGGTAAAGCTGCGGCCCATTTGCGG	Eco RI
148	Forward	AAAAAAGAATTC- ATGGCGTTAAAAACATCAAACCTTGAACACGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGCCCTTCATACAGCCTTCGTTTTG	Eco RI
149	Forward	CGCGGATCCCATATG-CTGCTTGACAACAAAGT	Xba I
			BamHI-



	Reverse	CCCGCTCGAG-AAACTTCACGTTACGCC	NdeI
150	Forward	CGCGGATCCCATATG-CAGAACACAAATCCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATAAACATCACGCTGATAGC	NdeI
151	Forward	AAAAAAGAATTC-	XhoI
		ATGAAACAAATCCGCAACATCGCCATCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAGCTTTTAAAGTGGCGGCG	Pst I
152	Forward	AAAAAAGAATTC-	Eco RI
		ATGAAAAACAAAACCAAAGTCTGGGACCTCCC	
	Reverse	AAAAAACTGCAG-TCAGGACAGGAGCAGGATGGCGGC	Pst I
153	Forward	AAAAAAGAATTC-ATGGCGTTTGCTTACGGTATGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTCATGTTTTCCGTTTCATT	Pst I
153a	Forward	AAAAAAGAATTC-CGGACTTCGGTATCGGTTCCCCAGCATTG	Eco RI
	Reverse	AAAAAACTGCAG-	Pst I
		TTACGCCGACGAAATACTCAGACTTTTCGG	
154	Forward	CGCGGATCCCATATG-ACTGACAACAGCCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGGCTTCCTTTCGGG	XhoI
155	Forward	AAAAAAGAATTC-ATGAAATCGGTATCCACGCGAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCCTTTCTTAAACATATTCAGCAT	Pst I
156	Forward	AAAAAAGAATTC-GCACAGCAAACGGTTTTGAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCAGCCGCGACAAACAGCCC	Pst I
157	Forward	CGCGGATCCCATATG-AGGAACGAGGAAAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAAACACAATATCCCCGC	XhoI
158	Forward	AAAAAAGAATTC-GCGGAGCAGTTGGCGATGGCAAATTCTGC	Eco RI
	Reverse	AAAAAATCTAGA-TTATCCACAGAGATTGTTCCAGTTC	Xba I
160	Forward	CGCGGATCCCATATG-GACATTCTGGACAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTTGTCCCGCCTTCTTT	XhoI
163	Forward	AAAAAAGGTACC-ACCGTGCCGGATCAGGTGCAGATGTG	Kpn I
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
163a	Forward	AAAAAAGAATTC-CGGCTGGTGCAGATAATGAGCCAGAC	Eco RI
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
164	Forward	CGCGGATCCCATATG-AACCGGACTTATGCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGTTTCCGTCAAACCTGC	XhoI
165	Forward	CGCGGATCCGCTAGC-GCTGAAGCGACAGACG	BamHI-
			NheI
	Reverse	CCCGCTCGAG-AATATCCAATACTTTCGCG	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAAGTATGTGC	XhoI
209	Forward	CGCGGATCCCATATG-CTGCGGCATTTAGGA	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-TACCCCTGAAGGCAAC	XhoI
211	Forward	AAAAAAGAATTC-ATGTTGCGGGTTGCTGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-CTATCCTGCGGATTGGCATTGAAA	Pst I
212	Forward	CGCGGATCCCATATG-GACAATCTCGTATGG	BamHI-
	Reverse	CCCGCTCGAG-AGGGGTTAGATCCTTCC	NdeI
215	Forward	CGCGGATCCCATATG-GCATGGTTGGGTCGT	XhoI
	Reverse	CCCGCTCGAG-CATATCTTTTGTATCATAAATC	BamHI-
216	Forward	CGCGGATCCCATATG-GCAATGGCAGAAAACG	NdeI
	Reverse	CCCGCTCGAG-TACAATCCGTGCCGCC	XhoI
217	Forward	CGCGGATCCCATATG-GCGGATGACGGTGTG	BamHI-
	Reverse	CCCGCTCGAG-ACCCCGAATATCGAATCC	NdeI
218	Forward	CGCGGATCCCATATG-GTCGCGGTTCGATC	XhoI
	Reverse	CCCGCTCGAG-TAACTCATAGAATCCTGC	BamHI-
219	Forward	CGCGGATCCGCTAGC-ACGGCAAGGTTAAG	NheI
	Reverse	CCCGCTCGAG-TTTAAACCATCTCCTCAAAAC	XhoI
223	Forward	CGCGGATCCCATATG-GAATTCAGGCACCAAGTA	BamHI-
	Reverse	CCCGCTCGAG-GGCTTCCCGCGTGTC	NdeI
225	Forward	CGCGGATCCCATATG-GACGAGTTGACCAACC	XhoI
	Reverse	CCCGCTCGAG-GTTCAGAAAGCGGGAC	BamHI-
226	Forward	AAAGAATTC-CTTGCGATTATCGTGCGCACGCG	NdeI
	Reverse	AAACTGCAG-TCAAAATCCCAAAACGGGGAT	XhoI
228	Forward	CGCGGATCCCATATG-TCGCAAGAAGCCAAACAG	Eco RI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	Pst I
229	Forward	CGCGGATCCCATATG-CAAGAGGTTTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-ACACAATATAGCGGATGAAC	NdeI
230	Forward	CGCGGATCCCATATG-CATCCGGGTGCCGAC	XhoI
	Reverse	CCCGCTCGAG-AAGTTTGGCGGCTTCGG	BamHI-
232	Forward	AAAAAAGAATTC-ATGTACGCTAAAAAGGCGGTTTGGG	NdeI
	Reverse	AAAAAACTGCAG-TCAAGGTTTTTCTGATTGCCGCCGC	XhoI
232a	Forward	AAAAAAGAATTC-GCCAAGGCTGCCGATACACAAATTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACATTGTCGTTGCCGCCAGATG	Pst I
233	Forward	CGCGGATCCCATATG-GCGGACAAACCCAAG	BamHI-
	Reverse	CCCGCTCGAG-GACGGCATTGAGCAG	NdeI
234	Forward	CGCGGATCCCATATG-GCCGTTTCACTGACCG	XhoI
			BamHI-

	Reverse	GCCCAAGCTT-ACGGTTGGATTGCCATG	NdeI
235	Forward	CGCGGATCCCATATG-GCCTGCCAAGTTCAAA	Hind III
	Reverse	CCCGCTCGAG-TTTGGGCTGCTCTTC	BamHI-
236	Forward	CGCGGATCCCATATG-GCGCGTTTCGCCTT	NdeI
	Reverse	CCCGCTCGAG-ATGGGTCGCGCGCCGT	XhoI
238	Forward	CGCGGATCCGCTAGC-AACGGTTTGGATGCCCCG	BamHI-
	Reverse	CCCGCTCGAG-TTTGTCTAAGTTCCTGATATG	NdeI
239	Forward	CCGGAATTCTACATATG-CTCCACCATAAAGGTATTG	XhoI
	Reverse	CCCGCTCGAG-TGGTGAAGAGCGGTTTAG	EcoRI-
240	Forward	CGCGGATCCCATATG-GACGTTGGACGATTTC	NdeI
	Reverse	CCCGCTCGAG-AAACGCCATTACCCGATG	XhoI
241	Forward	CCGGAATTCTACATATG-CCAACACGTCCAAC	BamHI-
	Reverse	CCCGCTCGAG-GAATGCGCCTGTAATTAATC	NdeI
242	Forward	CGCGGATCCCATATG-ATCGGCAAACCTTGTG	XhoI
	Reverse	GCCCAAGCTT-ACCGATACGGTCGCAG	BamHI-
243	Forward	CGCGGATCCCATATG-ACGATTTTTTCGATGCTGC	NdeI
	Reverse	CCCGCTCGAG-CGACTTGGTACCGCG	HindIII
244	Forward	CGCGGATCCCATATG-CCGTCTGAAGCCC	BamHI-
	Reverse	CCCGCTCGAG-TTTTTTCGGTAGGGGATT	NdeI
246	Forward	CGCGGATCCCATATG-GACATCGGCAGTGC	XhoI
	Reverse	CCCGCTCGAG-CCCGCGCTGCTGGAG	BamHI-
247	Forward	CGCGGATCCCATATG-GTCGGATCGAGTTAC	NdeI
	Reverse	CCCGCTCGAG-AAGTGTTCTGTTTGCGCA	XhoI
248	Forward	CGCGGATCCCATATG-CGAAACAGAACT	BamHI-
	Reverse	CCCGCTCGAG-CTCATCATTATTGCTAACA	NdeI
249	Forward	CGCGGATCCCATATG-AAGAATAATGATTGCTTC	XhoI
	Reverse	CCCGCTCGAG-TTCCCGACCTCCGAC	BamHI-
251	Forward	CGCGGATCCCATATG-CGTGCTGCGGTAGT	NdeI
	Reverse	CCCGCTCGAG-TACGAAAGCCGGTCGTG	XhoI
253	Forward	AAAAAAGAATTC-ATGATTGACAGGAACCGTATGCTGCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I

253a	Forward	AAAAAAGAATTC-AAAATCCTTTTGAAAACAAGCGAAAACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I
254	Forward	AAAAAAGAATTC-ATGTATACAGGCGAACGCTTCAATAC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATTACGTAACCGTACACGCTGAC	Xba I
255	Forward	CGCGGATCCCATATG-GCCGCGTTGCGTTAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-ATCCGCAATACCGACCAG	XhoI
256	Forward	CGCGGATCCGCTAGC-TTTTAACACCGCCGGAC	BamHI-
			NheI
	Reverse	CCCGCTCGAG-ACGCCTGTTTGTGCGG	XhoI
257	Forward	CGCGGATCCCATATG-GCGGTTTCTTTCTCTG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GCGCGTGAATATCGCG	XhoI
258	Forward	AAAAAAGAATTC-GATTATTTCTGGTGGATTGTTGCGTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
258a	Forward	AAAAAAGAATTC-GCGAAGGCGGTGGCGCAAGGCGA	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
259	Forward	CGCGGATCCCATATG-GAAGAGCTGCCTCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GGCTTTTCCGGCGTTT	XhoI
260	Forward	CGCGGATCCCATATG-GGTGCGGGTATGGT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AACAGGGGCGACACCCT	XhoI
261	Forward	AAAAAAGAATTC-CAAGATACAGCTCGGGCATTTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCAACAAGCCTTGGTCACT	Pst I
263	Forward	CGCGGATCCCATATG-GCACGTTTAACCGTA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GGCGTAAGCCTGCAATT	XhoI
264	Forward	AAAAAAGGTACC-GCCGACGCAGTGGTCAAGGCAGAA	Kpn I
	Reverse	AAACTGCAG-TCAGCCGGCGGTCAATACCGCCCCG	Pst I
265	Forward	AAAAAAGAATTC-GCGGAGGTCAAGAGAAGGTGTTTG	Eco RI
	Reverse	AAAAAACTGCAG-TTACGAATACGTCGTCAAATGGG	Pst I
266	Forward	AAAGAATTC-CTCATCTTTGCCAACGCCCCCTTC	Eco RI
	Reverse	AAACTGCAG-CTATTCCTGTTGCGCGTGTGCCA	Pst I
267	Forward	AAAGAATTC-TTCTTCCGATTTCGATGTTAATCG	Eco RI
	Reverse	AAACTGCAG-TTAGTAAAAACCTTTCTGCTTGGC	Pst I
269	Forward	AAAGAATTC-TGCAAACCTTGCGCCACGTGCCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
269a	Forward	AAAAAAGAATTC-GACTTTATCCAAAACACGGCTTCGCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
270	Forward	AAAGAATTC-GCCGTCAAGCTCGTTTTGTGCAATG	Eco RI
	Reverse	AAACTGCAG-TTATTCGGCGGTAAATGCCGTCTG	Pst I
271	Forward	CGCGGATCCCATATG-CCTGTGTGCAGCTCGAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCCCAGCCCCGTGGAG	XhoI

272	Forward	AAAGAATTC-ATGACCGCAAAGGAAGAACTGTTTCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAGCAGTTCCAAATCGGGGCT	Pst I
273	Forward	AAAGAATTC-ATGAGTCTTCAGGCGGTATTTATATACCC	Eco RI
	Reverse	AAACTGCAG-TTACGCGTAAGAAAAAACTGC	Pst I
274	Forward	CGCGGATCCCATATG-ACAGATTTGGTTACGGAC	BamHI-
	Reverse	CCCGCTCGAG-TTTGCTTTCAGTATTATTGAA	NdeI
276	Forward	AAAAAAGAATTC- ATGATTTTGCCGTCGTCATCACGATGATGCG	XhoI
	Reverse	AAAAAACTGCAG-CTACACCACCATCGGCGAATTTATGGC	Eco RI
277	Forward	AAAAAAGAATTC-ATGCCCCGCTTTGAGGACAAGCTCGTAGG	Pst I
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Eco RI
277a	Forward	AAAAAAGAATTC-GGGGCGGCGGCTGGGTTGGACGTAGG	Pst I
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Eco RI
278	Forward	AAAAAAGGTACC-GTCAAAGTTGTATTAATCGGGCCTTTGCC	Pst I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Kpn I
278a	Forward	AAAAAAGAATTC-AAAACTCTCCTAATTCGTCATAGTCG	Pst I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Eco RI
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT	Pst I
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA	BamHI-
280	Forward	AAAAAAGGTACC-GCCCCCTGCCGTTGTAACCAG	NdeI
	Reverse	AAAAAACTGCAG-TTATTGCTTCATCGCGTTGGTCAAGGC	XhoI
281	Forward	AAAAAAGAATTC-GCACCCGTCGGCGTATTCCTCGTCATGCG	Kpn I
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Pst I
281a	Forward	AAAAAAGAATTC-TCCTACCACATCGAAATTCCTTCCGG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
282	Forward	AAAAAAGAATTC-CTTTACCTTGACCTGACCAACGGGCACAG	Xba I
	Reverse	AAAAAACTGCAG-TCAACCTGCCAGTTGCGGGAATATCGT	Eco RI
283	Forward	CGCGGATCCCATATG-GCCGTCTTTACTTGGAAG	Pst I
	Reverse	CCCGCTCGAG-ACGGCAGTATTTGTTTACG	BamHI-
284	Forward	CGCGGATCCCATATG-TTTGCCTGCAAAAGAATCG	NdeI
	Reverse	CCCGCTCGAG-CCGACTTTGCAAAAACTG	XhoI
286	Forward	CGCGGATCCCATATG-GCCGACCTTTCCGAAAA	BamHI-
	Reverse	CCCGCTCGAG-GAAGCGCGTTCCCAAG	NdeI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG	XhoI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC	EcoRI-
288	Forward	CGCGGATCCCATATG-CACACCGGACAGG	NheI
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	XhoI
290	Forward	CGCGGATCCCATATG-GCGGTTTGGGGCGGA	BamHI-

	Reverse	CCCGCTCGAG-TCGGCGCGGCGGGC	NdeI
292	Forward	CGCGGATCCCATATG-TGCGGGCAAACGCC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTGATTTTTGCGGATGATT	NdeI
294	Forward	AAAAAAGAATTC-GTCTGGTCGATTCGGGTTGTCAGAAC	XhoI
	Reverse	AAAAAACTGCAG-TTACCAGCTGATATAAAACATCGCTTT	Eco RI
295	Forward	CGCGGATCCCATATG-AACCGGCCGGCCTCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CGATATTTGATTCCGTTGC	NdeI
297	Forward	AAAAAAGAATTC-GCATACATTGCTTCGACAGAGAG	XhoI
	Reverse	AAAAAACTGCAG-TCAATCCGATTGCGACACGGT	Eco RI
298	Forward	AAAAAAGAATTC-CTGATTGCCGTGTGGTTCAGCCAAAACCC	Pst I
	Reverse	AAAAAACTGCAG-TCATGGCTGTGTACTTGATGGTTGCGT	Eco RI
299	Forward	CGCGGATCCGCTAGC-CTACCTGTGCCTCCG	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-TTGCCTGATTGCAGCGG	NheI
302	Forward	AAAAAAGAATTC-ATGAGTCAAACCGATACGCAACG	XhoI
	Reverse	AAAAAACTGCAG-TTAAGGTGCGGGATAGAATGTGGGCGC	Eco RI
305	Forward	AAAAAAGGTACC-GAATTTTACCGATTTCAGCACCGGA	Pst I
	Reverse	AAAAAACTGCAG-TCATTCCCACTTATCCAGCCTGACAG	Kpn I
305a	Forward	AAAAAAGGTACC-TCCCGTTCGGGCAGTACGATTATGGG	Pst I
	Reverse	AAAAAACTGCAG-TTACAAACCGACATCATGCAGGGTGAA	Kpn I
306	Forward	CGCGGATCCCATATG-TTTATGAACAAATTTTCCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCGCATCGGCAGAC	NdeI
308	Forward	CGCGGATCCCATATG-TTAAATCGGGTATTTTATC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATCCGCCATTCCCTGC	NdeI
311	Forward	AAAAAAGGTACC-ATGTTCAGTTTTGGCTGGGTGTTT	XhoI
	Reverse	AAACTGCAG-ATGTTTCATATTCCCTGCCTTCGGC	Kpn I
312	Forward	AAAAAAGGTACC-ATGAGTATCCCATCCGGCGAAATT	Pst I
	Reverse	AAACTGCAG-TCAGTTTTTCATCGATTGAACCGG	Kpn I
313	Forward	AAAAAAGAATTC-ATGGACGACCCGCGCACCTACGGATC	Pst I
	Reverse	AAAAAACTGCAG-TCAGCGGCTGCCGCCGATTTTGCT	Eco RI
401	Forward	CGCGGATCCCATATG-AAGGCGGCAACACAGC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCTTACGTTTTTCAAAGCC	NdeI
402	Forward	AAAAAAGAATTC-GTGCCTCAGGCATTTTCATTTACCCTTGC	XhoI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
402a	Forward	AAAAAAGAATTC-AGGCTGATTGAAAACAAACACGG	Xba I
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG	Xba I
			BamHI-
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG	NdeI
			XhoI

501	Forward	CGCGGATCCCATATG-GCAGGCGGAGATGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGTGTGATGTTACCCC	XhoI
502	Forward	CGCGGATCCCATATG-GTAGACGCGCTTAAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCTGCATGGCGGCG	XhoI
503	Forward	CGCGGATCCCATATG-TGTTGCGGGAAAGGCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGCGCATTCCTCGCA	XhoI
504	Forward	CGCGGATCCCATATG-AGCGATATTGAAGTGACG	BamHI- NdeI
	Reverse	GCCCAAGCTT-TGATTCAAGTCCTTGCCG	HindIII
505	Forward	CGCGGATCCCATATG-TTTCGTTTACAATTCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGTTTTATAGCGG	XhoI
510	Forward	CGCGGATCCCATATG-CCTTCGCGGACAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCACTGGCAGCG	XhoI
512	Forward	CGCGGATCCCATATG-GGACATGAAGTAACGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGAATAGCCTTTGACG	XhoI
515	Forward	CGCGGATCCCATATG-GAGGAAATAGCCTTCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATGCCGCAAAGCATC	XhoI
516	Forward	CGCGGATCCCATATG-TGTACGTTGATGTTGTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCGGGCGGCATC	XhoI
517	Forward	CGCGGATCCCATATG-GGTAAAGGTGTGGAAATA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGCGCCCAGCCGT	XhoI
518	Forward	AAAGAATTC-GCTTTTTTACTGCTCCGACCGGAAGG	Eco RI
	Reverse	AAACTGCAG-TCAAATTCAGACTCTGCCAC	Pst I
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC	XhoI
520	Forward	CGCGGATCCCATATG-CCTGCGCTTCTTTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATTTACATTTAGTCGGC	XhoI
521	Forward	CGCGGATCCCATATG-GCCAAAATCTATACCTGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATACGCCCCAGTTCC	XhoI
522	Forward	CGCGGATCCCATATG-ACTGAGCCGAAACAC	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTCTGATTTCAAATCGGCA	HindIII
523	Forward	CGCGGATCCCATATG-GCTCTGCTTTCCGCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-AGGGTGTGTGATAATAAGAAG	XhoI
525	Forward	CGCGGATCCCATATG-GCCGAAATGGTTCAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCCGTGCATATCATAAA	XhoI
527	Forward	AAAGAATTC-TTCCCTCAATGTTGCCGTTTTTCG	Eco RI
	Reverse	AAACTGCAG-TTATGCTAAACTCGAAACAAATTC	Pst I
529	Forward	CGCGGATCCGCTAGC-TGCTCCGGCAGCAAAAC	BamHI- NheI
	Reverse	GCCCAAGCTT-ACGCAGTTCGGAATGGAG	HindIII
530	Forward	CGCGGATCCCATATG-AGTGCGAGCGCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGACCGACTGATTCCG	XhoI
531	Forward	AAAAAAGAATTC-TATGCCGCCGCTACCAAATCTACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACAGCGCCGTGCCGACGACAAG	Pst I
532	Forward	AAAAAAGAATTC-ATGAGCGGTCAGTTGGGCAAAGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTCCAAGTGGTCGGTATCAAA	Pst I
532a	Forward	AAAAAAGAATTC-TTGGGTGTCGCGTTTGAGCCGGAAGT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTCCAAGTGGTCGGTATCAAA	Pst I
535	Forward	AAAGAATTC-ATGCCCTTTCCCGTTTTTCAGAC	Eco RI
	Reverse	AAACTGCAG-TCAGACGACCCCGCCTTCCCC	Pst I
537	Forward	CGCGGATCCCATATG-CATACCCAAAACCAATCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCCTGCAAATAAAGGGTT	XhoI
538	Forward	CGCGGATCCCATATG-GTCGAGCTGGTCAAAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCATTTCGGTTTCGTC	XhoI
539	Forward	CGCGGATCCGCTAGC-GAGGATTTGCAGGAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TACCAATGTCGGCAAATC	XhoI
542	Forward	AAAGAATTC-ATGCCGTCTGAAACCGTGTC	Eco RI
	Reverse	AAACTGCAG-TTACCGCGAACCGGTCAGGAT	Pst I
543	Forward	AAAAAAGAATTC-GCCTTCGATGGCGACGTTGTAGGTAC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
543a	Forward	AAAAAAGAATTC-GGCAAACTCGTCATGAATTTGC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
544	Forward	AAAGAATTC-GCGCCCGCCTTCTCCCTGCCCCGACCTGCACGG	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
544a	Forward	AAAAAAGAATTC- GCAAATGACTATAAAAAACAAAACTTCCAAGTACTTGC	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
547	Forward	AAAGAATTC-ATGTTTCGTAGATAACGGATTTAATAAAAC	Eco RI
	Reverse	AAACTGCAG-TTAACAACAAAAACAAACCGCTT	Pst I
548	Forward	AAAGAATTC-GCCTGCAAACCTCAAGACAACAGTGCGGC	Eco RI



	Reverse	AAACTGCAG-TCAGAGCAGGGTCCTTACATCGGC	Pst I
550	Forward	AAAAAAGTCGAC- ATGATAACGGACAGGTTTCATCTCTTTCATTTTCC	Sal I
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAATCCCC	Pst I
550a	Forward	AAAAAAGAATTC-GTAAATCACGCCTTTGGAGTCGCAAACGG	Eco RI
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAATCCCC	Pst I
552	Forward	AAAAAAGAATTC-TTGGCGCGTTGGCTGGATAC	Eco RI
	Reverse	AAACTGCAG-TTATTTCTGATGCCTTTTCCCAAC	Pst I
554	Forward	CGCGGATCCCATATG-TCGCCCCGCGCCCAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCCCTGTCAGACAC	XhoI
556	Forward	AAAGAATTC-GCGGGCGGTTTTGTTGGACATCCCG	Eco RI
	Reverse	AAACTGCAG-TTAACGGTGCGGACGTTTCTGACC	Pst I
557	Forward	CGCGGATCCCATATG-TGCGGTTTCCACCTGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCCGCCTTCAGAAAGG	XhoI
558	Forward	AAAGAATTC-GAGCTTTATATGTTTCAACAGGGGACGGC	Eco RI
	Reverse	AAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
558a	Forward	AAAAAAGAATTC-ATTAGATTCTATCGCCATAAACAGACGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
560	Forward	AAAAAAGAATTC- TCGCCTTTCCGGGACGGGGCGCACAAAGATGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGCGGTTTTCAGACGGCATTTTGGC	Pst I
561	Forward	CCGGAATTCTACATATG-ATACTGCCAGCCCGT	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCAAGCTTTCTTCAGATG	XhoI
562	Forward	CGCGGATCCCATATG-GCAAGCCCGTCGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGACCAACTCCAACCTCGT	XhoI
565	Forward	CGCGGATCCCATATG-AAGTCGAGCGCGAAATAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCATTGATCGGCGGC	XhoI
566	Forward	CGCGGATCCCATATG-GTCGGTGGCGAAGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCATGGGCGAAGTCA	XhoI
567	Forward	CCGGAATTCTACATATG-AGTGCGAACATCCTTG	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCCCCGACACCCTCG	XhoI
568	Forward	CGCGGATCCCATATG-CTCAGGGTCAGACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGCGGCGTTTCAG	XhoI
569	Forward	AAAAAAGAATTC-CTGATTGCCTTGTGGGAATATGCCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATGCATAGACGCTGATAACGGCAAT	Pst I
570	Forward	CGCGGATCCCATATG-GACACCTTCCAAAAAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGGCGTTTCATTCTTT	XhoI

571	Forward	AAAAAAGAATTC- ATGGGTATTGCCGGCGCCGTAAATGTTTTGAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATGGCCGACGCGCGGCTACCTGACG	Pst I
572	Forward	CGCGGATCCCATATG-GCGCAAAAAGGCAAAACC	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-GCGCAGTGTGCCGATA	BamHI- NdeI XhoI
573	Forward	CGCGGATCCCATATG-CCCTGTTTGTGCCG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-GACGGTGTTCATTTCCGC	BamHI- NdeI XhoI
574	Forward	CGCGGATCCCATATG-TGTTTGC CGCCCGC	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AACTTCGATTTTATTCCGGG	BamHI- NdeI XhoI
575	Forward	CGCGGATCCCATATG-GTTTCGGGCGAGG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-CATTCCGAATCTGAACAG	BamHI- NdeI XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC	BamHI- NdeI XhoI
577	Forward	CGCGGATCCCATATG-GAAAGGAACGGTGTATTT	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AGGCTGTTTGGTAGATTCG	BamHI- NdeI XhoI
578	Forward	CGCGGATCCCATATG-AGAAGGTTTCGTACAG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-GCCAACGCCTCCACG	BamHI- NdeI XhoI
579	Forward	CGCGGATCCCATATG-AGATTGGGCGTTTCCAC	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AGAATTGATGATGTGTATGT	BamHI- NdeI XhoI
580	Forward	CGCGGATCCCATATG-AGGCAGACTTCGCCGA	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-CACTTCCCCCGAAGTG	BamHI- NdeI XhoI
581	Forward	CGCGGATCCCATATG-CACTTCGCCCAGC	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-CGCCGTTTGGCTTTGG	Eco RI
582	Forward	AAAAAAGAATTC-TTTGGAGAGACCGCGCTGCAATGCGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGATGCCGTCCCAGTCGTTGAA	Eco RI
583	Forward	AAAAAAGAATTC-ACTGCCGGCAATCGACTGCATAATCG	Pst I
	Reverse	AAAAAACTGCAG-TTAACGGAGGTCAATATGATGAAATTG	Eco RI
584	Forward	AAAAAAGAATTC- GCGGCTGAAGCATTGAATTACAATATTGTC	Pst I
	Reverse	AAAAAACTGCAG-TCAGAACTGAACCGTCCCATTGACGCT	Eco RI
585	Forward	AAAAAAGGTACC-TCTTTCTGGCTGGTGCAGAACACCCTTGC	Pst I
	Reverse	AAAAAACTGCAG-TCAGTTCGCACTTTTTTCTGTTTTGGA	BamHI- NdeI XhoI
586	Forward	CGCGGATCCCATATG-GCAGCCCATCTCG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-TTTCAGCGAATCAAGTTTC	BamHI-
587	Forward	CGCGGATCCCATATG-GACCTGCCCTTGACGA	

	Reverse	CCCGCTCGAG-AAATGTATGCTGTACGCC	NdeI
			XhoI
588	Forward	AAAAAAGAATTC-GCCGTCCTGACTTCCTATCAAGAACCAGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTGTTTTTGGGCAGTTTCACTTC	Pst I
589	Forward	AAAAAAGAATTC- ATGCAACAAAAAATCCGTTTCCAAATCGAAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAATCGATTTTACCCGTTTCAGGCG	Pst I
590	Forward	AAAAAAGAATTC-ATGAAAAAACCTTTGATTTCAGTTGCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCTGCGGCTCTGAAACCAT	Pst I
591	Forward	AAAAAAGAATTC-CACTACATCGTTGCCAGATTGTGCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAACCGAGCAGCCGGGTAACGTCGTT	Pst I
592a	Forward	AAAAAAGAATTC-CGCGATTACACCGCCAAGCTGAAAATGGG	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAAACGTCGGATTTGATACG	Pst I
593	Forward	CGCGGATCCGCTAGC-CTTGAACCTGAACGGACTC	BamHI- NheI
	Reverse	CCCGCTCGAG-GCGGAAGCGGACGATT	XhoI
594a	Forward	AAAAAAGAATTC-GGTAAGTTCGCCGTTTCAGGCCTTTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCGCCGTTTCTGACACTCGCG	Pst I
595	Forward	AAAAAAGAATTC-TGCCAGCCGCCGGAGGCGGAGAAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCAAGCCGAGTATGCCGCG	Pst I
596	Forward	CGCGGATCCCATATG-TCCCAACAATACGTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCGTTACCGGTTTGT	XhoI
597	Forward	CGCGGATCCCATATG-CTGCTTCATGTCAGC	BamHI- NdeI
	Reverse	GCCCAAGCTT-ACGTATCCAGCTCGAAG	HindIII
601	Forward	CGCGGATCCCATATG-ATATGTTCCCAACCGGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAACAATCCTCAGGCAC	XhoI
602	Forward	CGCGGATCCGCTAGC-TTGCTCCATCAATGC	BamHI- NheI
	Reverse	CCCGCTCGAG-ATGCAGCTGCTAAAAGCG	XhoI
603	Forward	AAAAAAGAATTC-CTGTCCTCGCGTAGGCGGGGACGGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAGATGCCGGCAAGTTCGGC	Pst I
604	Forward	CGCGGATCCGCTAGC-CCCGAAGCGCACTT	BamHI- NheI
	Reverse	CCCGCTCGAG-GACGGCATCTGCACGG	XhoI
606a	Forward	AAAAAAGAATTC-CGCGAATACCGCGCCGATGCGGGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTAAAGCGATTTGAGGCGGGCGATACG	Pst I
607	Forward	AAAAAAGAATTC-ATGCTGCTCGACCTCAACCGCTTTTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCCTTATGCGATCTGAC	Pst I
608	Forward	AAAAAAGAATTC-ATGTCCGCCCTCCTCCCATCATCAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGTCTATCCAAATGTCGCGTTC	Pst I
609	Forward	CGCGGATCCCATATG-GTTGTGGATAGACTCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-CTGGATTATGATGTCTGTC	XhoI
610	Forward	CGCGGATCCCATATG-ATTGGAGGGCTTATGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCTTCAACATCTTTGCC	XhoI
611	Forward	CGCGGATCCCATATG-CCGTCTCAAAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGACTTTGAACGCGCAA	XhoI
613	Forward	CGCGGATCCCATATG-TCGCGTTCGAGCCG3	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCCTGTAAAATAAGCGGC	XhoI
614	Forward	CGCGGATCCCATATG-TCCGTCGTGAGCGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCATACTGCGGCGTTC	XhoI
616	Forward	AAAAAAGAATTC-ATGTCAAACACAATCAAAATGGTTGTTCG	Eco RI
	Reverse	AAAAAATCTAGA-TTAGTCCGGGCGGCAGGCAGCTCG	Xba I
619a	Forward	AAAAAAGAATTC-GGGCTTCTCGCCGCTCGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTTTGTGTTTAAAACGAGATA	Pst I
622	Forward	CGCGGATCCCATATG-GCCGCCCTGCCTAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGTCCAAATGATAAATCTG	XhoI
624	Forward	CGCGGATCCCATATG-TCCCCGCGCTTTTACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGATTCCGGGCCTGCGC	XhoI
625	Forward	CGCGGATCCCATATG-TTTGCAACCAGGAAAATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCAAAATTACCGCCTT	XhoI
627a	Forward	AAAAAAGAATTC-AAAGCAGGCGAGGCAGGCGCGCTGGG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGAATGAAACAGGGTACCCGTCATCAAGGC	Pst I
628	Forward	AAAAAAGGTACC-GCCTTACAAACATGGATTTTGC GTTC	Kpn I
	Reverse	AAAAAACTGCAG-CTACGCACCTGAAGCGCTGGCAA	Pst I
629a	Forward	AAAAAAGAATTC-GCCACCTTTATCGCGTATGAAAACGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACAACACCGCCGTCCGGTTCAAACC	Pst I
630a	Forward	AAAAAAGAATTC-GCGGCTTTGGGTATTTCTTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGAGACTTCGCCAATGGAGCCGGG	Pst I
635	Forward	AAAAAAGAATTC- ATGACCCAGCGACGGGTCGGCAAGCAAAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATCCACTATAATCCTGTTGCT	Pst I
638	Forward	AAAAAAGAATTC-ATGATTGGCGAAAAGTTTATCGTAGTTGG	Eco RI
	Reverse	AAAAAACTGCAG-TCACGAACCGATTATGCTGATCGG	Pst I
639	Forward	CGCGGATCCCATATG-ATGCTTTATTTTGTTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCGCGGCTGCCGAC	XhoI
642	Forward	CGCGGATCCCATATG-CGGTATCCGCCGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGATTGCGGGGCATTA	XhoI

643	Forward	CGCGGATCCCATATG-GCTTCGCCGTCGGCAG	BamHI- NdeI XhoI Eco RI
	Reverse	CCCGCTCGAG-AACCGAAAAACAGACCGC	
644	Forward	AAAAAAGAATTC- ATGCCGTCTGAAAGGTCGGCGGATTGTTGCC	Pst I
	Reverse	AAAAAATCTAGA-CTACCCGCAATATCGGCAGTCCAATAT	Eco RI
645	Forward	AAAAAAGAATTC-GTGAACAGAGCAACACGTTAAATCG	Pst I
	Reverse	AAAAAACTGCAG-CTACGAGGAAACCGAAGACCAGGCCGC	Eco RI
647	Forward	AAAAAAGAATTC-ATGCAAAGGCTCGCCGCAGACGG	Pst I
	Reverse	AAAAAACTGCAG-TTAGATTATCAGGGATATCCGGTAGAA	Eco RI
648	Forward	AAAAAAGAATTC- ATGAACAGGCGCGACGCGCGGATCGAACG	Pst I
	Reverse	AAAAAACTGCAG-TCAAGCTGTGTGCTGATTGAATGCGAC	Eco RI
649	Forward	AAAAAAGAATTC-GGTACGTCAGAACCCGCCACCG	Pst I
	Reverse	AAAAAACTGCAG-TTAACGGCGGAAACTGCCGCCGTC	Eco RI
650	Forward	AAAAAAGAATTC-ATGTCCAAACTCAAACCATCGC	Pst I
	Reverse	AAAAAACTGCAG-TCAGACGGCATGGCGGTCTGTTTT	Kpn I
652	Forward	AAAAAAGGTACC- GCTGCCGAAGACTCAGGCCTGCCGCTTTACCG	Pst I
	Reverse	AAAAAACTGCAG-TTATTTGCCCAGTTGGTAGAATGCGGC	Eco RI
653	Forward	AAAAAAGAATTC-GCGGCTTTGCCGGTAATTTTCATCGG	Pst I
	Reverse	AAAAAACTGCAG-CTATGCCGGTCTGGTTGCCGGCGGCGA	Eco RI
656a	Forward	AAAAAAGAATTC-CGGCCGACGTCGTTGCGTCCTAAGTC	Pst I
	Reverse	AAAAAACTGCAG-CTACGATTTCCGCGATTTCACATCGT	Eco RI
657	Forward	AAAAAAGAATTC-GCAGAATTTGCCGACCGCCATTTGTGCGC	Pst I
	Reverse	AAAAAACTGCAG-TTATAGGGACTGATGCAGTTTTTTTGC	BamHI- NdeI XhoI Eco RI
658	Forward	CGCGGATCCCATATG-GTGTCCGGAATTGTG	
	Reverse	CCCGCTCGAG-GGCAGAATGTTTACCGTT	
661	Forward	AAAAAAGAATTC- ATGCACATCGGCGGCTATTTTATCGACAACCC	Pst I
	Reverse	AAAAAACTGCAG-TCACGACGTGTCTGTTCCGCGTCGGGC	BamHI- NdeI XhoI Eco RI
663	Forward	CGCGGATCCCATATG-TGTATCGAGATGAAATT	
	Reverse	CCCGCTCGAG-GTAAAAATCGGGGCTGC	
664	Forward	CGCGGATCCCATATG-GCGGCTGGCGCGGT	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AAATCGAGTTTTACACCAC	Eco RI
665	Forward	AAAAAAGAATTC-ATGAAATGGGACGAAACGCGCTTCGG	Pst I
	Reverse	AAAAAACTGCAG-TCAATCCAAAATTTTGCCGACGATTTC	Eco RI
666	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Eco RI
667	Forward	AAAAAAGAATTC- CCGCATCCGTTTGATTTCATTTCGTATTCGTCCG	Pst I
	Reverse	AAAAAACTGCAG-TTAATGACACAATAGGCGCAAGTC	

669	Forward	AAAAAAGAATTC-ATGCGCCGCATCATTAAAAAACACCAGCC	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTATCCGTTTGATGTCGGC	Pst I
670a	Forward	AAAAAAGAATTC-A AAAACGCTTCGGGCGTTTCGTCTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTAGGAGCTTTTGGAAACGCGTCGGACTGGC	Pst I
671	Forward	CGCGGATCCCATATG-ACCAGCAGGGTAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAACTATAAAAACGCAAG	XhoI
672	Forward	CGCGGATCCCATATG-AGGAAAATCCGCACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGGATAGGCGGTTG	XhoI
673	Forward	AAAAAAGAATTC-ATGGATATTGAAACCTTCCTTGCAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAACCCAGCTCGCGCAGGAA	Pst I
674	Forward	AAAAAAGAATTC-ATGAAAACAGCCCGCCGCGTTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAACGGCGTTTGGGCTCGTCGGG	Pst I
675	Forward	CGCGGATCCCATATG-AACACCATCGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCTTCGTCTTCAAACCTGT	XhoI
677a	Forward	AAAAAAGAATTC-AGACGGCATTCCCGATCAGTCGATTTTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGTATGCGCGAAATCGACCGCCGC	Pst I
680	Forward	CGCGGATCCGCTAGC-ACGAAGGGCAGTTCGG	BamHI- NheI
	Reverse	CCCGCTCGAG-CATCAAAAACCTGCCGC	XhoI
681	Forward	AAAAAAGAATTC-ATGACGACGCCGATGGCAATCAGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCGTCTTCCGCAAAAAACAGC	Pst I
683	Forward	CGCGGATCCCATATG-TGCAGCACACCGGACAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAGTTTTTTTCCGCATACG	XhoI
684	Forward	CGCGGATCCCATATG-TGCGGTACTGTGCAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTCGACCATCTGTTGCG	XhoI
685	Forward	CGCGGATCCCATATG-TGTTTGCTTAATAATAAACATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCA	XhoI
686	Forward	CGCGGATCCCATATG-TGCGGCGGTTTCGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGATTCTGATGAAG	XhoI
687	Forward	CGCGGATCCCATATG-TGCGACAGCAAAGTCCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCGCGGCTTTTTGTT	XhoI
690	Forward	CGCGGATCCCATATG-TGTTCTCCGAGCAAAGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TATTCGCCCCGTGTTTGG	XhoI
691	Forward	CGCGGATCCCATATG-GCCACGGCTTATATCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGGCAGGAAGAAAG	XhoI

694	Forward	CGCGGATCCCATATG-TTGGTTCCGCATCCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCTGCGTCGGTGCGGT	XhoI
695	Forward	CGCGGATCCCATATG-TTGCCTCAAACCTCGTCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCACACGGCT	XhoI
696	Forward	CGCGGATCCCATATG-TTGGGTGCCGGCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGATTGCCGCAATGATG	XhoI
700a	Forward	AAAAAAGAATTC-GCATCGACAGACGGTGTGTCGTGGAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCTACCGGCACGACTTCCAAACC	Pst I
701	Forward	CGCGGATCCCATATG-AAGACTTGTGTGGATACTTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGACAACAGCCTC	XhoI
702	Forward	AAAAAAGAATTC-ATGCCGTGTTCCAAAGCCAGTTGGATTTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACCCCATTCACCCGGAGAACCGA	Pst I
703	Forward	CGCGGATCCGCTAGC-CAAACGCTGGCAACCG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTTGCAGGTTTGATGTTTG	XhoI
704a	Forward	AAAAAAGAATTC-GCTTCTACCGGTACGCTGGCGCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGTTTTGCCGGATAATATGGCGGGTGCG	Pst I
707	Forward	CGCGGATCCGCTAGC-GAAATTATTAACGATGCAGA	BamHI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGA	XhoI
708	Forward	CGCGGATCCGCTAGC-CCTTTTAAGCCATCCAAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TTGACCGGTGAGGACG	XhoI
710	Forward	CGCGGATCCCATATG-GAAACCCACGAAAAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGGTTTCGGTCAG	XhoI
714	Forward	CGCGGATCCCATATG-AGCTATCAAGACATCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGTAGGTAAATCGGAT	XhoI
716	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTTGCC	XhoI
718	Forward	CGCGGATCCCATATG-GAGCCGATAATGGCAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGCGGGCATGGTCTTGTC	XhoI
720	Forward	CGCGGATCCCATATG-AGCGGATGGCATACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTTGCATAGCTGTTGACCA	XhoI
723	Forward	CGCGGATCCCATATG-CGACCCAAGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATGCGAATCCGCCGCC	XhoI

725	Forward	CGCGGATCCCATATG-GTGCGCACGGTTAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTATCCTTAAGGGTTA	XhoI
726	Forward	CGCGGATCCCATATG-ACCATCTATTTCAAAAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCGATGTTTAGCGTCC	XhoI
728	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	XhoI
729	Forward	CGCGGATCCCATATG-TGCACCATGATTCCCCA	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTGTCGGTTTGGGTATC	HindIII
731	Forward	CGCGGATCCGCTAGC-GCCGTGCCGGAGG	BamHI- NheI
	Reverse	CCCGCTCGAG-ACGGGCGCGGCAG	XhoI
732	Forward	CCGGAATTCTACATATG-TCGAAACCTGTTTTTAAGAA	EcoRI- NdeI
	Reverse	CCCGCTCGAG-CTTCTTATCTTTTTTATCTTTC	XhoI
733	Forward	CGCGGATCCCATATG-GCCTGCGGCGGCAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGCTTGCCTCCTTTAC	XhoI
734	Forward	CGCGGATCCCATATG-GCCGATACTTACGGCTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGATTTTGAATCAAAGAG	XhoI
735	Forward	CGCGGATCCCATATG-AAGCAGCAGGCGGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTCCGTAGCCGAGGG	XhoI
737	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	XhoI
739	Forward	CGCGGATCCCATATG-GCAAAAAAACCGAACA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGAGTTTGTGCGAGAATT	XhoI
740	Forward	CGCGGATCCCATATG-GCCAATCCGCCCGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAACGCGCCAAAATAGTG	XhoI
741	Forward	CGCGGATCCCATATG-TGCAGCAGCGGAGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTGGCGGCAAGGC	XhoI
743	Forward	CGCGGATCCCATATG-GACGGTGTGTGCCTGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTACGGATCAAATTGACG	XhoI
745	Forward	CGCGGATCCCATATG-TTTTGGCAACTGACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAATCAGATGCCTTTAGG	XhoI
746	Forward	CGCGGATCCCATATG-TCCGAAAACAAACAAAAC	BamHI-



	Reverse	CCCGCTCGAG-TTCATTCGTTACCTGACC	NdeI
747	Forward	CCGGAATTCTAGCTAGC-CTGACCCCTTGGG	XhoI
	Reverse	GCCCAAGCTT-TTTTGATTTTAATTGACTATAGAAC	EcoRI-
749	Forward	CGCGGATCCCATATG-TGCCAGCCGCCG	NheI
	Reverse	CCCGCTCGAG-TTCAAGCCGAGTATGC	HindIII
750	Forward	CGCGGATCCCATATG-TGTTCCGCCGAACCTG	BamHI-
	Reverse	CCCGCTCGAG-CTTTTCCCCGCCGCAA	NdeI
758	Forward	CGCGGATCCCATATG-AACAATCTGACCGTGT	XhoI
	Reverse	CCCGCTCGAG-TGGCTCAATCCTTTCTGC	BamHI-
759	Forward	CGCGGATCCGCTAGC-CGCTTCACACACACCAC	NdeI
	Reverse	CCCGCTCGAG-CCAGTTGTAGCCTATTTTG	XhoI
763	Forward	CGCGGATCCCATATG-CTGCCTGAAGCATGGCG	NheI
	Reverse	CCCGCTCGAG-TTCCGCAAATACCGTTTCC	XhoI
764	Forward	CGCGGATCCCATATG-TTTTCTCCGCCCTGA	BamHI-
	Reverse	CCCGCTCGAG-TCGCTCCCTAAAGCTTTC	NdeI
765	Forward	CGCGGATCCCATATG-TTAAGATGCCGTCCG	XhoI
	Reverse	CCCGCTCGAG-ACGCCGACGTTTTTTATTA	BamHI-
767	Forward	CGCGGATCCCATATG-CTGACGGAAGGGGAAG	NdeI
	Reverse	CCCGCTCGAG-TTTCTGTACAGCAGGGG	XhoI
768	Forward	CGCGGATCCCATATG-GCCCCGCAAAAACCCG	BamHI-
	Reverse	CCCGCTCGAG-TTTCATCCCTTTTTTGAGC	NdeI
770	Forward	CGCGGATCCCATATG-TGCGGCAGCGGCGAA	XhoI
	Reverse	CCCGCTCGAG-GCGTTTGTGCGAGATTTTC	BamHI-
771	Forward	CGCGGATCCCATATG-TCCGTATATCGCACCTTC	NdeI
	Reverse	CCCGCTCGAG-CGGTTCTTTAGGTTTGAG	XhoI
772	Forward	CGCGGATCCCATATG-TTTGCGGCGTTGGTGG	BamHI-
	Reverse	CCCGCTCGAG-CAATGCCGACATCAAACG	NdeI
774	Forward	CGCGGATCCCATATG-TCCGTTTCACCCGTTCC	XhoI
	Reverse	CCCGCTCGAG-TCGTTTGCACGCGCT	BamHI-
790	Forward	CGCGGATCCCATATG-GCAAGAAGGTCAAAAAC	NdeI
			XhoI
			BamHI-
			NdeI

	Reverse	CCCGCTCGAG-GGCGTTGTTCCGATTTCG	XhoI
900	Forward	CGCGGATCCCATATG-CCGTCTGAAATGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATGGAAAAGTCTGTTGTC	XhoI
901	Forward	CGCGGATCCCATATG-CCCGATTTTTTCGATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATGGAACAATACCAGG	XhoI
902	Forward	CCGGAATTCTACATATG-TTGCACTTTCAAAGGATAATC	EcoRI- NdeI
	Reverse	CCCGCTCGAG-AAAAATGTACAATGGCGTAC	XhoI
903	Forward	CGGGAATTCTAGCTAGC-CAGCGTCAGCAGCACAT	EcoRI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGAA	XhoI
904	Forward	AAAAAAGGTACC-ATGATGCAGCACAATCGTTTC	Kpn I
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
904a	Forward	AAAAAAGAATTC-CGGCTCGGCATTGTGCAGATGTTGCA	Eco RI
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
905	Forward	CGCGGATCCCATATG-AACAAAATATACCGCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCACTGATAACCGACAGAT	XhoI
907	Forward	CGCGGATCCCATATG-GGCGCGCAACGTGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCCACTGCCAGCG	XhoI
908	Forward	AAAGAATTC-GCAGAGTTAGTAGGCGTTAATAAAAATAC	Eco RI
	Reverse	AAACTGCAG-TTAATATGGTTTTGTCGTTTCG	Pst I
909	Forward	CGCGGATCCCATATG-TGCGCGTGGGAAACTTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGGTTTTTGAACTTTGGTTTT	XhoI
910	Forward	AAAGAATTC-GCATTTGCCGGCGACTCTGCCGAGCG	Eco RI
	Reverse	AAACTGCAG-TCAGCGATCGAGCTGCTCTTT	Pst I
911	Forward	AAAGAATTC-GCTTTCCGCGTGGCCGGCGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-GTCGACTTATTCGGCGGCTTTTCCGC	Pst I
912	Forward	AAAAAAGAATTC- CAAATCCGTCAAAACGCCACTCAAGTATTGAG	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTCCGTCCACGCCTTTTCGC	Pst I
913	Forward	CGCGGATCCCATATG-GAAACCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGTTGTGTTCCAGGTTG	XhoI
915	Forward	CGCGGATCCCATATG-TGCCGGCAGGCGGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAAAATATAGGTATCAGG	XhoI
914	Forward	AAAGAATTC-GACAGAATCGGCGATTGGAAGCACG	Eco RI
	Reverse	AAACTGCAG-CTATATGCGCGGCAGGACGCTCAACGG	Pst I
916	Forward	CGCGGATCCCATATG-GCAATGATGGCGGCTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI

917	Forward	AAAAAAGAATTC-CCTGCCGAAAAACCGGCACCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCCCCGCCTTCACATCCTG	Pst I
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC	BamHI-
	Reverse	CCCGCTCGAG-CGGGCGGTATTTCGGG	NdeI
920	Forward	CGCGGATCCCATATG-CACCGCGTCTGGGTC	XhoI
	Reverse	CCCGCTCGAG-ATGGTGCGAATGACCGA	BamHI-
921	Forward	AAAAAAGAATTC-TTGACGGAAATCCCGTGAATCC	NdeI
	Reverse	AAAAAACTGCAG-TCATTTCAAGGGCTGCATCTTCAT	XhoI
922	Forward	CGCGGATCCGCTAGC-TGTACGGCGATGGAGGC	Eco RI
2	Reverse	CCCGCTCGAG-CAATCCCGGGCCGCC	Pst I
923	Forward	CGCGGATCCCATATG-TGTTACGCAATATTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-GGACAAGGCGACGAAG	NheI
925	Forward	CGCGGATCCCATATG-AAACAAATGCTTTTAGCCG	XhoI
	Reverse	CCCGCTCGAG-GCCGTTGCATTTGATTTC	BamHI-
926	Forward	CGCGGATCCCATATG-TGCGCGCAATTACCTC	NdeI
	Reverse	CCCGCTCGAG-TCTCGTGCGCGCCG	XhoI
927	Forward	CGCGGATCCCATATG-TGCAGCCCCGCAGC	BamHI-
	Reverse	CCCGCTCGAG-GTTTTTTGCTGACGTAGT	NdeI
929a	Forward	AAAAAAGAATTC-CGCGGTTTGCTCAAAACAGGGCTGGG	XhoI
	Reverse	AAAAAATCTAGA-TTAAGAAAGACGGAACTACTGCC	Eco RI
931	Forward	AAAAAAGAATTC-GCAACCCATGTTTTGATGGAAAC	Xba I
	Reverse	AAAAAACTGCAG-TTACTGCCCCGACAACAACGCGACG	Eco RI
935	Forward	AAAAAAGAATTC-GCGGATGCGCCCGCGATTTTGGATGACAAGGC	Pst I
	Reverse	AAAAAACTGCAG-TCAAACCGCCAATCCGCGGACAC	Eco RI
936	Forward	CGCGGATCCCATATG-GCCGCCGTCGGCGC	Pst I
	Reverse	CCCGCTCGAG-GCGTTGGACGTAGTTTTG	BamHI-
937	Forward	AAAAAAGAATTC-CCGTTTACATTCAAACCGGCGCAAC	NdeI
	Reverse	AAAAAACTGCAG-TTAAAATGTATGCTGTACGCCAAA	XhoI
939a	Forward	AAAAAAGAATTC-GGTTCCGGCAGCTGTGATGAAACC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGCAAACCTTGGATAAAGTTGGC	Pst I
950	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	Eco RI
	Reverse	CCCGCTCGAG-TTAGAACCGCATTGTC	BamHI-
953	Forward	CGCGGATCCCATATG-GCCACCTACAAAGTGGAC	NdeI
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	XhoI
957	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI-

	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	NdeI
958	Forward	CGCGGATCCCATATG-GCCGATGCCGTTGCG	XhoI
	Reverse	GCCCAAGCTT-GGGTCGTTTGTGTCGTC	BamHI-
959	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	NdeI
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	HindIII
961	Forward	CGCGGATCCCATATG-GCCACAAGCGACGACG	BamHI-
	Reverse	CCCGCTCGAG-CCACTCGTAATTGACGC	NdeI
972	Forward	AAAAAAGAATTC- TTGACTAACAGGGGGGAGCGAAATTA AAAAC	XhoI
	Reverse	AAAAAATCTAGA-TTAAAAATAATCATAATCTACATTTTG	Eco RI
973	Forward	AAAAAAGAATTC-ATGGACGGCGCACAACCGAAAAC	Xba I
	Reverse	AAAAAACTGCAG-TTACTTCACGCGGGTCGCCATCAGCGT	Eco RI
982	Forward	CGCGGATCCCATATG-GCAGCAAAAGACGTAC	Pst I
	Reverse	CCCGCTCGAG-CATCATGCCGCCCATCC	BamHI-
983	Forward	CGCGGATCCCATATG-TTAGCTGTTGCAACAACAC	NdeI
	Reverse	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
987	Forward	CGCGGATCCCATATG-CCCCACTGGAAGAAC	BamHI-
	Reverse	CCCGCTCGAG-TAATAAACCTTCTATGGGC	NdeI
988	Forward	CGCGGATCCCATATG-TCTTTAAATTTACGGGAAAAAG	XhoI
	Reverse	GCCCAAGCTT-TGATTTGCCTTTCCGTTTT	BamHI-
989	Forward	CCGGAATTCTACATATG-GTCCACGCATCCGGCTA	NdeI
	Reverse	CCCGCTCGAG-TTTGAATTTGTAGGTGTATTGC	HindIII
990	Forward	CGCGGATCCGCTAGC-TTCAGAGCTCAGCTT	EcoRI-
	Reverse	CCCGCTCGAG-AAACAGCCATTTGAGCGA	NdeI
992	Forward	CGCGGATCCCATATG-GACGCGCCCGCCCG	XhoI
	Reverse	CCCGCTCGAG-CCAAATGCCCAACCATTC	BamHI-
993	Forward	CGCGGATCCCATATG-GCAATGCTGATTGAAATCA	NdeI
	Reverse	CCCGCTCGAG-GAACACATCGCGCCCG	XhoI
996	Forward	CGCGGATCCCATATG-TGCGGCAGAAAATCCGC	BamHI-
	Reverse	CCCGCTCGAG-TCTAAACCCCTGTTTTCTC	NdeI
997	Forward	CCGGAATTCTAGCTAGC-CGGCACGCCGACGTT	XhoI
	Reverse	CCCGCTCGAG-GACGGCATCGCTCAGG	EcoRI-
			NheI
			XhoI

Underlined sequences indicate restriction recognition sites.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1>:

```
g001.seq
1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG GTGTCGGCGA ACGAGGTGTC
51  CGGCAGGGCT TCGCCCCGA TGGTGCTGGT CATCTGCCAG ACGCTGCCGA
101 AACGCGATAC TTAAACGGC TCGGTACGC ATACTTTACC GGTTCGGCG
151 ATTTTGCCGA GGTCTGCG CAGCAAATCG ACAATCATCA CGTTTCGGC
201 GCGGTTTTTC GGTCTGCTT GTAACTCGGC GCGCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301 CCGTCTGAAG CGATGTTGAG GAAGAGTCG GCGGAGAAAC ACAGCGTCCA
351 CGCGGATTGC CCGGCTTCAT CGGCAGGTG GGACAATACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 2; ORF 001.ng>:

```
g001.pep
1  MLPOGKAARR VSANEVSGRA CARMVLVICQ TLPKRDTLNG SGHTTLPVWA
51  ILPRSLRSKS TIITFSARFF GSVNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEAMLRKSS GEKHSVHAD C PASSGRWDNT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3>:

```
m001.seq
1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
51  CGGcAssCTT ss.GCTTGA yGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101 AACGCGATAC TTAAACGGT TCGGTACGC ATACTGTGCC GGTTCGGCG
151 ATTTTGCCGA GATCGTTACG CAGCAAATCG ACAATCATCA CGTTTCGGC
201 GCGGTTTTTC GGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301 CCGTCCGAAC CGATTTTGAG GAAGAGTCG GCGGAGAAAC ACAGCGTCCA
351 CGCGGATTGC CCCTCCGCAT CGGCAGGTG GGACAAGACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 001>:

```
m001.pep
1  MLPOGKAARR MSANEVCGXL XAWXVLVICQ TLPKRDTLNG SGHTTVPVWA
51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEPILRKSS GEKHSVHAD C PSASGRWDKT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 5>:

```
a001.seq
1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
51  CGGCAAGGCT TGGGCTTGA TGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101 AACGCGATAC TTAAACGGT TCGGTACGC ATACTGTGCC GGTTCGGCG
151 ATTTTGCCGA GGTCTGCG CAGCAAATCG ACAATCATCA CGTTTCGGC
201 GCGGTTTTTC GGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301 CCGTCCGAAC CGATTTTGAG GAAGAGTCG GCGGAGAAAC ACAGCGTCCA
351 CGCGGATTGC CCTTGTGCAT CGGCAGGTG GGACAAAACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 6; ORF 001.a>:

```
a001.pep
1  MLPOGKAARR MSANEVCGKA WAWMVLVICQ TLPKRDTLNG SGHTTVPVWA
51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEPILRKSS GEKHSVHAD C PASGRWDKT A*
```

m001/a001 96.2% identity over a 131 aa overlap

	10	20	30	40	50	60
m001.pep	MLPOGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGHTTVPVWAILPRSLRSKS					
a001.pep	MLPOGKAARRMSANEVCGKAWWMVLVICQTLPKRDTLNGSGHTTVPVWAILPRSLRSKS					

	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
a001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
a001.pep	PCASGRWDKTAX					
	130					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 001 shows 89.3% identity over a 131 aa overlap with a predicted ORF (ORF 001.ng) from *N. gonorrhoeae*:

m001/g001

	10	20	30	40	50	60
m001.pep	MLPQGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS					
g001	MLPQGKAARRVSAANEVSGRACARMVLVICQTLPKRDTLNGSGTHTLPVWAILPRSLRSKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIITFSAREFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
g001	TIITFSAREFFGSVCNSAARRSSCPSPKIGAVPFIGSVLMVPSEAMLRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
g001	PASSGRWDNTAX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 7>:

g003.seq

```

1  ATGGTCGTAT TCGTGGCTGA AGGCGTATTC GGTGCGCTG TTTGGGTCA
51  CTTGGTATTG CTCTTCGGTC AGGGTGC GTT TGAGTTCGGC GTCAC TCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTG CCTTGC GGTG CGGCTTTGGT
151 TTTGCCCGGC AGCGGTTCTG CCGCTTTCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAGG TAGTCCTGAT GGTATTCCTC GCGCTCGTAG
251 AAGTTTTTCA GCGGTTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGG CCGCGATGAC GGCTTTTTCG GCGGGGTCGG
351 TGTAGTACAC GCCGCTGCGG TATTGCGTGC CCGTGTCGTT ACCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAA TAATATTGCA GGATGTCGTC
451 CAGGCTGagt TTGTCGGCAT CGTaggtcac tTTGACGGTC TCGGCATGAC
501 CCGTATGGCG GTaggacact tctTCgtanc TcGGGtTTTC CGTgttGCCG
551 TTGGCgttac cGGATACCGC gtcaACCACG CCGTcgatgc gttggaAATa
601 ggCTTCCAAG ccccaaaaagc agccgccggc gaagtaa atg gtgcccgtgt
651 tcatgattGC TGa

```

This corresponds to the amino acid sequence <SEQ ID 8; ORF 003.ng>:

g003.pep

```

1  MVVFVAEGVF GRAVLGHLVL LFGQGAFFG VTRFFIRCRV EAFALRCGFG
51  FARQRFVGEA DVDVAVAVGV FNQVLMVFL GVVEVFQRFV FNNEGQLVFL
101 LLAFEGGGDD GFFGGVGVVH AAAVLRAGVV TLFVEAGRIN DAEIILQDVF

```

151 QAEFVGIVGH FDGLGMTRMA VGHFFVRVFR VAVGVTGYRV NHAVDAL EIG  
201 FQAPKAAAGE VNGARVHDC

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 9>:

m003.seq  
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA  
51 CTTGgTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCACCTCGGT  
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGCAGGG CGGTCTTGGT  
151 TTTGCCCGGC AGCGGTTCGT CAGCkTTGCG GATGTCGATG TGGCAGTAGC  
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG  
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG  
301 CTGCTCGCGT TTGAGGGCGk CGGCGATGAC GGCTTTTTCG kCGGGGTCGG  
351 TGAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG  
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC  
451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTGACGGTT TCGGCGTGCG  
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCCG  
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA  
601 GGCTTCCAAG CCCAGAAGC AGCg.CCGGC GAGGTAAATG GTGCGCGTGT  
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 10; ORF 003>:

m003.pep Length: 221  
1 MVVFVAEGIF GRAVLGNLXL LFGQGAFFFG VTRFFIRCRV EAFALRGGLG  
51 FARQRFVSXA DVDVAVAVGV FNQVVLMLVFL GIVEVFQRLV FNNEGQLVFL  
101 LLAFEGGGDD GFFXGVGVVH AAALVLTGVV ALFVEAGRIN DAEEILQDVV  
151 \*AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVDAL E I  
201 GFQAPEAAXG EVNGARVHDF \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 11>:

a003.seq  
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA  
51 CTTGGTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCACCTCGGT  
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGCAGGTG CGGTCTTGGT  
151 TTTGCCCGGC AGCGGTTCGT CGGCTTTGCG GATATCGATG TGGCAGTAGC  
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG  
251 AAGTTTTTCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG  
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTCG GCGGGGTCGG  
351 TGAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG  
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC  
451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTGACGGTT TCGGCGTGCG  
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCCG  
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA  
601 GGCTTCCAAG CCCAGAAGC AGCCGCCGGC GAGGTAGATG GTGCGCGTGT  
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 12; ORF 003.a>:

a003.pep  
1 MVVFVAEGIF GRAVLGNLVL LFGQGAFFFG VTRFFIRCRV EAFALRCGLG  
51 FARQRFVGFA DIDVAVAVGV FNQVVLMLVFL GIVEVFQRLV FNNEGQLVFL  
101 LLAFEGGGDD GFFGGGVVH AAALVLTGVV ALFVEAGRIN DAEEILQDVV  
151 \*AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVDAL E I  
201 GFQAPEAAAG EVDGARVHDF \*

m003/a003 95.9% identity over a 220 aa overlap

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXLLFGQGAFFFGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
a003	MVVFVAEGIFGRAVLGNLVLFLFGQGAFFFGVTRFFIRCRVEAFALRCGLGFARQRFVGFA					
	10	20	30	40	50	60

	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGXGDDGFFXGVGVVH					
a003	DIDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGGDDGFFGGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
a003	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDLEIGFQAPEAAAXGEVNGARVHDFX					
a003	RVAVGVAGYRVNHAVDLEIGFQAPEAAAXGEVDGARVHDFX					
	190	200	210	220		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 003 shows 88.6% identity over a 219 aa overlap with a predicted ORF (ORF 003.ng) from *N. gonorrhoeae*:

m003/g003

	10	20	30	40	50	60
m003.pep	MVFVFAEGIFGRAVLGNLXLLFGQGAFFGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
g003	MVFVFAEGVFGRAVLGHLVLLFGQGAFFGVTRFFIRCRVEAFALRCGFGFARQRFVGFA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGXGDDGFFXGVGVVH					
g003	DVDVAVAVGVFNQVVLVFLGVVEVFQRFVFNNEGQLVFLLLAFEGGDDGFFGGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
g003	AAAVLRAGVVTLFVEAGRINDAEIILQDVVQAEFVGIVGHFDGLGMTRMAVGHFFV-RVF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDLEIGFQAPEAAAXGEVNGARVHDFX					
g003	RVAVGVGTGYRVNHAVDLEIGFQAPKAAAGEVNGARVHDC					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 13>:

g004.seq

```

1  ATGgtagAAC GGCATATCCA GCATTTCGGG AACGGTCATC TTCATTGAT
51  GCGCCCATGC CAACAagtga gccAAAtgtT CGGCGGCAGG GCCTacgatT
101 TCCGCGCCGA TAAagcggcc gGTGgctTTT tcgGCataca ggcgcaTatg
151 gCCTTTGTTT ACCAgcatca cgcggtcgcg accttgaTTT TTGAACGATA
201 CTTCGCCgaT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTCAAAC CGACAAAGCC GATTTCGgga ctggtaaACA CCACGCCAAT
301 GGTgctgcg cGCAAAACCGC TGCCGATATt cgGtagcgg ccccgcgtaa
351 ttgcccggca atcttacctt ggtcggcggc ttcGtGAGC AGGGGCagtt
401 ggttgacgc gtcgcccgcg ataAAGATAT GCGGAATgct ggtCTGCATg
451 gtCAGCGGAT CGGCAACGGG tacgccgcgc gcgtctttgT CGATATTGAT
501 GTTTTCCAAA CCGATATtgT CAACGTTCGG ACGGCgACCT ACGGCTGCCA

```



```

551 ACATATATTC GGCAACAAAT ACGCCTTTTT CGCCATCCTG CTCCCAATGG
601 ACTtctACAT TGCCGTCTGC GTCGAGTTTG ACCTCGGTTT TAGCATCCAG
651 ATGCAGTTTC AATtctTCTC CGAACACGGC TTTGCGCTCG TCTGAAACAA
701 CGGGGTCGGA AATGCCGCCG ATGATTCCGC CCAAACCGAA AATTCAACT
751 TTCACACCCA AACGGTGCAA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF 004.ng>:

**g004.pep**

```

1 MVERHIQHLR NGHLLMRPC QVSQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVYQHHAHA TLIFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAN
101 GAAQAADTI RVAAPRYCPA ILPWSAASCS RGSWLDASPA IKICGMLVCM
151 VSGSATGTFR ASLSILMFSK PILSTFGRFP TAANIYSATN TPFSPSCSQW
201 TSTLPSASSL TSVLASRCSF NSSPNTAFAS SETTGSEMPF MIPKPKIST
251 FTKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 15>:

**m004.seq**

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCAGG GCCTACGATT
101 TCCGCGCCGA TAAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTTCAGAC CGACAAAGCC GATTTGCGGA CTGGTAAACA CCACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGCAATC TTGCCTTGGT CGGCAGCTTC ATGCAGCAGA GGCAGTTGGT
401 TGGACGCATC GCCTGCGATG AAGATATGCG GAATACTGGT CTGCATGGTC
451 AGCGGGTCGG CAACAGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATATT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTAG CATCCAGATG
651 CAGTTTCAAT TCTTCGCCGA ACACGGCGTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCGCATG ATTCGCCCA AACCGAAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 16; ORF 004>:

**m004.pep**

```

1 MVERHIQHLR NGHLLMCPs QVVRQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVHQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAD
101 GAAPQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPA KICGILVCMV
151 SGSATGTFR SFSILIFSKP ILSTFGRFP AASIYSATN PFSPPSCSQW
201 STLPSASSLT SVLASRCSFN SSPNTAFAS ETTGSEMPM IPEKPKISTF
251 TPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>:

**a004.seq**

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCCG ACCTACGATT
101 TCTGCGCCGA TGAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTGCGGA CTGGTGAACA CTACGCCGAT
301 GGTGCTGCGG CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGCAATC TTGCCTTGGT CGGCGGCTTC ATGCAGCAGG GGCAGTTGGT
401 TGGACGCGTC GCCGCAATA AAGATATGCG GAATACTGGT CTGCATAGTC
451 AGCGGATCGG CAACGGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATGTT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCTACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCGTC GAGTTTGACC TCGGTTTAG CATCCAAATG
651 CAGTTTCAAT TCTTCACCGA ACACGGCTTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCGCATG ATGCCACCA AACCGAAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 18; ORF 004.a>:

```
a004.pep
1  MVERHIQHLR NGHLLHMCPS QQVRQMFGR TYDFCADEAA GGFFGIQAHM
51 AFVYQHAAA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGEHYAD
101 GAAQAQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPAI KICGILVCIV
151 SGSATGTPRA SFSILMFSKP ILSTFGRRPT AASIYSATNT PFSPPSCSQWT
201 STLPSASSLA SVLASKCSFN SSPNTAFASS ETTGSEMPPM MPPKPKISTF
251 TPKRCNA*
```

m004/a004 94.9% identity over a 257 aa overlap

```

      10      20      30      40      50      60
m004.pep MVERHIQHLRNGHLLHMCPSQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA
a004      MVERHIQHLRNGHLLHMCPSQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA
      10      20      30      40      50      60

      70      80      90     100     110     120
m004.pep ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAALSPAI
a004      ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGEHYADGAAQAQTAADIRVAAALSPAI
      70      80      90     100     110     120

      130     140     150     160     170     180
m004.pep LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTTPRASFSILIFSKPILSTFGRRPT
a004      LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTTPRASFSILIFSKPILSTFGRRPT
      130     140     150     160     170     180

      190     200     210     220     230     240
m004.pep AASIYSATNTPFSPPSCSQWTSTLPSASSLSVLASCSFNSSPNTAFASSETTGSEMPPM
a004      AASIYSATNTPFSPPSCSQWTSTLPSASSLSVLASCSFNSSPNTAFASSETTGSEMPPM
      190     200     210     220     230     240

      250
m004.pep IPPKPKISTFTPKRCNAX
a004      :|||||
      250
m004.g004 MPPKPKISTFTPKRCNAX
      250
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 004 shows 93.4% identity over a 258 aa overlap with a predicted ORF (ORF 004.ng) from *N. gonorrhoeae*:

m004/g004

```

      10      20      30      40      50      60
m004.pep MVERHIQHLRNGHLLHMCPSQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA
g004      MVERHIQHLRNGHLLHMCPSQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA
      10      20      30      40      50      60

      70      80      90     100     110     119
m004.pep ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAA-LSPA
g004      :||:|||||
      70      80      90     100     110     120

      120     130     140     150     160     179
m004.pep ILPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTTPRASFSILIFSKPILSTFGRRP
```

```

|||||
g004      ILPWSAASCSRGSWLDASPAIKICGMLVCMVSGSATGTTPRASLSILMFSPILSTFGRRP
           130      140      150      160      170      180

180      190      200      210      220      230      239
m004.pep  TAASIYSATNTFFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
|||||
g004      TAANIYSATNTFFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
           190      200      210      220      230      240

240      250
m004.pep  MIPPKPKISTFTPKRCNAX
|||||
g004      MIPPKPKISTFTPKRCNA
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 19>:

```

g005.seq
1  ATGGGGATGG ACAATATTGA TATGTTTCATG CCTGAACAAG AGGAAATCCA
51  ATCAATGTGG AAAGAAATTT TACTGAATTA CGGTATTTTC CTGCTCGAAC
101 TGCTTACCGT GTTCGGCGCA ATTGCGCTGA TTGTGTTGGC TATCGTACAG
151 AGTAAGAAAC AGTCGGAAAG CGGCAGTGTC GACTGACAG ATTTTTCGGA
201 AAATTATAAA AAACAGCGGC AATCGTTTGA AACATTCTTT TTAAGCGAGG
251 AAGAGACAAA ACATCAGGAA AAAAAAGAAA AGAAAAAGGA AAAGGCGGAA
301 GCCAAAGCAG AGAAAAAGCG TTTGAAGGAG GCGGGGAGA AATCTGCCGA
351 AACGCAAAAA TCCCGCCTTT TTGTGTTGGA TTTTGACGGC GATTTGTATG
401 CACACGCCGT AGAATCCTTG CGTCATGAGA TTACGGCGGT GCTTTTGATT
451 GCCAAGCCTG AAGATGAGGT TCTGCTCAGA TTGGAAGTC CGGGCGGCGT
501 GGTTACGGT TACGGTTTGG CGGCTTCGCA GCTTAGGCGT TTGCGCGAAC
551 GCAATATTCC GCTGAcgctc gccgTCGATA AGGTCGCGGC AAGCGcggc
601 tatatgatgg cgtgtgtgGC GGATAAAATT GTTCCGctc cgtttgcggt
651 catcggttcg gtgggtgtgg tgGcggaagt gcCGAATATC CaccgCctGT
701 TGAAAAAACA TGATATTGAT GTGGATGTGA TGACGGCGGG CGAATTTAAG
751 CGCACGGTTA CTTTTATGGG TGAAATACG GAAAAGGGCA AACAGAAATT
801 CCGCAGGAA CTGGAGGAAA CGCATCAGTT GTTCAAGCAG TTTGTCAGTG
851 AAAACCGCCC CGGGTTGGAT ATTGAAAAAA TAGCGACGGG CGAGCATTGG
901 TTCGGCCGGC AGGCGTTGGC GTTGAAGTTG ATTGACGAGA TTTGACCCAG
951 TGATGATTG TTGTTGAAAG CGTTTGAAAA CAAACAGGtt aTCGAAGTGA
1001 AATATCAGGA GAAGCGAAGC CTGATCCAGC GCATTGTTTT GCAGGCGGAA
1051 GCTTCCGTTG AAAAGTTGTT TGCCAAACTT GTCAACCGGC GAGCGGATGT
1101 GATGTAG

```

This corresponds to the amino acid sequence <SEQ ID 20; ORF 005.ng>:

```

g005.pep
1  MGMDNIDMFV PEQEEIQSMW KEILLNYGIF LLELLTVFGA IALIVLAIVQ
51  SKKQSESGSV VLTDFSENK KQRQSFETFF LSEEETKHQE KKEKKKEKAE
101 AKAEKKRLKE GGEKSAETQK SRLFVLDFDG DLYAHAVESL RHEITAVLLI
151 AKPEDEVLLR LSPGGVVHG YGLAASQLRR LRERNIPLTV AVDKVAASGG
201 YMMACVADKI VSAPFAVIGS VGVVAEVPNI HRLLKKHDID VDVMTAGEFK
251 RTVTFMGENT EKGKQKFRQE LEETHQLFKQ FVSENRPGLD IEKIATGEHW
301 FGRQALALNL IDEISTDDL LLKAFENKQV IEVKYQEKRS LIQRIQLQAE
351 ASVEKLFACL VNRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 21>:

```

m005.seq
1  ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51  GTGGAAAGAA ATTTACTGTA ATTACGGTAT TTTCCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AWAGCGGCAG TGTCGTACTG ACGGATTTTT CGGAAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CACAACATCA GAAAAAGAG GAAAAGAAA AGGAAAAGGC GGAAGCCAAA

```

```

301 GCAGAGAAAA A.CGTTTGAA GGAGGGTGGG GAGAAATCTG CCGAAACGCA
351 nAAATCACGC CTTTTGTGT TGGANNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNGCGAGCGG CGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGCTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGGTGGGT GTGGTGGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGG GGCAACAGA AATCCGACA
801 GGAACGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGCGAGCA TTGTTCCGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTGCA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTGTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGT A
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 22; ORF 005>:

**m005.pep**

```

1 MDNIDMFPE QEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQXSGSVVL TDFSENYKKQ RQSFEAFFLS GEEAQHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKSAETXKSR LFVLXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXASGGYM
201 MACVADKIAS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQLE ETHQLFKQFV SENRPQLDIE EVATGEHWFG
301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIGLQAEAS
351 VEKLFARKLVN RRADV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 23>:

**a005.seq**

```

1 ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51 GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AAAGCGGCAG TGTCGACTG ACGGATTTT CGGAAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CAAACATCA GGAAGAAAGAG GAAAGAAAA AGGAAAAGGC GGAAGCCAAA
301 GCAGAGAAAA AGCGTTTGAA GGAGGGTGGG GAGAAATCTT CCGAAACGCA
351 AAAATCCGC CTTTTGTGT TGGATTTGA CGGCGATTG TATGCACACG
401 CCGTAGAATC CTTGCGTCAT GAGATTACGG CGGTGCTTTT GATTGCCAAG
451 CCTGAAGATG AGGTTCTGCT TAGATTGGAA AGTCCGGGCG GCGTGGTTCA
501 CGGTACGGT TTGGCGGCTT CGCAGCTTAG GCGTTTGC GCACGCAATA
551 TTCCGCTGAC CGTCGCCGTC GATAAGGTGG CGGCGAGCGG TGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGTTCC GCTCCGTTT CGATTGTCGG
651 TTCGGTGGGT GTTGTAGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGG GGCAACAGA AATCCGACA
801 GGAACGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGCGAGCA TTGTTCCGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTGCA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTT AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTGTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGA
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF 005.a>:

**a005.pep**

```

1 MDNIDMFPE QEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSESGSVVL TDFSENYKKQ RQSFEAFFLS GEEAKHQEKE EKKKEKAEAK
101 AEKKRLKEGG EKSSSETQKSR LFVLDFDGLD YAHAVESLRH EITAVLLIAK
151 PEDEVLLRLE SPGGVVHGYG LAASQLRRLR ERNIPLTAV DKVAASGGYM
201 MACVADKIVS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQLE ETHQLFKQFV SENRPQLDIE EVATGEHWFG

```

301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIQLQAEAS  
 351 VEKLFKLVN RRADVM\*

m005/a005 79.2% identity over a 366 aa overlap

m005.pep	MDNIDMFMEQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSXSGSVVL
a005	MDNIDMFMEQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESXSGSVVL
m005.pep	TDFSENYKKQRQSFEAFFLSGEEAQHQEKEEKKKEKAEAKAEKKRLKEGGEKSAETXKSR
a005	TDFSENYKKQRQSFEAFFLSGEEAKHQEKEEKKKEKAEAKAEKKRLKEGGEKSSSETQKSR
m005.pep	LFVLXX
a005	LFVLDFDGLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPGGVVHGYGLAASQLRRLR
m005.pep	XXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSGVVAEVPNIHRLKKHDIDVD
a005	ERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAIVGSGVVAEVPNIHRLKKHDIDVD
m005.pep	VMTAGEFKRTVTFMGENTEGKQKFRQELEETHQLFKQFVSENRPQLDIEEVATGEHWFG
a005	VMTAGEFKRTVTFMGENTEGKQKFRQELEETHQLFKQFVSENRPQLDIEEVATGEHWFG
m005.pep	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFKLVN
a005	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFKLVN
m005.pep	RRADVMX
a005	RRADVMX

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 005 shows 77.0% identity over a 366 aa overlap with a predicted ORF (ORF 005.ng) from *N. gonorrhoeae*:

m005/g005

m005.pep	MDNIDMFMEQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSXSGSV
g005	MGMDNIDMFMEQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESXSGSV
m005.pep	VLTDFSENYKKQRQSFEAFFLSGEEAQHQEKEEKKKEKAEAKAEKKRLKEGGEKSAETXK
g005	VLTDFSENYKKQRQSFETFFLSEETKHQEKKEKKKEKAEAKAEKKRLKEGGEKSAETQK

	120	130	140	150	160	170
m005.pep	SRLFVLXX					
			:			
g005	SRLFVLDFDGLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPPGVVHGYGLAASQLRR					
		130	140	150	160	170 180
	180	190	200	210	220	230
m005.pep	XXXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDID					
	:					
g005	LRERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHDID					
		190	200	210	220	230 240
	240	250	260	270	280	290
m005.pep	VDVMTAGEFKRTVTFMGENTEKQKQFRQLEETHQLFKQFVSENRPQLDIEEVATGEHW					
g005	VDVMTAGEFKRTVTFMGENTEKQKQFRQLEETHQLFKQFVSENRPGLDIEKIATGEHW					
		250	260	270	280	290 300
	300	310	320	330	340	350
m005.pep	FGRQALALNLIDEISTSDDLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFACL					
g005	FGRQALALNLIDEISTSDDLKAFENKQVIEVKYQEKSLIQRIGLQAEASVEKLFACL					
		310	320	330	340	350 360
	360					
m005.pep	VNRRADVMX					
g005	VNRRADVMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 25>:

```

g006.seq
1  ATGCTGCTGG TGCTggaatt ttggttCGGc gtGtCGGCGG TGGGCatact
51  tgCGTTGTTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCT CCTGAACAAC AGCTTGGAAC gcgACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GTACCGCCAT TACGGACTGG TTTCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGCGTCGGCG
251 CGGCGATGGG TATTTTGTTT GCCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACGGCA GCGCGGGGCA TATTTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATG AGTTTGACG ATGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451 GCCGGAATT GA

```

This corresponds to the amino acid sequence <SEQ ID 26; ORF 006.ng>:

```

g006.pep
1  MLLVLEFWFG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDERQLYRH YGLVSRRLVL ISNREAFGYL CVGAAMGILF GFVFMVMTLK
101 GYGSAGHIYS VGTYLWMFAM SLDDVPRLVE QYSLKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 27>:

```

m006.seq
1  ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGCCTTGTTC TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCT CCTGAACAAC AGCTTGGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACC GCGGCAGCT GTACCGCCAT TACGGACTGC TTGCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGCGTCGGCA
251 CGGCGATGGG TATTTTGTTT GCCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT

```

351 GTTTGCCATG AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA  
 401 ATTTGAAAGA CATCGACAA CGGATAGAGT GGTGGAACG GAACATCAAA  
 451 GCCGGAACCTGA

This corresponds to the amino acid sequence <SEQ ID 28; ORF 006>:

**m006.pep**

1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR  
 51 KGDRRQLYRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK  
 101 GYSSAGHVYS VGTYLWMFAM SLDDVPRLVE QYSNLKDIGQ RIEWSERNIK  
 151 AGT\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 29>:

**a006.seq**

1 ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT  
 51 TCGGTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC  
 101 TGTATTCCG CCTGAAGAAC AGCTTGGAAC GCGACAACCA CTTTATCCGA  
 151 AAAGGCGACG AGCGGCAGCT GGACCGCCAT TACGGAAGTC TTGCGCGCCT  
 201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGCTCGGCA  
 251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA  
 301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT  
 351 GTTTGCCATA AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA  
 401 ATTTGAAAGA CATCGACAA CGGATAGAGT GGTGGAACG GAACATCAAA  
 451 GCCGGAACCT GA

This corresponds to the amino acid sequence <SEQ ID 30; ORF 006.a>:

**a006.pep**

1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLKN SLERDNHFIR  
 51 KGDERQLDRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK  
 101 GYSSAGHVYS VGTYLWMFAI SLDDVPRLVE QYSNLKDIGQ RIEWSKRNIK  
 151 AGT\*

**m006/a006** 96.7% identity over a 153 aa overlap

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS					
a006	MLLVLEFWVGVS					
	10	20	30	40	50	60
	SAVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGD					
	RRQLYRH					
	70	80	90	100	110	120
m006.pep	YGLLARLRVLISNREAFGYLCVGTAMGILF					
a006	YGLLARLRVLISNREAFGYLCVGTAMGILF					
	70	80	90	100	110	120
	GFAFVMMTLKGYSSAGHVYSVGTYLWMFAM					
	SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
	130	140	150			
m006.pep	SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
a006	SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 006 shows 95.4% identity over a 153 aa overlap with a predicted ORF (ORF 006.ng) from *N. gonorrhoeae*:

**m006/g006**

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS					
	SAVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGD					
	RRQLYRH					

g006	MLLVLEFWFGVSAVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDRLYRHH	10	20	30	40	50	60
		70	80	90	100	110	120
m006.pep	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGYTYLWMFAM						
g006	YGLVSRRLVLISNREAFGYLCVGAAMGILFGFAFVMMTLKGYGSAGHIYSVGYTYLWMFAM	70	80	90	100	110	120
		130	140	150			
m006.pep	SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX						
g118	SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGT	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 31>:

g006-1.seq

```

1  ATGTGGA AAA TGTGGA AACA CATAGCCAAA ACCCACC GCA AGCGATTGAT
51  TGGCACATTT TCCCGGTCG GACTGGAAAA CCTTTTGATG CTGGGGTATC
101 CGGTGTTTGG CGGCTGGGCG ATTAATGCCG TGATTGCGGG GAGGGTGTGG
151 CAGGCGTTGC TGTACGCTTT GGTGTGATTT TTGATGTGGC TGGTCGGTGC
201 GGCACGGCGG ATTGCCGATA CGCGCACGTT TACGCGGATT TATACCGAAA
251 TCGCCGTGCC GGTGTGTGTT GAACAACGGC AGCGGCAAGT CCCGCATTCA
301 GCGGTAAC TG CACGGGTGCT CCTGTGCGCT GAATTTGTCA GCTTTTTTGA
351 AGAACACCTG CCGATTGCCG CGACATCCGT CGTATCCATA TTCGGCGCGT
401 GCATCATGCT GCTGGTGCTG GAATTTTGGG TCGGCGTGTC GGCGGTGGGC
451 ATACTGCGT TGTTTTATG GCTTTTGCCA CGTTTGTCCG CCATCAGCGA
501 AAACCTGTAT TTCCGCCTGA ACAACAGCTT GGAACGCGAC AACCACCTTA
551 TCCGAAAAGG CGACGAGCGG CAGCTGTACC GCCATTACGG ACTGGTTTCG
601 CGCCTGCGTG TGCTGATTTT CAACCGCGAA GCCTTCGGCT ATCTCTGCGT
651 CGGCGCGGCG ATGGGTATTT TGTTCGGCTT TGCTTTGTG ATGATGACGC
701 TCAAAGGCTA CGGCAGCGCG GGGCATATTT ATTCGGTCGG CACTTATCTG
751 TGGATGTTT CCATGAGTTT GGACGATGTG CCGCGATTGG TCGAACATA
801 TTCCAATTG AAAGACATCG GACAACGGAT AGAGTGGTCG GAACGGAACA
851 TCAAAGCCGG AACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 32; ORF 006-1.ng>:

g006-1.pep

```

1  MWKMLKHI AK THRKRLIGTF SPVGLNLLM LGYPVFGGWA INAVIAGR VVW
51  QALLYALVVF LMWLVG AARR IADTRTFTRI YTEIAPVVL EQRQRQVPHS
101 AVTARVALSR EFVSFFEEHL PIAATSVVSI FGACIMLLVL EFWVGVS AVG
151 ILALFLWLLP RFAAISENLY FRLNNSLERD NHFIRKGDRL QLYRHYGLVS
201 RLRVLISNRE AFGYLCV GAA MGILFGFAFV MMTLKGYGSA GHIYSVGYTYL
251 WMFAMSLDDV PRLVEQYSNL KDIGQRIEWS ERNIKAGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 33>:

m006-1.seq

```

1  ATGTGGA AAA TGTGGA AACA CATAGCCCAA ACCCACC GCA AGCGATTGAT
51  TGGCACATTT TCCCTGGTCG GACTGGAAAA CCTTTTGATG CTGGGTGATC
101 CGGTGTTTGG CGGCCGGGCG ATCAATGCCG TGATTGCGGG GGAGGTGTGG
151 CAGGCGTTGC TGTACGCTTT GGTGTGCTT TTGATGTGGC TGGTCGGTGC
201 GGTGCGGCGG ATTGCCGATA CGCGCACGTT TACGCGGATT TATACCGAAA
251 TCGCCGTGCC GGTGCTGTTG GAACAGCGGC AGCGACAAGT CCCGCATTG
301 GCGGTAAC TG CGCGGGTTCG CCTGTGCGCT GAGTTGTGCA GCTTTTTTGA
351 AGAACACCTG CCGATTGCCG CGACATCCGT CGTATCCATA TTCGGCGCGT
401 GCATCATGCT GCTGGTGCTG GAATTTTGGG TCGGCGTGTC GGCGGTGGGC
451 ATACTGCGT TGTTTTATG GCTTTTGCCA CGTTTGTCCG CCATCAGCGA
501 AAACCTGTAT TTCCGCCTGA ACAACAGCTT GGAACGCGAC AACCACCTTA
551 TCCGAAAAGG CGACGCGCGG CAGCTGTACC GCCATTACGG ACTGCTTGCG
601 CGCCTGCGTG TGCTGATTTT CAACCGCGAA GCCTTCGGCT ATCTCTGCGT

```



```

651 CGGCACGGCG ATGGGTATTT TGTCGGCTT TGCTTTGTG ATGATGACGC
701 TCAAAGGCTA CAGCAGCGCG GGGCATGTCT ATTCGGTCGG CACTTATCTG
751 TGGATGTTTG CCATGAGTTT GGACGACGTG CCGCGATTGG TCGAACAATA
801 TTCCAATTTG AAAGACATCG GACAACGGAT AGAGTGGTCG GAACGGAACA
851 TCAAAGCCGG AACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 34; ORF 006-1>:

```

m006-1.pep
  1 MWKMLKHIAQ THRKLIGTF SLVGLENLLM LVYPVFGGRA INAVIAGEVW
  51 QALLYALVVL LMWLVGAVRR IADTRTFTRI YTEIAPVVVL EQRQRQVPHS
 101 AVTARVALSR EFVSFFEEHL PIAATSVVSI FGACIMLLVL EFWVGVSavg
 151 ILALFLWLLP RFAAISENLY FRLNNSLERD NHFIRKGD RR QLYRHYGLLA
 201 RLRVLISNRE AFGYLCVGTA MGILFGFAFV MMTLKGYS SA GHVYSVGTYL
 251 WMFAMSLDDV PRLVEQYSNL KDIGQRIEWS ERNIKAGT*

```

m006-1/g006-1 95.5% identity in 288 aa overlap

m006-1.pep	10	20	30	40	50	60
	MWKMLKHIAQTHRKLIGTFSLVGLENLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL					
g006-1	10	20	30	40	50	60
	MWKMLKHIAKTHRKLIGTFSPVGLENLLMLGYPVFGGWAINAVIAGRvwQALLYALVVF					
m006-1.pep	70	80	90	100	110	120
	LMWLVGAVRRRIADTRTFTRIYTEIAPVVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
g006-1	70	80	90	100	110	120
	LMWLVGAARRIADTRTFTRIYTEIAPVVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
m006-1.pep	130	140	150	160	170	180
	PIAATSVVSIFGACIMLLVLEFWVGVSavgGILALFLWLLPRFAAISENLYFRLNNSLERD					
g006-1	130	140	150	160	170	180
	PIAATSVVSIFGACIMLLVLEFWVGVSavgGILALFLWLLPRFAAISENLYFRLNNSLERD					
m006-1.pep	190	200	210	220	230	240
	NHFIRKGD RRQLYRHYGLLARLV LISNREAFGYLCVGTA MGILFGFAFVMMTLKGYS SA					
g006-1	190	200	210	220	230	240
	NHFIRKGD RRQLYRHYGLVSR LV LISNREAFGYLCVGA MGILFGFAFVMMTLKGYS SA					
m006-1.pep	250	260	270	280	289	
	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
g006-1	250	260	270	280		
	GHIYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 35>:

```

a006-1.seq (partial)
  1 ..AGCCAAAACC ACCGCAAGCG ATTGATTGGC ACATTTTTC TGGTCGGACT
  51 GGAAAACCTT TTGATGCTGG TGTATCCGGT GTTTGGCGGC TGGGCGATTA
 101 ATGCCGTGAT TGCAGGGCAG GCGTGGCAGG CGTTGCTGTA CGCTTTGGTT
 151 GTGCTTTTGA TGTGGCTGGT CCGTGGCGCG CCGCGGATTG CCGATACGCG
 201 CACGTTTACG CGGATTTATA CCGAAATCGC CGTGCCGTT GTGTTGGAAC
 251 AGCGGCAGCG GCAAGTCCCG CATTCGGCGG TAACTGCGCG GGTGCGCTG
 301 TCGCGTGAGT TTGTCAGCTT TTTTGAAGAA CACCTGCCGA TTGCCGCGAC
 351 ATCCGTCGTA TCCATATTCG GCGCGTGCAT CATGCTGCTG GTGCTGGAAT
 401 TTTGGGTCGG CGTGTGGCGG GTGGGCATAC TTGCGTTGTT TTTATGGCTT
 451 TTGCCACGTT TTGCCGCCAT CAGCGAAAAC CTGTATTTC GCCTGAAGAA
 501 CAGCTTGGA CCGGACAACC ACTTTATCCG AAAAGGCGAC GAGCGGCAGC
 551 TGGACCGCCA TTACGGACTG CTTGCGCGCC TGCGTGTGCT GATTTC AAC
 601 CGCGAAGCCT TCGGCTATCT CTGCGTCGGC ACGGCGATGG GTATTTGTT
 651 CGGCTTTGCT TTTGTGATGA TGACGCTCAA AGGCTACAGC AGCGCGGGG

```

701 ATGTCTATTC GGTCCGCACT TATCTGTGGA TGTTGCCAT AAGTTGGAC  
 751 GACGTGCCGC GATTGGTCGA ACAATATTC AATTGAAAG ACATCGGACA  
 801 ACGGATAGAG TGGTCGAAAC GGAACATCA AGCCGGAAC TGA

This corresponds to the amino acid sequence <SEQ ID 36; ORF 006-1.a>:

a006-1.pep (partial)  
 1 ..SQNHRKRLIG TFFLVGLENL LMLVYPVFGG WAINAVIAGQ AWQALLYALV  
 51 VLLMWLVGAA RRIADTRTFT RIYTEIAVPV VLEQRQRQVP HSAVTARVAL  
 101 SREFVSFFEE HLPFAATSVV SIFGACIMLL VLEFWVGSA VGILALFLWL  
 151 LPRFAAISEN LYFRLKNSLE RDNHFIRKGD ERQLDRHYGL LARLRVLISN  
 201 REAFGYLCVG TAMGILFGFA FVMMLTKGYS SAGHVYSVGT YLWMFAISLD  
 251 DVPRLVEQYS NLKDIGQRIE WSKRNIKAGT \*

a006-1/m006-1 95.7% identity in 280 aa overlap

	10	20	30	40	50
a006-1.pep	SQNHRKRLIGTFFLVGLENLMLVYPVFGGWAINAVIAGQAWQALLYALVVL				
m006-1	MWKMLKHIAQTHRKRLLIGTFFSLVGLNLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL				
	10	20	30	40	50
	60	70	80	90	100
a006-1.pep	LMWLVGAAARRIADTRTFTRIYTEIAVPVLEQRQRQVP HSAVTARVALSREFVSFFEEHL				
m006-1	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVP HSAVTARVALSREFVSFFEEHL				
	70	80	90	100	110
	120	130	140	150	160
a006-1.pep	PIAATSVVSIFGACIMLLVLEFWVGSAVGILALFLWLLPRFAAISENLYFRLKNSLERD				
m006-1	PIAATSVVSIFGACIMLLVLEFWVGSAVGILALFLWLLPRFAAISENLYFRLKNSLERD				
	130	140	150	160	170
	180	190	200	210	220
a006-1.pep	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSA				
m006-1	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSA				
	190	200	210	220	230
	240	250	260	270	280
a006-1.pep	GHVYSVGTLYWMFAISLDDVPRLVEQYSNLKDIGQRIEWSKRNIKAGTX				
m006-1	GHVYSVGTLYWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 37>:

g007.seq  
 1 atgaACACAA CCCGACTGCC GACCGCCTTC ATCTGTGCT GCCTCTGcgc  
 51 CGCcGCTTCT GCCGccgaca acAGCatcat gaCaAAAGGG CAAAAAGTGT  
 101 ACGAATCcAa ctGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC  
 151 ACTGCGtTTC CTccgctTTT CCggtcgGac tgtattatga acaAACCGCa  
 201 cgTCctgctg cacagcatgg tcaaaggcAt cgacgggaca ttcaaagtgg  
 251 agcggcaaaa cctacgacgg atttatgCcc gcaaccgcca tcagcgATGC  
 301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

This corresponds to the amino acid sequence <SEQ ID 38; ORF 007.ng>:

g007.pep  
 1 MNTTRLPTAF ILCCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG  
 51 TAFPPLFRSD CIMNKPVLL HSMVKGIDGT FKVERQNLRR IYARNRHQRC  
 101 GHCRRRHLYH ERL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>:

**m007.seq**

```

1 ATGAACACAA CCGACTGCC GACCGCCCTC GTCTTGGGCT GCTTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACC GCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTC.
251 AACGGCAAAA CCTACAACGG ATTCATGCCC GCAACCGCCA TCAGCGATGC
301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 40; ORF 007>:

**m007.pep**

```

1 MNTTRLPTAL VLGCFCAAA AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVXRQNLQR IHARNRHQRC
101 GHCRRRHLHY ERL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 41>:

**a007.seq**

```

1 ATGAACACAA CCGACTGCC GACCGCCCTC GTCTTGGGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACC GCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTC.
251 AACGGCAAAA CCTACAACGG ATTCATGCCC GCCACTGCCA TCAGCGATGC
301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 42; ORF 007.a>:

**a007.pep**

```

1 MNTTRLPTAL VLGCFCAAA AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVXRQNLQR IHARNRHQRC
101 GHCRRRHLHY ERL*

```

**m007/a007** 97.3% identity over a 113 aa overlap

	10	20	30	40	50	60
m007.pep	MNTTRLPTALVLGCFC	AAAADNSIMTKGQKV	YESNCVACHGKKGE	GRGTMFPPLYRSD		
a007	MNTTRLPTALVLGCL	CAASAADNSIMTKGQKV	YESNCVACHGKKGE	GRGTMFPPLYRSD		
	10	20	30	40	50	60
m007.pep	FIMKKPQVLLHSMVK	GINGTIKVXRQNLQRI	HARNRHQRCGHCRR	RRHLHYERLX		
a007	FIMKKPQVLLHSMVK	GINGTIKVXRQNLQRI	HARNRHQRCGHCRR	RRHLHYERLX		
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 007 shows 86.7% identity over a 113 aa overlap with a predicted ORF (ORF 007.ng) from *N. gonorrhoeae*:

**m007/g007**

	10	20	30	40	50	60
m007.pep	MNTTRLPTALVLGCFC	AAAADNSIMTKGQKV	YESNCVACHGKKGE	GRGTMFPPLYRSD		
g007	MNTTRLPTAFILCCL	CAASAADNSIMTKGQKV	YESNCIACHGKKGE	GRGTAFPPFLFRSD		
	10	20	30	40	50	60
m007.pep	FIMKKPQVLLHSMVK	GINGTIKVXRQNLQRI	HARNRHQRCGHCRR	RRHLHYERLX		

g007                    CIMNKPVLLHSMVKGIDGTFKVERQNLRRYYARNRHQRCGHCRRLHYHERL  
                               70                    80                    90                    100                    110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 43>:

g007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC
151 ACTGCGTTTC CTCCGCTTTT CCGGTCGGAC TATATTATGA ACAAACCGCA
201 CGTCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGGC AAAAAAAC.
```

This corresponds to the amino acid sequence <SEQ ID 44; ORF 007-1.ng>:

g007-1.pep (partial)

```

1  MNTTRLPTAF ILCLCAAAS AADNSIMTKG QKYESNCIA CHGKKGEGRG
51 TAFPFLFRSD YIMNKPVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKG KKN...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 45>:

m007-1.seq

```

1  ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCTTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGC AAAAAAACT
401 AA
```

This corresponds to the amino acid sequence <SEQ ID 46; ORF 007-1>

m007-1.pep

```

1  MNTTRLPTAL VLGCFAAAS AADNSIMTKG QKYESNCVA CHGKKGEGRG
51 TMFPFLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKS KKN*
```

m007-1 / g007-1 91.7% identity in 133 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFAAASAADNSIMTKGQKYESNCVACHGKKGEGRGTMFPFLYRSD					
g007-1	MNTTRLPTAFILCLCAAASAADNSIMTKGQKYESNCIACHGKKGEGRGTAFPFLFRSD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGTIKVNKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	:     :     :     :     :     :					
g007-1	YIMNKPVLLHSMVKGINGTIKVNKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
	:					
g007-1	TEKDVQAKGKKN					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 47>:

a007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
```

```

151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CCACTGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAACA GGCAAAAAAC AAAAAA..

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF 007-1.a>:

**a007-1.pep (partial)**

```

1 MNTTRLPTAL VLGLCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVKQAKN KK..

```

m007-1/a007-1 98.5% identity in 132 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGLCAAAS	AAADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
a007-1	MNTTRLPTALVLGLCAAAS	AAADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGT	IKVNGKTYNGFMPATAISDADIAAVATYIM	NAFDNGGGSV			
a007-1	FIMKKPQVLLHSMVKGINGT	IKVNGKTYNGFMPATAISDADIAAVATYIM	NAFDNGGGSV			
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVKQAKSKKNX					
a007-1	TEKDVKQAKNKK					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 49>:

**g008.seq**

```

1 ATGAACAACA GACATTTTGC CGTCAtcgCC TTGGGCAGCA ACCTTGACAA
51 CCCCACACAA CAAATacgcg gcgcattaga cgcgctctcg tcccatcctg
101 acatccggct tgaaCaggtt tcctcactgt aTatgaccgc acctgtcgggt
151 tacgAcaaTC agcccgATTT CATCaatgcc gTCTgcaccg TTCCACCAC
201 CtTGGACGGC ATTGcccTGC TTGCCgaACT CAAccgTATC GAAGCCGATT
251 TCGGACGCGA aCGCAGTTTC CGCAATGCAC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCCGCC TTACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATAcGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAATACG GAAAGGTTGT CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGACA GGTA

```

This corresponds to the amino acid sequence <SEQ ID 50; ORF 008.ng>:

**g008.pep**

```

1 MNNRHFAVIA LGSNLDNPAQ QIRGALDALS SHPDIRLEQV SSLYMTAPVG
51 YDNQPDFINA VCTVSTLDG IALLAELNRI EADFGRETSF RNAPRTLDD
101 IIDFDGISSD DPLRLPHPR AHRSFVIRP LAEILPDFIL KYGKVVELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 51>:

**m008.seq**

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCTCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTT TGTCAATGCC GTCTGCACCG TTCCACCAC
201 TCTGGACGGC ATTGCCyTGC TTGCCGAAct CAACCGTATC GAGGCTGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GkATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACACsCGAC TcACCTTGCC

```

```

351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATCCGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTGTTTTA GGAAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGyTGG GCAATCAAGG TATCCGTCTT TTACCGGACA GGTAAAT

```

This corresponds to the amino acid sequence <SEQ ID 52; ORF 008>:

```

m008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFRERSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFVL GKHKVLAELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 53>:

```

a008.seq
  1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
 51 CCCTGCCCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATT CGTCAATGCC GTCTGCACCG TTTCCACCAC
201 CTTGGACGGC ATTGCCCTGC TTGCCGAAT CAACCGTATC GAAGCCGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT TCACGCGAC GACCCCGGAC TCACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CACACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTATTTTG GGAAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGATA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 54; ORF 008.a>:

```

a008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFRERSF RNAPRTLDLD
101 IIDFDGISSD DPRLTLPHPR AHERSFVIRP LAEILPDFIL GKHKVLAELS
151 KRLGNQGIRL LPDK*

```

m008/a008 97.6% identity over a 164 aa overlap

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYDNQPDFVNA					
a008	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYDNQPDFVNA					
	10	20	30	40	50	60
m008.pep	VCTVSTTLDGIALLAELNRIEADFRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
a008	AHERSFVIRPLAEILPDFILGKHGKVAELSKRLGNQGIRLLPDKX					
	130	140	150	160		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 008 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF008.ng) from *N. gonorrhoeae*:

m008/g008

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYDNQPDFVNA					
g008	MNNRHFAVIALGSNLDNPAQQIRGALDALSSHPDIRLEQVSSLYMTAPVGYDNQPDFINA					

	10	20	30	40	50	60
m008.pep	70	80	90	100	110	120
	VCTVSTTLDGIALLAELNRIEADFRGRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
g008	70	80	90	100	110	120
	VCTVSTTLDGIALLAELNRIEADFRGRERSFRNAPRTLXLDIIDFDGISSDDPRLTLPHPR					
m008.pep	130	140	150	160		
	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
g008	130	140	150	160		
	AHERSFVIRPLAEILPDFILGKYGKVVELSKRLGNQGIRLLPDRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 55>:

g009.seq

```

1  ATGCCCGCG CTGCGGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GCGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGAAA TCAGCACACG CAGGCGCGAA ACCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTcg cGTTCCAAGC
201 TGTTGTTCAG GCGGAAATAC AGGTTTTTCGC TGATGGCGGC AAAACGTGGC
251 AaaaGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 56; ORF 009.ng>:

g009.pep

```

1  MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFAVGNQHT QARNQSVMAV
51  QLPLVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>:

m009.seq

```

1  ATGCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC CGGTCGCCTT TTCGGATAAA GTGGTTGTcg CGTTCGAAGC
201 TGTTGTTCAG GCGGAAATAC AGGTTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 58; ORF 009>:

m009.pep

```

1  MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFAVGNQHT QARKQSVMAV
51  QLPPVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 009 shows 97.7% identity over a 86 aa overlap with a predicted ORF (ORF 009.ng) from *N. gonorrhoeae*:

m009/g009

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
g009	MPRAAVAFAERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARNQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
m009.pep	70	80				
	VVVAFAQVVQAEIQVFADGGKTWQKPX					
g009	70	80				
	VVVAFAQVVQAEIQVFADGGKTWQKPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 59>:

```
a009.seq
1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAT TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTC
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTCG CGTTCCAAGC
201 TGTCTCTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A
```

This corresponds to the amino acid sequence <SEQ ID 60; ORF 009.a>:

```
a009.pep
1  MPRAAFAFER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
51  QLPLVAFSDK VVVAFAQVLQ AEIQVFADGG KTWQKP*
```

m009/a009 97.7% identity over a 86 aa overlap

	10	20	30	40	50	60
m009.pep	MPRAAFAFERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
a009	MPRAAFAFERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009.pep	VVVAFAQVVAEIQVFADGGKTWQKPX					
	:					
a009	VVVAFAQVLQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 61>:

```
g010.seq
1  ATGGGTTTTC CTGTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTC CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GCGGGTATTT CCGCTCTCTT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTTCGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTGC TATTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGATATTC TGTGAacgc
801 cgacggcgaa cgcTTTATGG AAcgctatgc GCcgACCGta aAagaCTTGG
851 CTTCTCGCga cgtGGTTTCA CgcgcGatgG CGatggaAAT ctatgaaggt
901 cgcggctgTG GtaaaAAcaA agaCCacgtC TTACTGAAAA TCGACcAtAt
951 cggTGcAGAA AAAATTATGG AAAAAGTCCG GGCATCCGC GAGATTTCa
1001 TTCagtttgc cGGTATCGAT CCGATTAAAG ACCCGATTcc ggttgTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCg aCCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTCCGTAC ACGGTGCGAA CCGTTGGGT
1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga
```

This corresponds to the amino acid sequence <SEQ ID 62; ORF 010.ng>:

g010.pep



```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDDHMY DTVKGSWDLG DQDAIEFMCR AAPEAVIELE
101 HMGMPPDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENGDVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGCKNKDHF LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPPIVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>:

```

m010.seq (PARTIAL)
1  ..nTCCAATTAT CCAAATCCGG TCTGAATTGT GCCGTTTTGT CTAAAGTGTT
51  CCCGACCCGT TCGCATACCG TAGCGGCGCA GGGCGGTATT TCCGCCTCTn
101 TGGGTAATGT GCAGGAAGAC CGTTGGGACT GGCACATGTA CGATACCGTG
151 AAAGGTTCCG ACTGGTTGGG CGACCAAGAT GCGATTGAGT TTATGTGCCG
201 CGCCGCGCCT GAAGCCGTAA TTGAGTTGGA ACACATGGGT ATGCCTTTTG
251 ACCGTGTGGA AAGCGGTAAA ATTTATCAGC GTCCTTTCGG CGGCCATACT
301 GCCGAACACG GTAAACGCGC GGTAAGACGC GYCTGTGCGG TTGCCGACCG
351 TACAGGTCAT GCGATGCTGC ATACTTTGTA CCAACAAAAC GTCCGTGCCA
401 ATACGCAATT CTTGTGGAA TGGACGGCAC AAGATTTGAT TCGTGATGAA
451 AACGGCGATG TCGTCGGCGT AACCGCCATG GAAATGGAAA CCGGCGAAGT
501 TTATATTTTC CACGCTAAAG CTGTGATGTT TGCTACCGGC GCGGCGGGTC
551 GTATTTATGC GTCTTCTACC AATGCCTATA TGAATACCGG CGATGGTTTG
601 GGTATTTGTG CGCGTGCAGG TATCCCGTTG GAAGACATGG AATTCTGGCA
651 ATTCCAGCCG ACCGGCGTGG CGGGTGCGGG CGTGTGATT ACCGAA...

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF 010>:

```

m010.pep (PARTIAL)
1  ..XQLSKSGLNC AVLSKVFPTR SHTVAAQGGI SASXGNVQED RWDWHMYDTV
51  KGSDDLGDQD AIEFMCRAP EAVIELEHMG MPFDRVESGK IYQRPFGGHT
101 AEHGKRAVER XCAVADRTGH AMLHTLYQQN VRANTQFFVE WTAQDLIRDE
151 NGDVVGVTAM EMETGEVYIF HAKAVMFATG GGGRIYASST NAYMNTGDGL
201 GICARAGIPL EDMFVQFQP TGVAGAGVLI TE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 65>:

```

a010.seq
1  ATGGGCTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTG TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTGTGTC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTCCA
1001 TTCAGTTGCG CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CCGTATTCCG ACCAACTACC ATGGCGAAGT
1101 TGTGTTTCCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTGGGT
1201 ACCAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCT TTGCTGCTA

```

```

1301 ATGCCGCGCA ACTGACCCGC CAACGTATCG AGCGTTTGA CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GGCGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATCA GATGCCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 66; ORF 010.a>:

```

a010.pep
1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKV F PTRSHTVAAQ
51  GGISASLGNV QEDRWWHMY DTVKGS DWLG DQDAIEFMCRA APEAVIELE
101 HMGMFPDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLASRDVVS RAMAMEIYEG
301 RCGCKNKDHY LLKIDHIGAE KIMEKLP GIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEV PVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWK P LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQSVQLHA GVFRTEILS KGVREVM AIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKR VY*

```

m010/a010 98.7% identity over a 231 aa overlap

```

                                10      20      30
m010.pep                                XQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASXGNV
                                |||
a010      MGFPVRKFDAVIVGGGGAGLRAXLQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m010.pep      QEDRWWHMYDTVKGSDWLG DQDAIEFMCRA APEAVIELEHMGMFPDRVESGKIYQRPFG
                                |||
a010      QEDRWWHMYDTVKGSDWLG DQDAIEFMCRA APEAVIELEHMGMFPDRVESGKIYQRPFG
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m010.pep      GHTAEHGKRAVERXCAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENG DVVG V
                                |||
a010      GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENG DVVG V
                                130     140     150     160     170     180

                                160     170     180     190     200     210
m010.pep      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                |||
a010      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                190     200     210     220     230     240

                                220     230
m010.pep      FQPTGVAGAGVLITE
                                |:|
a010      FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPT VKDLASRDVVS RAMAMEIYEG
                                250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 010 shows 98.7% identity over a 231 aa overlap with a predicted ORF (ORF 010.ng) from *N. gonorrhoeae*:

m010.pep/g010.pep

m010.pep				10	20	30	
				XQLSKSGLNCAVL	SKVF	PTRSHTVAAQGGISASXGNV	
g010	MGFPVRKFD	DAVIVGGG	GAGLRAAL	QLSK	SGLNCAVL	SKVF	PTRSHTVAAQGGISASLGNV
	10	20	30	40	50	60	
m010.pep	40	50	60	70	80	90	
	QEDRW	DWHMYD	TVKGS	DWLGDQ	DAIEF	MCRAAPEAVIE	LEHMGMPFDRVESGKIYQRPFG
g010	QEDRW	DWHMYD	TVKGS	DWLGDQ	DAIEF	MCRAAPEAVIE	LEHMGMPFDRVESGKIYQRPFG
	70	80	90	100	110	120	
m010.pep	100	110	120	130	140	150	
	GHTAE	HGKRA	VERXC	CAVADR	TGHAML	HTLYQQNVRANTQFF	VEWTAQDLIRDENG
g010	GHTAE	HGKRA	VERXC	CAVADR	TGHAML	HTLYQQNVRANTQFF	VEWTAQDLIRDENG
	130	140	150	160	170	180	
m010.pep	160	170	180	190	200	210	
	TAMEM	ETGEV	YIFHA	KAVMF	FATGGG	GRIYASSTNAYMNTG	DGLGICARAGIPLEDMEFWQ
g010	TAMEM	ETGEV	YIFHA	KAVMF	FATGGG	GRIYASSTNAYMNTG	DGLGICARAGIPLEDMEFWQ
	190	200	210	220	230	240	
m010.pep	220	230					
	FQPTG	VAGAGV	LITE				
g010	FHPTG	VAGAGV	LITEG	VRGEG	GILLN	ADGERF	MERYAPT
	250	260	270	280	290	300	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 67>:

g010-1.seq..

```

1  ATGGGTTTTC CTGTTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTGTGC TAAAGTGTTT CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAGAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCT TATTTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACGGGT GACGGTTTGG GCATTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTGAACGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTGGTTTCA CGCGCATGG CGATGGAAAT CTATGAAGGT
901 CGCGGCTGTG GTAAAAACAA AGACCACGTC TTAAGTAAAA TCGACCATAT
951 CCGTGAGAAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCCT
1001 TTCAGTTTGC CGGTATCGAT CCGATTAAAG ACCCGATTCC GGTGTGCGCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT

```

1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga

This corresponds to the amino acid sequence <SEQ ID 68; ORF 010-1.ng>:

g010-1.pep  
 1 MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVFP TRSHTVAAQ  
 51 GGISASLGNV QEDRDWHMY DTVKGSDDLQ DQDAIEFMCR AAPEAVIELE  
 101 HMGMFPDRVE SGKIYQRPFG GHAEHGKRA VERACAVADR TGHAMLHTLY  
 151 QQNVRAQTQF FVEWTAQDLI RDENGDVVG V TAMEMETGEV YIFHAKAVMF  
 201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG  
 251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG  
 301 RCGGKNDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP  
 351 TTHYMMGGIP TNYHGEVVVP QGDEYEVFVK GLYAAGECAC ASVHGANRLG  
 401 TNSLLDLVVF RPTPR\*

g010-1 / P10444

sp|P10444|DHSA\_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT  
 gnl|PID|d1015210 (D90711) Succinate dehydrogenase, flavoprotein [Escherichia coli] gi|1786942  
 (AE000175) succinate dehydrogenase flavoprotein subunit [Escherichia coli] Length = 588  
 Score = 1073 (495.6 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169  
 Identities = 191/303 (63%), Positives = 238/303 (78%)

Query: 1 MGFPVRKFDAVIVXXXXXXXXXXXXXSKSLNCVLSKVFP TRSHTVAAQGGISASLGNV 60  
 M PVR+FDVAV++ S+SG CA+LSKVFP TRSHTV+AQGGI+ +LGN  
 Sbjct: 1 MKLPVREFDAVVIGAGGAGMRAALQISQSGQTCALLSKVFP TRSHTVSAQGGITVALGNT 60  
 Query: 61 QEDRDWHMYDTVKGSDDLQDQDAIEFMCR AAPEAVIELEHMGMFPDRVESGKIYQRPFG 120  
 ED W+WHMYDTVKGS++GDQDAIE+MC+ PEA++ELEHMG+PF R++ G+IYQRPFG  
 Sbjct: 61 HEDNWEWHMYDTVKGS DYIGDQDAIEYMCKTGPEAILELEHMG LPPSRLLDDGRIYQRPFG 120  
 Query: 121 GHAEHGKRAVERACAVADRTGHAMLHTLYQQNVRAQTQFFVEWTAQDLIRDENG DVVG 180  
 G + G R A ADRTGHA+LHTLYQQN++ +T F E W A DL++++G VVG  
 Sbjct: 121 GQSKNFGGEQAARTAAADRTGHALLHTLYQQNLKNHTTIFSEWYALDLVKNQDGA VVG 180  
 Query: 181 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ 240  
 TA+ +ETGEV F A+A + ATGG GRIY S+TNA++NTGDG+G+ RAG+P++DME WQ  
 Sbjct: 181 TALCIETGEVVYFKARATVLTGAGRIYQSTTNAHINTGDGVGM AIRAGVPVQDMEMWQ 240  
 Query: 241 FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG 300  
 FHPTG+AGAGVL+TEG RGE G LLN GERFMERYAP KDLA RDVV+R++ +EI EG  
 Sbjct: 241 FHPTGIAGAGVLTEGCRGEGGYLLNKHGERFMERYAPNAKDLAGRDVVAR SIMIEIREG 300  
 Query: 301 RGC 303  
 RGC  
 Sbjct: 301 RGC 303

Score = 249 (115.0 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169  
 Identities = 53/102 (51%), Positives = 62/102 (60%)

Query: 309 HVLLKIDHIGAEKIMEKLPGIREISIQFAGXXXXXXXXXXXXTTHYMMGGIPTNYHGEVV 368  
 H LK+DH+G E + +LPGI E+S FA T HYMMGGIPT G+ +  
 Sbjct: 310 HAKLKLHLGKEVLESRLPGILELSRTFAHVDVPVKEPIPVIP TCHYMMGGIPTKV TQAL 369  
 Query: 369 VPQGDEYEVFVKGLYAAGECACASVHGANRLGTNSLLDLVVF 410  
 +V V GL+A GE AC SVHGANRLG NSLLDLVVF  
 Sbjct: 370 TVNEKGEDVVVPG LFAVG E IACVSVHGANRLGNSLLDLVVF 411

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 69>:

m010-1.seq..  
 1 ATGGGTTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG  
 51 TGCAGGTTTA CGCGCAGCCC TCCAATTATC CAAATCCGGT CTGAATTGTG  
 101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG  
 151 GCGCGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG  
 201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG  
 251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA  
 301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG  
 351 TCCTTTCCGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACCGG  
 401 CCTGTGCCGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC

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451 CAACAAAACG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGTTCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCAGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTGTAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CCGCGCTGCG GTAAAAACAA AGACCATGTC TTACTGAAAA TCGACCATAT
951 CCGCGCAGAA AAAATTATGG AAAAAGTCCG GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTACC ACGGCGAAGT
1101 TGTGCTTCCG CAAGGTGAAG ATTACGAAGT GCCTGTAATA GGTCTGTATG
1151 CCGCAGGTGA GTGCGCTTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACCAACTCCC TGTGGACTT GGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGAGGTGGA GTTACCCGCG CAACGTATCG AGCGTTTGGG CAACCAAACC
1351 GATGGTGAAA ACCTTGATGC ATTGCGTCCG GAACTGCAAC GCTCTGTACA
1401 ACTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGCGGTTT
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTGATTGAA GTGCGGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TCGCACGCT TCAGACGACC ATCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATATCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGATGA

```

This corresponds to the amino acid sequence <SEQ ID 70; ORF 010-1>:

m010-1.pap..

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVFP TRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGSDDLW GDQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIIYQRPFG GHTAETHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRANTQF FVEWTAQDLI RDENGDVVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGGKKNKDHV LLKIDHIGAE KIMEKLPKIR EISIQFAGID PIKDPPIVVP
351 TTHYMMGGIP TNYHGEVVPV QGEDYEVVPK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFTDEILS KGVREVMAIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPPERDDE
551 NWMKHTLYHS DINTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010-1 / g010-1 99.5% identity in 410 aa overlap

	10	20	30	40	50	60
m010-1.pap	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV					
g010-1	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV					
	10	20	30	40	50	60
m010-1.pap	QEDRWDWHMYDTVKGSDDLWGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
g010-1	QEDRWDWHMYDTVKGSDDLWGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
	70	80	90	100	110	120
m010-1.pap	GHTAETHGKRAVERACAVADR TGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDVVGV					
g010-1	GHTAETHGKRAVERACAVADR TGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDVVGV					
	130	140	150	160	170	180
m010-1.pap	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDLGICARAGIPLEDMEFWQ					
g010-1	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDLGICARAGIPLEDMEFWQ					
	190	200	210	220	230	240

190

	190	200	210	220	230	240
m010-1.pep	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
g010-1	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
	250	260	270	280	290	300
m010-1.pep	310	320	330	340	350	360
	RGCGRKNKHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIFVVPPTHYMMGGIP					
g010-1	RGCGRKNKHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIFVVPPTHYMMGGIP					
	310	320	330	340	350	360
m010-1.pep	370	380	390	400	410	420
	TNYHGEVVVPQGEDYEVPVKGLYAAGECACASVHGARNLGTNSLLDLVVFGKAAGDSMIK					
g010-1	TNYHGEVVVPQGEDYEVPVKGLYAAGECACASVHGARNLGTNSLLDLVVFRPTPRX					
	370	380	390	400	410	
m010-1.pep	430	440	450	460	470	480
	FIKEQSDWKPLPANAGELTRQIERLDNQTGDNVDALRRELQRSVQLHAGVFRTEILS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 71>:

a010-1.seq..

```

1  ATGGGCTTTC CTGTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTTC TAAAGTGTTC CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGATATT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGCG GGCCTACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGCGGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAT CTACGAAGGT
901 CGCGGCTCGG GTAAAAACAA AGACCATGTC TTACTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTCC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGTATTCCG ACCAACTACC ATGGCGAAGT
1101 TGTGTTTCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCT TTGCCTGCTA
1301 ATGCCGCGCA ACTGACCCGC CAACGTATCG AGCGTTTGGG CAATCAAAC
1351 GATGGTGAAA ACCTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GGCATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 72; ORF 010-1.a>:

a010-1.pep..

```

1  MFFPVRKFDA VIVGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDDHMY DTVKGSWDLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY

```

151 QQNVRANTQF FVEWTAQDLI RDENGDVVG TAMEMETGEV YIFHAKAVMF  
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG  
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG  
301 RCGGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDFIPVVP  
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG  
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT  
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMAIA ERVKRTEIKD  
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE  
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY\*

m010-1 / a010-1 99.3% identity in 587 aa overlap

	10	20	30	40	50	60
a010-1.pep	MGFPVRKFD	AVIVGGGAGL	RAXLQLSKS	GLNCAVL	SKVFPTR	SHTVAAQGGISASLGNV
m010-1	MGFPVRKFD	AVIVGGGAGL	RAALQLSKS	GLNCAVL	SKVFPTR	SHTVAAQGGISASLGNV
	10	20	30	40	50	60
a010-1.pep	QEDRW	DWHMYD	TVKGS	DWLGDQ	DAIEFMC	RAAPEAVIELEHMGMPFDRVESGKIYQRPFG
m010-1	QEDRW	DWHMYD	TVKGS	DWLGDQ	DAIEFMC	RAAPEAVIELEHMGMPFDRVESGKIYQRPFG
	70	80	90	100	110	120
a010-1.pep	GHTAEHGKRA	VERACAVAD	RTGHAMLH	TLYQQN	VRANTQ	FFVEWTAQDLIRDENGDVVG
m010-1	GHTAEHGKRA	VERACAVAD	RTGHAMLH	TLYQQN	VRANTQ	FFVEWTAQDLIRDENGDVVG
	130	140	150	160	170	180
a010-1.pep	TAMEMETGEV	YIFHAKAV	MFATGGG	GRIYAS	SSTNAYM	NTGDGLGICARAGIPLEDMEFWQ
m010-1	TAMEMETGEV	YIFHAKAV	MFATGGG	GRIYAS	SSTNAYM	NTGDGLGICARAGIPLEDMEFWQ
	190	200	210	220	230	240
a010-1.pep	FHPTGVAGAG	VLITEGVR	EGGILLN	ADGERF	MERYAP	TVKDLASRDVVS RAMAMEIYEG
m010-1	FHPTGVAGAG	VLITEGVR	EGGILLN	ADGERF	MERYAP	TVKDLASRDVVS RAMAMEIYEG
	250	260	270	280	290	300
a010-1.pep	RGCGKNKDH	VLLKIDH	IGAEKIM	EKLPGIR	EISIQF	AGIDPIKDFIPVVP TTHYMMGGIP
m010-1	RGCGKNKDH	VLLKIDH	IGAEKIM	EKLPGIR	EISIQF	AGIDPIKDFIPVVP TTHYMMGGIP
	310	320	330	340	350	360
a010-1.pep	TNYHGEVV	VPQGDEY	EVVPVK	GLYAAGE	CACASV	HGANRLGTNSLLDLVVF GKAAGDSMIK
m010-1	TNYHGEVV	VPQGEDY	EVVPVK	GLYAAGE	CACASV	HGANRLGTNSLLDLVVF GKAAGDSMIK
	370	380	390	400	410	420
a010-1.pep	FIKEQSDW	KPLPAN	AGELTR	QRIERLD	NQTDGE	NVDALRR ELQRSVQLHAGVFRTEILS
m010-1	FIKEQSDW	KPLPAN	AGELTR	QRIERLD	NQTDGE	NVDALRR ELQRSVQLHAGVFRTEILS
	430	440	450	460	470	480
a010-1.pep	KGVREVMA	IAERVKR	TEIKDK	SKVWNT	ARIEAL	ELDNLIEVAKATLVSAE ARKESRGAHA
m010-1	KGVREVMA	IAERVKR	TEIKDK	SKVWNT	ARIEAL	ELDNLIEVAKATLVSAE ARKESRGAHA
	490	500	510	520	530	540
a010-1.pep	SDDHPERD	DENW	MKHTLY	HS	DANTLS	YKPVHTKPLSVEYI KPAKRVYX
m010-1	SDDHPERD	DENW	MKHTLY	HS	DANTLS	YKPVHTKPLSVEYI KPAKRVYX
	550	560	570	580		

m010-1 SDDHPERDDENWMKHTLYHSDINTLSYKPVHTKPLSVEYIKPAKRVYX  
550 560 570 580

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 73>:

g011.seq  
1 ATGAAGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC  
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA  
101 GCCTGAAAAC CCGCCTTACC GAAGATATGA AAACCGCGAT GCGCGCCAAA  
151 GATCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAATGCCG CCGTCAAACA  
201 GTTTGAAGTA GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA  
251 TCCTGACCAA AATGGTCAAA CAGCGCAAAG ACGCGCGGAA AATCTACACT  
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGACGT  
351 GCTGCACCGC TACCTGCCGC AAATGCTCTC CGCCGGCGAA ATCCGCACCG  
401 CCGTCGAAGC AGCCGTGTCG GAAACCGCGC CGGCAGGTAT GCGCGATATG  
451 GGCAAAGTGA TGGTCGTATT GAAAaccGC CTCGCCGCA AAGccgATAT  
501 GGGCGAAGTC AACAAATCT TGAaaaccGt aCTGACCGCC tga

This corresponds to the amino acid sequence <SEQ ID 74; ORF 011.ng>:

g011.pep  
1 MKTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKTRLT EDMKTAMRAK  
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDGAKIYT  
101 EAGRQDLADK ENAEIDVLHR YLPQMLSAGE IRTAVEAAVA ETGAAGMADM  
151 GKVMVVLKTR LAGKADMGV NKILKTVLTA \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 75>:

m011.seq (partial)  
1 ATGAGGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC  
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA  
101 GCCTGAAAAT CCGCCTTACC GAAGACATGA AAACCGCGAT GCGCGCCAAA  
151 GACCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAACGCCG CCGTCAAACA  
201 GTTTGAAGTG GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA  
251 TCCTGACCAA AATGGTCAAA CAGCGAAAAG ACAGCGCGAA AATCTACACT  
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGAGGT  
351 ACTGCACCGC TACCTTCCCC AAATGCTTTC CGCCGGCGAA ATCCGTACCG  
401 AGGTCGAAGC TGCCGTGTCG GAAACCGCGC CGGCAGGTAT GCGCGATATG  
451 GGTAAAGTCA TGGGGCTGCT GAAAACCGC CTCGCAGGTA AAGCCGA...

This corresponds to the amino acid sequence <SEQ ID 76; ORF 011>:

m011.pep (partial)  
1 MRTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKIRLT EDMKTAMRAK  
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDSAKIYT  
101 EAGRQDLADK ENAEIEVLHR YLPQMLSAGE IRTEVEAAVA ETGAAGMADM  
151 GKVMGLLKTR LAGKA.....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 011 shows 95.8% identity over a 165 aa overlap with a predicted ORF (ORF 011.ng) from *N. gonorrhoeae*:

m011/g011

	10	20	30	40	50	60
m011.pep	MRTHRKTCSAVCF	AFQTASKPAVSIR	HPSEDIMSLKIR	LTEDMKTAMRAK	DQVSLGTIRL	
	:	:	:	:	:	:
g011	MKTHRKTCSAVCF	AFQTASKPAVSIR	HPSEDIMSLKTR	LTEDMKTAMRAK	DQVSLGTIRL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m011.pep	INAAVKQFEVDER	TEADDAKITAIL	TKMVKQRKDSAK	IYTEAGRQDLAD	KENAEIEVLHR	
	:	:	:	:	:	:
g011	INAAVKQFEVDER	TEADDAKITAIL	TKMVKQRKDGAK	IYTEAGRQDLAD	KENAEIDVLHR	



193

	70	80	90	100	110	120
	130	140	150	160		
m011.pep	YLPQMLSAGEIRTEVEAAVAETGAAGMADMGKVMGLLKTRLAGKA					
	:					
g011	YLPQMLSAGEIRTAVEAAVAETGAAGMADMGKVMVVLKTRLAGKADMGVEVNKILKTVLTA					
	130	140	150	160	170	180
g011	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 77>:

**g012.seq**

```

1  ATGCTCGCCC GTCGCTATTT TTTCAATATC CAACCCGGGG CGGTTTTCAC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGCCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACa
201 gGcggTGGAT ATTCGgcact tccgCcacca caccaccga accgatgacc
251 gcaaacggaG CGGAACAAT TTTATCCGcC acacacgcca tcatatagcc
301 gCGCTTGCC GCGACCTTAT CGAcggcgac ggTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CGCCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATTT TTGCGTTTCG
551 GCAGATTCTT CCCCACCCTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CTTTTTTTTC CTGATGTTT GTCTCTTCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 78; ORF 012.ng>:

**g012.pep**

```

1  MLARRYFNI QPGAVFTDKL LEQLMRFLQF LPEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRFRHHHTHR TDDRKRSGNN FIRHTRHHIA
101 AACRDLIDGD QQRNIAFAQT PKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPAL LQTLFLCFGF
201 RLFLFLFFFF LMFCLFLA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>:

**m012.seq**

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCGGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCGCTCGCn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
401 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
451 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
501 nnnnnnnnnn nnnnnnnnnC AACACAAAAA GGCGTGATTT nTGCCTTTCG
551 GCAGATTCTT CCCCACCCTC CTTCAAACGT TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTGT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 80; ORF 012>:

**m012.pep**

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRHHHTR TDNRKRSGSN FIRHTRHHIT
101 AARXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XXXXQHKKA*F XRFRFLPTL LQTFFLCFGF
201 RLFLFLFLFF LMLCLFPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 81>:

```
a012.seq
1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAACTG  CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTGCGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCCT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTACGCGGA ATATTGCGTT
351 CCGCAAACG  CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TCGCGTTTCG
551 GAAGATTCT  CCCCACCTC CTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 82; ORF 012.a>:

```
a012.pep
1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRYNTHR TDNRKRSGNN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKRRNLMTQ  GFYGVCIQIA VKIQHKKAGF LRFRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*
```

m012/a012 64.2% identity over a 218 aa overlap

	10	20	30	40	50	60
m012.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
a012	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m012.pep	NIMFFQQAVIDIRYFRHHTRTDNRKRSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXXXX					
a012	NIMFFQQAVIDIRYFRYNTHRTDNRKRSGNNFIRHTRHHITTARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m012.pep	XXQHKKAXF					
a012	PKLRSRQTVTVNHAARTFQSKQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
m012.pep	XRFRFLPTLLQTLFLCFGRFLFLFLFLFFLMLCLFPAX					
a012	LRFRFLPTLLQTLFLCFGRFLFLFLFLFFLMLCLFPAX					
	190	200	210			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 012 shows 58.7% identity over a 218 aa overlap with a predicted ORF (ORF 012.ng) from *N. gonorrhoeae*:

m012/g012

	10	20	30	40	50	60
m012.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					

195

	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHHTRTDNRKRSNFIHTRHHITAARXXXXXXXXXXXXXXXXXXXX					
g012	NIMFFQQAVDIRHFRHHHTRTDDRKRSGNNFIHTRHHIAAACRDLDGDGQRNIAFAQT					
	70	80	90	100	110	120
m012.pep	130	140	150	160	170	180
	XXQHKKAXF					
g012	PKLRSRQTVTVNHAARTFQSEQNLIIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
m012.pep	190	200	210	219		
	XRFGRFLPTLLQTFFLCFGRFLFLFLFLMLCLFPA					
g012	LRFGRFLPALLQTLFLCFGRFLFLFLFLMFLCLFLAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 83>:

m012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGTTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCCGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCCGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCC GCCACCTTAT CGACGGCGAC GGTACGCGGA ATATTGCGTT
351 CGCGCAAACG CyTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATTT TTGCGTTTCG
551 GCAGATTCTC CCCCAACCTC CTTCAAACGC TTTTCTCTG CTTTGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 84; ORF 012-1>:

m012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRHHTHR TDNRKRSNFI FIRHTRHHIT
101 AARRHLIDGD GQRNIAFAQT XKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*

```

m012-1/g012 91.7% identity in 218 aa overlap

	10	20	30	40	50	60
m012-1.pep	MLARCHFLNIQLRAVLADKLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
m012-1.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHHTRTDNRKRSNFIHTRHHITAARRHLIDGDGQRNIAFAQT					
g012	NIMFFQQAVDIRHFRHHHTRTDDRKRSGNNFIHTRHHIAAACRDLDGDGQRNIAFAQT					
	70	80	90	100	110	120
m012-1.pep	130	140	150	160	170	180
	XKLRSRQTVTVNHAARTFQSEQNLIIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
g012	PKLRSRQTVTVNHAARTFQSEQNLIIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					

196

	130	140	150	160	170	180
	190	200	210	219		
m012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFLFFLMFCLFPAX					
	:     :     :     :					
g012	LRFGRLPALLLQTLFLCFGRFLFLFLFLFFLMFCLFLAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>:

a012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCCGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCAGTGGAT ATTCCGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAACAAT TTTATCCGCC ACACAGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTACGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TCGCGTTTCG
551 GAAGATTTCT CCCCACCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTTC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 86; ORF 012-1.a>:

a012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVID IRYFRYNTHR TDNRKRSNGN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*

```

a012-1/m012-1 97.2% identity in 218 aa overlap

	10	20	30	40	50	60
a012-1.pep	MLARCHFLNIQLRAVLADKLL	EQLMRFLQFLSEFLFALFR	IFTHKSNRALKFARRHHIHI			
m012-1	MLARCHFLNIQLRAVLADKLL	EQLMRFLQFLSEFLFALFR	IFTHKSNRALKFARRHHIHI			
	10	20	30	40	50	60
	70	80	90	100	110	120
a012-1.pep	NIMFFQQAVIDIRYFRYNTHR	TDNRKRSNGNFIRHTRHHIT	TARRHLIDGDGQRNIAFAQT			
m012-1	NIMFFQQAVIDIRYFRHHTHR	TDNRKRSNGNFIRHTRHHIT	AARRHLIDGDGQRNIAFAQT			
	70	80	90	100	110	120
	130	140	150	160	170	180
a012-1.pep	PKLRSRQTVT VNHAARTFQSK	QNLIFRLGNQKHRRNLMTQ	GFYGVCIQIAVKIQHKKAGF			
m012-1	XKLRSRQTVT VNHAARTFQSE	QNLIFRLGNQKHRRNLMTQ	GFYGVCIQIAVKIQHKKAGF			
	130	140	150	160	170	180
	190	200	210	219		
a012-1.pep	LRFGRLPTLLQTLFLCFGRFL	FLFLFLFFLMFCLFPAX				
m012-1	LRFGRLPTLLQTLFLCFGRFL	FLFLFLFFLMFCLFPAX				
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 87>:

g013.seq

```

1  aTgcctttga ccatgctgtg cagcaGGAcg tGCGGTTtgt tcataatata
51  gtCcgaccGG AAAagcggAG GAAaCGCAGT GCCGCGCCCT TCCCTTTTCT
101 TGCCGTGGCA GGCGATGCag tTgGATTCGT AACTTTTTTG CCCTTTtGtc

```

```

151 atgatGCTgt tgtcggCGGC AGAAGCgGCG GcgCAGAGGC AGCACAAGAT
201 GAAGGCGGTC GGCAGTCGGG TTGTGTtcat tGgcgTTTCC cctaatgttt
251 tgaaaccttg ttttttgatt Ttgcctttac ggggtgaaaa gtttttTtgg
301 cccaaatccg gaatttag

```

This corresponds to the amino acid sequence <SEQ ID 88; ORF 013.ng:

```

g013.pep
  1 MPLTMLCSRT CGLFIIQSDR KSGGNAVPRP SPFLPWQAMQ LDSYTFCPFV
  51 MMLLSAAEAA AQRQHMKAV GSRVVFIVGS PNVLKPCFLI LPLRGEKFFV
 101 PKSGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 89>:

```

m013.seq
  1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TGCGGTTTTT TCATGATGAA
  51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
 101 TGCCGTGGCA GGCACGCAG TTGGATTTCG ACACTTTTTG CCCTTTTGTC
 151 ATGATGCTGT TGTCGGCGGC AGAAGCGGCG GCGCAGAAGC AGCCCAAGAC
 201 GAGGGCGGTC GGCAGTCGGG TTGTGTTCAT TGGTGTTCCT TTCATGTTTG
 251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT TTTGCCGAAT
 301 CAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 90; ORF 013>:

```

m013.pep
  1 MPLTMLCSST CGFFMMKSER XSGGNMVRP SPFLPWQATQ LDSYTFCPFV
  51 MMLLSAAEAA AQKQPKTRAV GSRVVFIVGS FMFETLLLLIL RSGXKIFLPN
 101 Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 91>:

```

a013.seq
  1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TGCGGTTTTT TCATGATGAA
  51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
 101 TGCCGTGGCA GGCACGCAG TTGGATTTCG ACACTTTTTG CCCTTTTGTC
 151 ATGATGCTGT TGTCGGCGGC AGAAGCGGCG GCGCAGAGGC AGCCCAAGAC
 201 GAGGGCGGTC GGCAGTCGGG TTGTGTTCAT TGGTGTTCCT TTAATGTTTG
 251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT CTTGCCGAAT
 301 CGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 92; ORF 013.a>:

```

a013.pep
  1 MPLTMLCSST CGFFMMKSER *SGGNMVRP SPFLPWQATQ LDSYTFCPFV
  51 MMLLSAAEAA AQRQPKTRAV GSRVVFIVGS LMFETLLLLIL RSG*KIFLPN
 101 R*

```

m013/a013 97.0% identity over a 101 aa overlap

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
a013	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFIVGSFMFETLLLLILRSGXKIFLPNQX					
	:					
a013	AQKQPKTRAVGSRVVFIVGSFMFETLLLLILRSGXKIFLPNRX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 013 shows 73.3% identity over a 101 aa overlap with a predicted ORF (ORF 013.ng) from *N. gonorrhoeae*:

## m013/g013

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	:   : :: :					
g013	MPLTMLCSRTCGLFIIQSDRKSGGNAVPRPSPFLPWQAMQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60

  

	70	80	90	100
m013.pep	AQKQPKTRAVGSRVVFIVGSF-MFETLLILR-SGXKIFLPNQX			
	:    :            : :           :    :			
g013	AQRQHKMAVGSRVVFIVGSPNVLKPCFLILPLRGEKFFWPKSGIX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 93>:

g015.seq

```

1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TTCAACATCC GTTTTTCCT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGT CGGCTTTTGG AAAGCACTGC CCCACCTCAA CGACACGATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAG ATTACCCATT TCTCCCGGTT
201 CAACGCGCCT TGGCTCGGCA CAAAATCCT GCTCCTGTTC GCCTACATCG
251 CACTGGGCAT GGTAAATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCTAT GTGTGCATC GCCTGCATCG TTTACCTTGC
351 CAAAACCAA GTCCTGCCAT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 94; ORF 015.ng>:

g015.pep

```

1  MQYLIVKYSH QIEVTITILV FNIRFLLWK NPEKPLVGFW KALPHLNDTM
51  LLFTGLWLMK ITHFSPFNAP WLGTKILLF AYIALGMVMM RARPRSTKFY
101 TVYLLAMCCI ACIVYLAKTK VLPF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 95>:

m015.seq (partial)

```

1  ..AAAATCAGAA AAGCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA
51  CGACACCATG CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT
101 TCTCCCGGTT CAACGCGCCT TGGCTCGGTA CAAAATCCT GCTTCTGCTC
151 GCCTATATCG CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC
201 CAAGTTCTAC ACCGTTTACC TGCTCGCCAT GTGTTGCGTC GCCTGCATCG
251 TTTACCTTGC CAAAACCAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 96; ORF 015>:

m015.pep (partial)

```

1  ..KIRKALAGFW KALPHLNDTM LLFTGLWLMK ITHFSPFNAP WLGTKILLLL
51  AYIALGMMM RARPRSTKFY TVYLLAMCCV ACIVYLAKTK VLPF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 97>:

a015.seq

```

1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TTCAACATCC GTGTTTCNT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA CGACACCATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT TCTCCCGGTT
201 CAACGCGCCT TGGCTCGGTA CAAAATCCT GCTTCTGCTC GCCTATATCG
251 CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCCAT GTGTTGCGTC ACCTGCATCG TTTACCTTGC
351 CAAAACCAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 98; ORF 015.a>:

a015.pep

1 MQYLIVKYSH QIFVTITILV FNIRVFXLWK NPEKPLAGFW KALPHLNDTM  
 51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLL AYIALGMMM RARPRSTKFY  
 101 TVYLLAMCCL TCIVYLAKTK VLPF\*

m015/a015 96.7% identity over a 91 aa overlap

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
a015	LIVKYSHQIFVTITILVFNIRVFXLWKNPEKPLAGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep	40	50	60	70	80	90
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP					
a015	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCLTCIVYLAKTKVLP					
	70	80	90	100	110	120
m015.pep	FX					
a015	FX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 015 shows 94.5% identity over a 91 aa overlap with a predicted ORF (ORF 015.ng)

from *N. gonorrhoeae*:

m015/g015

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
g015	LIVKYSHQIFVTITILVFNIRFFLLWKNPEKPLVGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep	40	50	60	70	80	90
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP					
g015	FSPFNAPWLGTKILLLLFAYIALGMVMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP					
	70	80	90	100	110	120
m015.pep	FX					
g015	FX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 99>:

g018.seq

1 atGCAGCAGG GGCagttggt tggacgcgtc gcccgcaata AAGATATGCG  
 51 GAATgctggt CTGCATggtC AGCGGATCGG CAACGGGtac gccgcgcgcg  
 101 tctttgTCGA TATTGATGTT TTCCAAACCG ATATgtCAA CGTTCGGACG  
 151 GCgACCTACG GCTGCCAACA TATATTCGGC AACAAATACG CCTTTTTCGC  
 201 CATCCTGCTC CCAATGGACT tctACATTGC CGTCTGCGTC GAGTTTGACC  
 251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT tctTCTCCGA ACACGGCTTT  
 301 CGCCTCGTCT GA

This corresponds to the amino acid sequence <SEQ ID 100; ORF 018.ng>:

g018.pep

1 MQQGQLVGRV ARNKDMRNAG LHGQRIGNGY AARVFVDIDV FQTDIVNVRT  
 51 ATYGCQHIFG NKYAFFAILL PMDFYIAVCV EFDLGFSIQM QFQFFSEHGF

101 RLV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 101>:

## m018.seq

```

1   ATGCAGCAGA GGCAGTTGGT TGGACGCATC GCCTGCGATG AAGATATGCG
51  GAATACTGGT CTGCATGGTC AGCGGGTCGG CAACAGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATATT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCCACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCATC GAGTTTGACC
251 TCGGTTTtag CATCCAGATG CAGTTTCAAT TCTTCGCCGA ACACGGCGTT
301 CGCCTCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 102; ORF 018>:

## m018.pep

```

1   MQQRQLVGRI ACDEDMRNTG LHGQRVGNRY AARIFFDIDI FQTDIVNVRT
51  AAHGCGHIFG NKYAFFAILL PMDFYIAVCI EFDLGFSIQM QFQFFAEHGV
101 RLV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 103>:

## a018.seq

```

1   ATGCAGCAGG GGCAGTTGGT TGGACGCGTC GCCCGCAATA AAGATATGCG
51  GAATACTGGT CTGCATAGTC AGCGGATCGG CAACGGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATGTT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCTACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCGTC GAGTTTGCCG
251 TCGGTTTtag CATCCAAATG CAGTTTCAAT TCTTCACCGA ACACGGCTTT
301 CGCCTCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 104; ORF 018.a>:

## a018.pep

```

1   MQQGQLVGRV ARNKDMRNTG LHSQRIGNGY AARIFFDIDV FQTDIVNVRT
51  AAYGCGHIFG NKYAFFAILL PMDFYIAVCV EFGLGFSIQM QFQFFTEHGF
101 RLV*

```

m018/a018 86.4% identity over a 103 aa overlap

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG					
	:  ::   :     : :       : : : : : : : : : : : : : : : : :					
a018	MQQGQLVGRVARNKDMRNTGLHSQRIGNGYAARIFFDIDVFQTDIVNVRTAAYGCGHIFG					
	10	20	30	40	50	60
	70	80	90	100		
m018.pep	NKYAFFAILLPMDFYIAVCIEFDLGFSIQMQFQFFAEHGVRLVX					
	: :					
a018	NKYAFFAILLPMDFYIAVCVEFGLGFSIQMQFQFFTEHGFRLVX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 018 shows 84.5% identity over a 103 aa overlap with a predicted ORF (ORF 018.ng) from *N. gonorrhoeae*:

## m018/g018

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG					
	:  ::   :     : :       : : : : : : : : : : : : : : : : :					
g018	MQQGQLVGRVARNKDMRNAGLHGQRIGNGYAARVFVDIDVFQTDIVNVRTATYGCQHIFG					
	10	20	30	40	50	60



	70	80	90	100
m018.pep	NKYAFFAILLPMDFYIAVCIEFDLGFSIQMQQFFAEHGVRLVX			
	:     :     :			
g018	NKYAFFAILLPMDFYIAVCVEFDLGFSIQMQQFFSEHGFRLVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 105>:

g019.seq (partial)

```

1  ..ctgctggcgg ccctggtgct tgcgcgtgt tcttcgACAA ACacacTGCC
51  AGCCGGCAAG ACCCCGGCAG ACAATATAGA AActgcCgAC CTTTCGGCAA
101 GCGTTCCAC ccgcCCTGCC GAACCGGAAG GAAAAACGCT GGCAGATTAC
151 GGCGGCTACC CGTCCGCACT GGATGCAGTG AAACAGAACA ACGATGCGGC
201 AGCCGCCGCC TATTTGGAAÀ Acgcaggaga cagCGcgatg gcGGAAAatg
251 tccgcaagga gtgGCTGa

```

This corresponds to the amino acid sequence <SEQ ID 106; ORF 019.ng>:

g019.pep (partial)

```

1  ..LLAALVLAAC SSTNTLPAGK TPAENIETAD LSASVPTRPA EPEGKTLADY
51  GGYPSALDAV KQNNDAÀAAA YLENAGDSAM AENVRKEWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 107>:

m019.seq (partial)

```

1  ATGTACCTAC CCTCTATGAA GCATTCCCTG CCGCTGCTGG CGGCCCTGGT
51  GCTTGCCGCG TGTCTTCGA CAAACACACT GCCAGCCGGC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCCGCCCT
151 GCCGAACCCG AAAGAAAAAC GCTGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCACGCG ACAGTGGACG CTGTTGCAC AGGAATACGC
351 CAAACTCGAA CCGGCAGGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCTG AACTGGTCAA AAATACGGGC
451 AACTGCCTT CGGGCTGCAC CAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGC GCGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCAAT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTAAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCCT TGGACTATTA
801 CGGCAAGGTT GCCGACCGCC GCCAAGTAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCCTTGCGC GCCCGACGTT GGGACGAGCT GGCCTCCGTT
901 ATCTCGCATA TGCCCGAAAA ACTGCAAAAA AGCCCGACCT GGCTCTACTG
951 GCTGGCACGC AGCCGCGCCG CAACGGGCAA CACGCAAGAG GCGGAAAAAC
1001 TTTACAAACA GGCGGCAGCG ACGGCAGGA ATTTTATGC GGTGCTGGCA
1051 GGGGAAGAAT TGGGTCGGAA AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAAAC AGCGTCCGCC GCATGGCGGA AGACGGTGCA GTCAAACGCG
1151 CACTGGTACT GTTCCAAAAC AGCCAATCTG CCGGTGATGC AAAAATGCGC
1201 CGTCAGGCTC AGGCGGAATG GCGTTTGGC ACACGCGGCT TTGACGAAGA
1251 CAAGCTGCTG ACCGCGCGC AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCAGC GCAAACTCAA CTACACCTTG
1351 CGCTATATTT CGCGTTTAA AGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCTTGGG TTTATGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATAGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGCG AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCCGACG GG...

```

This corresponds to the amino acid sequence <SEQ ID 108; ORF 019>:

m019.pep (partial)

```

1  MYLPSMKHSL PLLAALVLAA CSSTNTLPAG KTPADNIETA DLSASVPTRP

```

```

51  AEPERKTLAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARROWT LFAQEYAKLE PAGRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYYGKV ADRRLTDDQ IEWYARAALR ARRWEDELASV
301 ISHMPEKLQK SPTWLYWLR SRAATGNTQE AEKLYKQAAA TGRNIFYAVLA
351 GEELGRKIDT RNNVPDAGKN SVRRMAEDGA VKRALVLFQV SQSAGDAKMR
401 RQAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL
451 RYISPFKDTV IRHAQNVNVD PAWVYGLIRQ ESRFVIGAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADG...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 109>:

a019.seq

```

1  ATGTACCCAC CCTCTCTGAA GCATTCCCTG CCGCTGCTGG TGGNCTGGT
51  GCTTGCCGCG TGTCTTNGA CAAACACACT GTCAGCCGAC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCNGCCCT
151 GCCGAACCCG AANGAAAAAC GTNGGCAGAT TACGGCGGGT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCGCGCAG ACAGTGGACG CTGTNTGCAC ANGAATATGC
351 NAAACTCGAA CCGGCANGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCCGCG AACTGGTCAA AAATACGGGC
451 AAAGTGCCTT CCGGCTGCAC CAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGCGCGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCC
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAGGAA GCACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTAAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCTT TGGACTATTA
801 NGGCAAGGTT GCCGACCGCC GCCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCNTNNGC NNNCGNNGT NGNANGANN NTGNNCCGNN
901 ANCNCGNNN TGCNNGANAA ACNNNNNNAN AGNCNNANT NGNTNNANTG
951 NNTGGCACGC AGCCGCGCCG CNACGGGCAA CACGCAANAN GCGGANAAC
1001 TNTACAAACA GCGGCGAGCA NCGGGCANGA ATTTTATGC NGTGTGNCN
1051 GGGGAAGAGT TGGGCGGCAN AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAANC AGCGTCTTCC GTATGGCGGA AGACGGCGCG ATTAAGCGCG
1151 CGCTGGTGCT GTTCCGAAAC AGCCGAACCG CCGCGATGC GAAAATGCGC
1201 CGTCNNGGCTC AGCGGGAATG GCGTTTCGCC ACACGCGGCT TCGATGAAGA
1251 CAAGCTGCTG ACCGCGCGCG AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTTG
1351 CGCTACATTT CGNNNNNTNA NGACACGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGCGGTGGG TTTACGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATGGG CCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCTTGCCA CCGCGCGCGA AATCGCCGCG AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCCGACG GCAATATCCG TATGGGGACG TGGTATATGG
1601 CGGACACCAA ACGCCGCTG CAAAACAACG AAGTCTCGC CACCGCAGGC
1651 TATAACGCGG GTCCCGGCGA GCGCGCCGA TGGCAGGCGG ACACGCCCTT
1701 CGAAGGCGCG GTATATGCCG AAACCATCCC GTTTTCCGAA ACGCGCGACT
1751 ATGTCAAAAA AGTGATGGCC AATGCCGCTC ACTACGCTC CCTCTTCGGC
1801 GCGCCGCACA TCCCGCTCAA ACAGCGTATG GGCATTGTCC CCGCCCGCTG
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 019.a>:

a019.pep

```

1  MYPPSLKHSL PLLVXLVLAA CSXTNTLSAD KTPADNIETA DLSASVPTXP
51  AEPEKTXAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARROWT LXAXEYAKLE PAXRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDXXGKV ADRRLTDDQ IEWYARAAXX XXXXXXXXXX
301 XXXXXXXXXX XXXXXXXXAR SRAATGNTQX AXKLYKQAAA XGXNIFYAVLX
351 GEELGRXIDT RNNVPDAGKX SVLRMAEDGA IKRALVLFVN SRTAGDAKMR
401 RQAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL

```

451 RYISXXXTV IRHAQNVNVD PAWVYGLIRQ ESRFVMGAQS RVGAQGLMQV  
 501 MPATAREIAG KIGMDAAQLY TADGNIRMGW WYMADTKRRL QNNEVLATAG  
 551 YNAGPGRARR WQADTPLEGA VYAETIPFSE TRDYVKKVMA NAAYYASLFG  
 601 APHIPLKQRM GIVPAR\*

m019/a019 88.9% identity over a 524 aa overlap

m019.pep	10	20	30	40	50	60
	MYLPSMKHSLPLLAALVLAACSSNTNLPAGKTPADNIETADLSASVPTRPAPERKTLAD					
a019	10	20	30	40	50	60
	MYPPSLKHSLPLLVXLVLAACSXTNTLSADKTPADNIETADLSASVPTXPAEPEXKTXAD					
m019.pep	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSGLGARRQWTLFAQEYAKLE					
a019	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSGLGARRQWTLXAXEYAKLE					
m019.pep	130	140	150	160	170	180
	PAGRAQEVECYADSSRNDYTRAAELVKNTGKLPSCGCTKLLEQAAASGLLDGNDAWRRVRG					
a019	130	140	150	160	170	180
	PAXRAQEVECYADSSRNDYTRAAELVKNTGKLPSCGCTKLLEQAAASGLLDGNDAWRRVRG					
m019.pep	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
a019	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
m019.pep	250	260	270	280	290	300
	EQRSAFWGVLGHYQSQNLNVPALDYXGKVADRRQLTDDQIEWYARAALRARRWDELASV					
a019	250	260	270	280	290	300
	EQRSAFWGVLGHYQSQNLNVPALDYXGKVADRRQLTDDQIEWYARAAXXXXXXXXXXX					
m019.pep	310	320	330	340	350	360
	ISHMPEKLQKSPTWLYWLARSRAATGNTQEAELKLYKQAAATGRNFYAVLAGEELGRKIDT					
a019	310	320	330	340	350	360
	XXXXXXXXXXXXXXXXXARSRAATGNTQXAXKLYKQAAAXGXNFYAVLXGEELGRKIDT					
m019.pep	370	380	390	400	410	420
	RNNVPDAGKNSVRRMAEDGAVKRALVLFQNSQSAGDAKMRRQAQAEWRFATRGFDEDKLL					
a019	370	380	390	400	410	420
	RNNVPDAGKXSVLRMAEDGAIKRALVLFNRSRTAGDAKMRRXAQAEWRFATRGFDEDKLL					
m019.pep	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLNLYTLRYISPFKDTVIRHAQNVNVDPAWVYGLIRQ					
a019	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLNLYTLRYISXXXTVIRHAQNVNVDPAWVYGLIRQ					
m019.pep	490	500	510	520		
	ESRFVIGAQS RVGAQGLMQVMPATAREIAGKIGMDAAQLYTADG					
a019	490	500	510	520	530	540
	ESRFVIGAQS RVGAQGLMQVMPATAREIAGKIGMDAAQLYTADGNIRMGWYMAADTKRRL					
a019	550	560	570	580	590	600
	QNNEVLATAGYNAGPGRARRWQADTPLEGAVYAETIPFSETRDYVKKVMANAAYYASLFG					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 019 shows 95.5% identity over a 89 aa overlap with a predicted ORF (ORF 019.ng) from *N. gonorrhoeae*:

g019/m019

		10	20	30	40	49
g019.pep		LLAALVLAACSSNTLPAGKTPADNIETADLSASVPTRPAEPEGKTLAD				
m019	MYLPSMKHSLPLLAALVLAACSSNTLPAGKTPADNIETADLSASVPTRPAEPEKTLAD					
		10	20	30	40	50 60
	50	60	70	80	89	
g019.pep	YGGYPSALDAVKQNDAAAAYLENAGDSAMAENVRKEWL					
	:    :    :    :					
m019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLFAQEYAKLE					
		70	80	90	100	110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 111>:

g023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  AATGCAGCGT GCGACTGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAG CTTGGGTAAA AGTATTTACC CAAGTGAGCT TTATCGCCGT
201 ATTCTTGCAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCCTCGG CGTGC GTTTG TTTTGCAGG TTGCCACCAT TGtctGGCTG
301 GTCGGCTGCC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 023.ng>:

g023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVL FAL PKEYPAWQAF
51  FSQAWVKVFT QVSFIAVFLH AWVGIRDLWM DYIKPFGVRL FLOVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

m023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  GATGCAACGT GCGACTGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTTCCCTG CCTAAAGAAT ATTCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT
201 ATTCTTGCAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCCTCGG CGTGC GTTTG TTTTGCAGG TTGCCACCAT CGTTTGGCTG
301 GTCGGCTGTC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 023>:

m023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVL FSL PKEYSAWQAF
51  FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYIKPFGVRL FLOVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

a023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GGGATTGGGC
51  GATGCAACGT GCGACCGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCTCTG CCTAAAGAAT ATTCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT

```

201 ATTCTTGCAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATNA  
 251 AACCTTCGG CGTGCGTTG TTTTGCAGG TTGCCACCAT CGTCTGGCTG  
 301 GTCGGCTGCT TGGTGTATTC AATTAAAGTA ATTTGGGGT AA

This corresponds to the amino acid sequence <SEQ ID 116; ORF 023.a>:

a023.pep  
 1 MVERKLTGAH YGLRDWAMQR ATAVIMLIYT VALLVVLFL PKEYSAWQAF  
 51 FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYXKPGVRL FLQVATIVWL  
 101 VGCLVYSIKV IWG\*

m023/a023 96.5% identity over a 113 aa overlap

	10	20	30	40	50	60
m023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFLSLPKEYSAWQAFSSQTWVKVFT					
a023	MVERKLTGAHYGLRDWAMQRATAVIMLIYTVALLVVLFLALPKEYSAWQAFSSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
m023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
a023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSIKVIWGX					
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 023 shows 97.3% identity over a 113 aa overlap with a predicted ORF (ORF 023.ng) from *N. gonorrhoeae*:

g023/m023

	10	20	30	40	50	60
g023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFLALPKEYPAWQAFSSQAWVKVFT					
m023	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFLSLPKEYSAWQAFSSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
g023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
m023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 117>:

g025.seq

1 ATGTTGAAAC AAACgACACT TTTGGCAGCT TGTACCGCCG TTGCCGCTCT  
 51 GTTGGGCGGT TGcGCCACCC AACAGCCTGC TccTGTCATT GCAGGCAATT  
 101 CAGGTATGCA GACCGTATCG TCTGCGCCGG TTTACAATCC TTATGGCGCA  
 151 ACGCCGTACA ATGCCGCTCC TGCCGCCAac gatgcGCCgT ATGTGCCGCC  
 201 CGTGCAAact gcgcgggttT ATTGCGCTCC TGCTTATGTT CCGCcgTCTG  
 251 CACCTGCCGT TTCGGgtaca tatgtTCCTT CTTACGCACC CgtcgACATC  
 301 aacgCGCGCa cgCataCTAT TGTGCGTGGC GACACgGtgt acaACATTTC  
 351 caaAcgCtAc CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA  
 401 CCGACAATAC GTTGAGCATC GGTcAGATTG TTAAAGTCAA ACCGGCaggA  
 451 TATGCCGCAC CGAAAACCGC AGCCGTAGAA AGCAGGCCCG CCGTACCGGC  
 501 TGCCCGCAA ACCCTGTGA AACCgCCGC gcaACCGCCC GTTCAGTCCG  
 551 CGCCGCAACC TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCCCCC  
 601 GCGCCGCCCC CGCAATCTCC TGCCGCTTCG CCTTCCGCA CGCGTTCGGT  
 651 CGGCGGCATT GTTTGGCAGC GTCCGACCCA AGGTAAAGTG GTTGCCGATT

```

701 TCGGCGGCGG CAACAAGGGT GTCGATATTG CCGGCAATGC CGGACAACCC
751 GTTTTGGCGG CGGCTGACGG CAAAGTGGTT TATGCCGGTT CAGGTTTGAG
801 GGGATACGGA AACTTGGTCA TCATCCAGCA CAATTCCTCT TTCCTGACCG
851 CGTACGGGCA CAACCAAAA TTGCTGGTCG GCGAAGGTCA GCAGGTCAAA
901 CGCGGTACAG AGGTGCTTT GATGGGTAAT ACCGATGCTT CCAGAACGCA
951 GCTTCATTTC GAGGTGCGTC AAAACGGCAA ACCGGTTAAC CCGAACAGCT
1001 ATATCGCGTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 025.ng>:

```

g025.pep
1 MLKQTTLLAA CTAVAALLGG CATQQPAPVI AGNSGMQTVS SAPVYNPYGA
51 TPYNAAPAAAN DAPYVPPVQT APVYSPPAYV PPSAPAVSGT YVPSYAPVDI
101 NAATHTIVRG DTVYNISKRY HISQDDFRW NGMTDNTLSI GQIVKVKPAG
151 YAAPKTAAVE SRPAVPAAQ TPVKPAAQPP VQSAPQPAAP AAENKAVPAP
201 APAPQSPAAS PSGTRSVGGI VWQRPTQGV VADFGGNGK VDIAGNAGQP
251 VLAAADGKVV YAGSGLRGY NLVIIQHNSS FLTAYGHNQK LLVGEQGVK
301 RGQQVALMGN TDASRTQLHF EVRQNGKPVN PNSYIAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

```

m025.seq (partial)
1 ..GTGCCGCGG TGCAAAGCGC GCCGGTTTAT ACGCCTCCTG CTTATGTTCC
51 GCCGTCTGCA CCTGCCGTTT CGGGTACATA CGTTCCTTCT TACGCACCCG
101 TCGACATCAA CGCGGCGACG CATACTATTG TCGCGGCGCA CACGGTGTAC
151 AACATTTCOA AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA
201 CGGCATGACC GACAATACGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC
251 CGGCAGGATA TGCCGCAACG AAAGCCGCG CCGTAAAAAG CAGGCCCGCC
301 GTACCGGCTG CGCGCAACC GCCCGTACAG TCCGCACCCG TCGACATTAA
351 CGCGGCGACG CATACTATTG TCGCGGCGCA CACGGTGTAC AACATTTCOA
401 AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA CGGCATGACC
451 GACAATATGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC CGGCAGGATA
501 TGCCGCACCG AAAACCGCG CCGTAGAAAG CAGGCCCGCC GTACCGGCTG
551 CCGTGCAAAC CCCTGTGAAA CCGCGCGCGC AACCGCCTGT GCAGTCCGCG
601 CCGCAACCTG CCGCGCCCGC TCGGAAAAAT AAAGCGGTTT CCGCGCCCGC
651 CCGCAATCT CCTGCCGCTT CGCCTTCCGG CACGCGTTCG GTCGGCGGCA
701 TTGTTTGGCA GCGTCCGACG CAAGGTAAAG TGGTTGCCGA TTTCGGCGGC
751 AACAACAAGG GTGTCGATAT TGCCGGTAAT GCGGGACAGC CCGTTTGGC
801 GGCGGCTGAC GGCAAAGTGG TTTATGCCGG TTCAGTTTG AGGGGATACG
851 GAAACTTGGT CATCATCCAG CATAATTCTT CTTTCCTGAC CGCATACGGG
901 CACAACCAAA AATTGCTGGT CGGCGAGGGG CAGCAGGTCA AACCGCGTCA
951 GCAGGTTGCT TTGATGGGCA ATACCGATGC TTCCAGAACG CAGCTTCATT
1001 TCGAGGTGCG TCAAACCGG AAACCGGTTA ACCCGAACAG CTATATCGCG
1051 TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 025>:

```

m025.pep (partial)
1 ..VPPVQSAPVY TPPAYVPPSA PAVSGTYVPS YAPVDINAAT HTIVRGDTVY
51 NISKRYHISQ DDFRAWNGMT DNTLSIGQIV KVKPAGYAAP KAAAVKSRPA
101 VPAAQPPVQ SAPVDINAAT HTIVRGDTVY NISKRYHISQ DDFRAWNGMT
151 DNLSIGQIV KVKPAGYAAP KTAAVESRPA VPAAVQTPVK PAAQPPVQSA
201 PQPAAPAAEN KAVPAPAPQS PAASPSGTRS VGGIVWQRPT QGKVVADFGG
251 NNKGVDIAGN AGQPVLAAD GKVVYAGSGL RGYGNLVIIQ HNSSFLLTAYG
301 HNQKLLVGEQ QQVKRGQOVA LMGNTDASRT QLHFVVRQNG KPVNPNSYIA
351 F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

a025.seq
1 ATGTTGACAC CAACAACACT TTAGGTAGCT TGTACCGCCC TTGCCGCTCA
51 GTTGGGCGGA TGCCCCACCC AACACCCTTC TCCTGTCAAT GCAGGCAATT
101 CAGGTATGCA GACCGTACCG TCTGCGCCGG TTTACAAATCC TTATGGCGCA

```

```
151 ACGCCGTACA ATGCCGCTCC TGCCGCCAAC GATGCGCCGT ATGTGCCGCC
201 GGTGCAAAGC GCGCCGGTTT ATANGCCTCC TGCTTATGTT CCGCCGTCTG
251 CACCTGCCGT TTCGGGTACA TACGTTCTT CTTACGCANC CGTCGACATC
301 AACGCGGCGA CCCATACTAT TGTGCGCGGC GACACCGTGT ACAAGATTTC
351 CAAATGCTAC CATATCTCTC AAGACGATTT CCGTGCGTGG AACGCGATGA
401 CCGACAATAC GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA
451 TATGCCGCAC CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC
501 TGCCGCGCAA CCGCTCGTAC AGTCCGCACC CGTCGACATC AACGCGGCGA
551 CGCATACTAT TGTGCGCGGC GACACGGTGT ACAACATTTC CAAACGCTAC
601 CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA CCGACAATAC
651 GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA TATGCCGCAC
701 CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC TGCCGTGCAA
751 ACCCCTGTGA AACC CGCCG GCAACCGCCT GTGCAGTCCG CGCCGCAACC
801 TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCGCCC GCCCCGCAAT
851 CTCCTGCCGC TTCGCCTTCC GGCACGCGTT CCGTGCGCGG CATTGTTTGG
901 CAGCGTCCGA CGCAAGGTAA AGTGGTTGCC GATTTCGGCG GCAACAACAA
951 GGGTGTCGAT ATTGCAGGAA ATGCGGGACA GCCCGTTTGG GCGGCGGCTG
1001 ACGGCAAAGT GGTATTATGCA GGTTCGGTT TGAGGGGATA CGGCAATTG
1051 GTCATCATCC AGCATAATTC TTCCTTCTG ACCGCATACG GGCACAACCA
1101 AAAATTGCTG GTCGCGAAG GCCAGCAGGT CAAACGCGG CAGCAGGTCG
1151 CTTTGATGGG CAATACCGAG GCTTCTAGAA CGCAGCTTCA TTTGAGGTCG
1201 CGGCAAAACG GCAAACCGGT TAATCCGAAC AGCTATATCG CGTTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 025.a>:

```
a025.pep
1 MLTP TTL*VA CTALAAQLGG CPTQHPSPIV AGNSGMQTVS SAPVYNPYGA
51 TPYNAA PAAN DAPYVPPVQS APVYXPPAYV PPSAPAVSGT YVPSYAXVDI
101 NAATH TIVRG DTVYKISKCY HISQDD FRAW NGMTDNTLSI QIVKVKPAG
151 YAAPKA AAVK SRPAVPAAQ PLVQSAPVDI NAATH TIVRG DTVYNISKRY
201 HISQDD FRAW NGMTDNTLSI QIVKVKPAG YAAPKA AAVK SRPAVPAAVQ
251 TPVKPA AQPP VQSAPQPAAP AAENKAVPAP APQSPAASPS GTRSVGGIVW
301 QRPTQ GKVVA DFGGNNKGVD IAGNAGQPV LAAADGKVVA GSGLRGYGNL
351 VTIQHNS SFL TAYGHNQKLL VEGEQQVKRG QQVALMGNT EASRTQLHFEV
401 RQNGKPV NPN SYIAF*
```

m025/a025 97.4% identity over a 351 aa overlap

```

                                     10      20      30
m025.pep                               VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
                                     |||:|||:|||:|||:|||:|||:|||
a025      GMQTVPSAPVYNPYGATPYNAAPAANDAPYVPPVQSAPVYXPPAYVPPSAPAVSGTYVPS
               40      50      60      70      80      90

               40      50      60      70      80      90
m025.pep      YAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMTDNTLSI QIVKVKPAGYAAP
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025      YAXVDINAATH TIVRGDTVYKISKCYHISQDD FRAWNGMTDNTLSI QIVKVKPAGYAAP
               100     110     120     130     140     150

               100     110     120     130     140     150
m025.pep      KAAAVKSRPAVPAAQPPVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025      KAAAVKSRPAVPAAQPLVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
               160     170     180     190     200     210

               160     170     180     190     200     210
m025.pep      DNMLSIGQIVKVKPAGYAAPKTA AVESRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025      DNTLSIGQIVKVKPAGYAAPKAAAVKSRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
               220     230     240     250     260     270

               220     230     240     250     260     270
m025.pep      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQ GKVVADFGGNNKGVDIAGNAGQPVLAAD
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
```

```

a025      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLAAD
           280      290      300      310      320      330

m025.pep      280      290      300      310      320      330
GKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDASRT
|||||
a025      GKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTEASRT
           340      350      360      370      380      390

m025.pep      340      350
QLHFEVRQNGKPVNPNSYIAFX
|||||
a025      QLHFEVRQNGKPVNPNSYIAFX
           400      410

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 025 shows 75.6% identity over a 353 aa overlap with a predicted ORF (ORF 025.ng) from *N. gonorrhoeae*:

m025/g025

```

m025.pep      10      20      30
               VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
               |||||:||||:|||||
g025      GMQTVSSAPVYNPYGATPYNAAPAANDAPYVPPVQTAPVYSPPAYVPPSAPAVSGTYVPS
           40      50      60      70      80      90

m025.pep      40      50      60      70      80      90
YAPVDINAATHITVRGDTVYNISKRYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
|||||
g025      YAPVDINAATHITVRGDTVYNISKRYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
           100     110     120     130     140     150

m025.pep      100     110     120     130     140     150
KAAAVKSRPAVPAAPAAQPPVQSAPVDINAATHITVRGDTVYNISKRYHISQDDFRAWNGMT
|
g025      K-----

m025.pep      160     170     180     190     200     210
DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
|||||
g025      -----TAAVESRPAPVPAAPAAQTPVKPAAQPPVQSAPQPAAPAAEN
           160     170     180     190

m025.pep      220     230     240     250     260
KAVPAPAP--QSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
|||||
g025      KAVPAPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
           200     210     220     230     240     250

m025.pep      270     280     290     300     310     320
ADGKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDAS
|||||
g025      ADGKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDAS
           260     270     280     290     300     310

m025.pep      330     340     350
RTQLHFEVRQNGKPVNPNSYIAFX

```



g025                    |||||  
                          RTQLHFEVRQNGKPVNPNSYIAFX  
                          320                    330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 113>:

g031.seq  
 1 ATGGTGTCCC TCCGCTTCAG ATTCGGCAAC CACTTTAAAC GCCGACATTC  
 51 TGACAATTTC CTTTTCGCC AGCCAAATAT CATGCGTATC TTTTCGGTTTCG  
 101 GGCTTGTTGG GCATGGCAAC CTTCAACAGC CGCGCCATCA CAGGAATCGT  
 151 CGTTCCCTGA ATCAGCAGCG ACAGCACCAC CACGGCAAAC GCCACATCAA  
 201 ACAGCAGGTG CGAATTGGGA ACGCCCATCA CCAGCGGCAT CATCGCCAGC  
 251 GAAATCGGTA CGGCTCCTCG CAAGCCCAAC CAACTGATAT ACGCCTTTTC  
 301 ACGCAGGCTG TAATTGAATT TCCACAAACC GCCGAACACT GCCAGCGGAC  
 351 GCGCGACCAG CATCAGGAAC GCCGCAATCG CCAAGGCTTC CGCCGCCCTG  
 401 TCCAACACGC CGCGGGGAGA AACCAGCAGA CCGAGCATGA CGAACAAAGT  
 451 TGCCTGCGCC AGCCAAGCCA AACCGTCCAT CACACGCAA ACCTGTTCCG  
 501 TcgcACGGTT GCGCTGGTTA CCGACAATGA TGCCGGCAAG GTAAACCGCC  
 551 AAAAAGCCGC TGCCGCCTAT GGTATTGGTA AACGCAAACA CAAGCAGCCC  
 601 GCCCGACACA ATCATCAGCG CGTACAGACC TTCCGtacac acctccaatt  
 651 cccaatcaac gtcatagtg tctcccggtg taaaatgttc ttcaacttcag  
 701 aatccccccc ttcttcccag cccgaaacct tcatgtgtta nacctggtg  
 751 tgccccaacg gatttagtaa cctcccaatg actctggtg tcgccccctt  
 801 cgccccgttt ctccttcggt gaaaacttgt tgtccccgtc ttacattaa

This corresponds to the amino acid sequence <SEQ ID 114; ORF 031.ng>:

g031.pep  
 1 MVSRLRFREGN HFKRRHSDNF LFRQPNIMRI FRFGLVGHGN LQQPRHHRNR  
 51 RSLNQQRQHH HGKRHIKQV RIGNAHHRH HRQRNRYGSS QAQPTDIRLF  
 101 TQAVIEFPQT AEHCQRTRDQ HQERRNRQGF RRPVQHAGGR NQQTEDHEQS  
 151 CLRQPSQTVH HTQNVFRRTV ALVTDNDAGK VNRQKAAAY GIGKRKHQKQ  
 201 ARHNHQRVQT FRTHLQFPIN VIAVSRVKMF FTSESPPSSQ PETFMCXTLG  
 251 CPNGFSNLPM TLLVAPFARF LLPGKLVVPV LH\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

m031.seq (partial)  
 1 ...CGCCTGAAGC ACGGTGTCGG ACTGCATTTT TATTCGGCTA TACGCCTTTT  
 51 CACGCAGGCT GTAATTGAAT TTCCACAAAC CGCCGAACAC TGCCGACGGA  
 101 CGCGCGACCA GCATCAGGAA CGCCGCAATC GCCAAGGCTT CCGCCGCCCT  
 151 GTCCAACACG TTGGCAGGAG AAACCAGCAG CAAAGGCATT CCCAAACGTG  
 201 CGGACAAAGT GGTGCAAAAC ACGCTCAGAA ACAACAGTGC GCCACCCGGC  
 251 AG....

This corresponds to the amino acid sequence <SEQ ID 116; ORF 031>:

m031.pep (partial)  
 1 ...RLKHGVLGHF YSAIRLFTQA VIEFPQTAEH CRRTRDQHQE RRNRQGFRRP  
 51 VQHVGRNRQQ QRHSQTCGQS GRNHAQKQOC ATRQ....

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

a031.seq  
 1 ATACGCCTTT TCACGCAGGC TGTAATTGAA TTTCCACAAA CCGCCGAACA  
 51 CTGCCGCGCG ACGCGCGACC AGCATCAGGA ACGCCGCAAT CGCCAAGGCT  
 101 TCCGCCGCCG CGTCCAACAC GTTGGCAGGA GAAACCAGCA GCAAAGGCAT  
 151 TCCCAAACGT GCGGACAAAG TGCTCGAAAC CACGCTCAGA AACAACAGTG  
 201 CGCCACCCGG CAG

This corresponds to the amino acid sequence <SEQ ID 118; ORF 031.a>:

a031.pep (partial)  
 1 IRLFTQAVIE FPQTAEHCRR TRDQHQRERN RQGFRFPVQH VGRNRQQQRH  
 51 SQTGQSGRN HAQKQCATR Q

**m031/a031** 100.0% identity over a 71 aa overlap

10 20 30 40 50 60  
 m031.pep RLKHGVLGHFYSAIRLFTQAVIEFPQTAEHCRRTRDQHQERRNRQGFRRPVQHVGRNRQQ  
 |||||  
 a031 IRLFTQAVIEFPQTAEHCRRTRDQHQERRNRQGFRRPVQHVGRNRQQ  
 10 20 30 40  
 70 80  
 m031.pep QRHSQTCGQSGRNHAQKQQCATRQ  
 |||||  
 a031 QRHSQTCGQSGRNHAQKQQCATRQ  
 50 60 70

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 031 shows 60.0% identity over a 85 aa overlap with a predicted ORF (ORF 031.ng) from *N. gonorrhoeae*:

m031/g031

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 119>:

g032.seq

1	ATGCGGCGAA	ACGTGCCTGC	CGTCGCCGTA	TTGCCCGGCC	CACGATTCGA
51	GGCGTTTTTG	GATTTGGCGT	TGGCTCAGGG	GGGTGCCGTT	CCTGCCGGTA
101	AACAGGGCTT	TGCCGTCGGA	TGCCGTCGTA	CGCAGCGGCA	GATAGTTTTT
151	CAAGGCTTCC	ACGCTTTTTG	CGGCTCAGCG	AACCTGACGC	TGATTGCGCC
201	CTTTGCCGGT	AACGTGTACC	CACGCTTCGT	CCAAATATAC	ATCATCTGCA
251	TTCAAGCCGT	GTATCTCGTT	CGCCGCGAAA	CCGCTGCCGT	ACATCAGCTC
301	GAACAGCGCG	TGGTCGCGCA	CCGCCAGCGG	GTCCGCCCGC	TCCACGGGGA
351	AATCCAACAT	CCGGTTCAGC	CATTCTCGCG	GCAGGGCTTT	GGTAGCGCGC
401	TCGGGCTGCT	TCGGCGGTTT	GATGTCGGCG	GTCCGGTCGG	CGCGCATCAG
451	CCCGCGCTTG	ACCAGCCAGG	CGCAATACTG	CCGCCACCGC	CACAGCTTGC
501	GCGCCAGCGT	CCGACCGTCC	AAACCGCGCT	CGCAGACCGC	GGCAGACGCG
551	GcggTAAAGT	CGCGCCGCGA	CAAGTCTGCG	GGCAGCGcgc	ctgcaTCTTC
601	AGACGGCATT	TGTGCCAACA	GTGCAAAACG	TTCTTCCAAA	TGGCGCCGGT
651	ATGCCGCAAC	CGTGTGCTCG	GACTTGCCCT	CGCGCACGAT	GTTTTCCAAA
701	TAAGCTGTCAA	AATAcgcgcC	AAACcgcTCC	AAAACCATAA	CCGTCCCACA
751	CAAAATATCAA	AAAACACAGT	A		

This corresponds to the amino acid sequence <SEQ ID 110; ORF 032.ng>:

**g032.pap**

1 MRRNVPAAVAV LRRPRFEAF L DLA LAQARAV PAGKQGF A VR CRLTQRQIVF  
51 QGFHAFAGQR NLTL LAPFAG NVYPRFVQIY IICIQAVYLA HAOTAAVHOL

101 EQRVVAHRQR VAAVHGQIQH PVQPFLRQGF GYALGLLRRF DVGGRVGAHQ  
151 PAFDPQGAIL PPRRLARQR PTVQTALRQP PQRRLKIAPR QVLRHAACIF  
201 RRHLCQCKQ FFQIAPVCRN RVLRLALAHQ VFQISVKIRR KPVQNHNRPT  
251 QISKNQ\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

m032.seq	(partial)					
1	ATGCGGCGAA	ACGTGcMTCG	mGTCGCCGTT	kTGCGCCGCC	CATTGCGCCA	
51	AACGTTTTTG	GATTTGGCGT	TGGCTCAGGC	GCGTGCCGTT	CCTGCCGGTA	
101	AACAGGGGCTT	TGCCGTCCGA	TGCCGTCTGA	CGCAGCGGCA	GATAGTTTTT	
151	CAGGCGCTTC	ACCGCTTTTG	CGACCACGG	CACCTGCCGC	TgTT.CGC	
201	CTTTGCCGAT	AAcGTGTACC	CACGcYTCGT	CCAAATAGAC	ATCATCTGCA	
251	TTCAAGCCGT	GTATCTCGCT	CACGCGCAA	CCGCTGCCGT	ACATCAGTTC	
301	GAACAGGGCG	TGGTCGCGCA	CGCCAGCGG	GTCCGCGCCG	TCCACGGGCA	
351	AATCCAGCAT	CCGGTTCAGC	CATTCTGCG	GCAGGGCTTT	GGGTACGCGC	
401	TCGGGCTGCT	TCGGCGGTTT	GATGTCGGC	GTCCGGTTCG	CGTGCATCAG	
451	GCCGCGCTTT	ACGAGCAAA	CGAATACTG	CCGCAAGAC	GAAGCTTGC	
501	GAGCCAGCGT	CCGTTCCCC	AAACCGCG...			

This corresponds to the amino acid sequence <SEQ ID 112; ORF 032>:

```
m032.pep (partial)
1 MRRNVXAVAV XRRPLRQTFE DLALAQARAV PAGKQGFVR CRLTQRQIVF
51 QGFHAFADQR HLPLXAPFAD NVYPRXVQID IICIQAVYLA HAQTAAVHQF
101 EQGVVAHRQR VAAVHGQIQH VPQPFRLRQF GYALGLLRRF DVGGRGVGHQ
151 AALYQPNAIL PPRRKLASQR FFPQTA...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

```
a032.seq
1  ATGCGGCGAA  ACGTGCGCTGC  CGTCGCCGTT  TTGCGCGCCG  CATTGCGCCA
51  AACGTTTTTG  GATTTGGCGCT  TGCGTCAGCG  GCGTGCCGTT  CCTGCCGGTA
101 AACAGGGCTT  TGCCGTCCGA  TGGCGTCTGA  CGCAGCGCGA  GATAGTTTTT
151 CAGGGCTTCC  ACGCTTTTGC  CGGTCAAGCG  AACCTGCCGC  TGCTTGCGTC
201 CTTTGCCGGT  AACGTGTACC  CACGCCCTCG  CCAAATATAC  ATCATCTGCA
251 TTCAAGCCGT  GTATCTCGCT  CACGCGCAA  CCGCTGCCGT  ACATCAGTTC
301 GAACAGCGCG  TGATCGCGCA  CCGCAGCGG  GTCGCGCGC  TCCACGGGCA
351 AATCCAGCAT  CCGGTTCAAG  CATTCTGCG  GCAGGGCTTT  GGGTACGCGC
401 TCGGGCTGCT  TCGGCGGTTT  GATGTCGGCG  GTCGGGTCGG  TATGCAGCAG
451 ACCGCGTTTG  ACCAGCCAGG  CGCAATACTG  CCGCCAAGAC  GACAGCTTGC
501 GCGCCACGCT  CCGCGCATTC  AAACCGCGCT  CGCAGACGCG  CCGCAACGCC
551 GCCGTAAAT  CGCGCTCGCA  CAAGCCCTGC  GGCAGCGCGC  CTGCATCTTC
601 AGACGGCATT  TGTGCCAACA  GCGCAAACAG  TTCTTCCAAA  TCGCGCCGGT
651 ATGCCGCCAC  CGTGTGCTCC  GACTTGCCCT  CGCGCAGCAT  GTTTTCCAAA
701 TAAGCGTCAA  AATGCGCCGC  AAACCCGTCC  AAAACCATAA  CCGCCCCACA
751 CAAATATCAA  AAAAACAGTG  A
```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 032.a>:

```
a032.pep
1  MRRNPVAVAV LRRPLRQTFL DLALAQARAV PAGKQGFVAV CRLTQRQIVF
51  QGFHAFAGQR NLPLLASFAG NVYPRLVQIY IICIQAVYLA HAQTAAVHQF
101 EQRVIAHRQR VAAVHHGQIQH PVQPLRQGF GYALGLLRRF DVGGRVGMQQ
151 TAFDQPGARL PPRRQLARQR PRIQTALRQP PQRRRKIALR QALRHAACIF
201 RRHLCQQRKQ FFQIAPVCRH RVLRLALAH DVFQISVKMRR KPVQNHNRPT
251 QISKKO*
```

**m032/a032**      **88.1% identity over a 176 aa overlap**

```

              10      20      30      40      50      60
m032.pep  MRRNVXAVAVXRRPLRQTFDLALAQAARAVPAGKQGFAVRCRLTORQIVFQGFHAFADQR
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a032      MRRNVPAAVAVLRRLRQTFDLALAQAARAVPAGKQGFAVRCRLTORQIVFQGFHAFAGQR
              10      20      30      40      50      60

```

212

```

              70      80      90      100      110      120
m032.pep    HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQ RVAAVHGQIQH
              :||| | || ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a032         NLPLLASFAGNVYPRLVQIYIICIQAVYLAHAQTAAVHQFEQQRVIAHRQ RVAAVHGQIQH
              70      80      90      100      110      120

              130      140      150      160      170
m032.pep    PVQPFLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFPQTA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a032         PVQPFLRQGFYALGLLRRFDVGGRVGMQQTAFDQPGAILPPRRQLARQRPRIQTALRQP
              130      140      150      160      170      180

a032         PQRRLKIALRQALRHAACIFRRHLCCQQRKQFFQIAPVCRHRLRLALAHDFQISVKMRR
              190      200      210      220      230      240

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 032 shows 86.4% identity over a 176 aa overlap with a predicted ORF (ORF 032.ng) from *N. gonorrhoeae*:

m032/g032

```

              10      20      30      40      50      60
m032.pep    MRRNVXAVAVXRRPLRQTFLDLALAQAARAVPAGKQGFVAVRCRLTQRQIVQGFHAFADQR
              ||||| ||||| ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g032         MRRNVFAVAVLRRPRFEAFDLALAQAARAVPAGKQGFVAVRCRLTQRQIVQGFHAFAGQR
              10      20      30      40      50      60

              70      80      90      100      110      120
m032.pep    HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQ RVAAVHGQIQH
              :| | ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g032         NLTLLAPFAGNVYPRFVQIYIICIQAVYLAHAQTAAVHQLEQRVVAHRQ RVAAVHGQIQH
              70      80      90      100      110      120

              130      140      150      160      170
m032.pep    PVQPFLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFPQTA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g032         PVQPFLRQGFYALGLLRRFDVGGRVGAHQPAFDQPGAILPPRRQLARQRPVQTALRQP
              130      140      150      160      170      180

g032         PQRRLKIAPRQVLRHAACIFRRHLCCQCKQFFQIAPVCRNRVRLRLALAHDFQISVKIRR
              190      200      210      220      230      240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 115>:

g033.seq

```

1  ATGGCGGCGG CGGACAACT CTTGGGCGGC GACCGCCGCA GCGTCGCCAT
51  CATCGGAGAC GGCGCGATGA CGGCGGGGCA GGCGTTTGAA GCCTTGAATT
101 GCGCGGGCGA TATGGATGTG GATTGTGCTGG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAACGT CGGCGCGTTG CCCAAATATC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAACgg
251 GCAAGGTATT AGACAAAATA CCCGGCGCGA TGGagtTTG CCAAAAAGTC
301 GAACAcaaa TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAAAACAGTC
351 GCTGTCGCTG TTGAAAATT TCGGCTTCCG CTACACCGGC CCGTGGACG
401 GACACAACGT CGAGAATCTG GTGGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCcg tcaAATACCA CGCCGTGCGc aACCTGCcta
551 AAGAAGGCGG GGCGCAAATg ccGTCTGAAA AAGAACCcAA GCCCGCCgCc
601 aaaccgACCT ATACCCAAGT ATTCGGCAAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG

```

```

701 GACTGGTGGG GTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT tacCTTTGCC GCGGTTTGG CGTGCGAAGG
801 CATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTGCCCGT TTTGTTTGCC
901 GTCGACCGTG CGGGCATCGT CGGCGCGGAC GGTCCGACCC ATGCCGGCTT
951 GTACGATTTG AGCTTCTTGC GCTGTGTGCC GAACATGATT GTTGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCTGCTGC TTTGACCTG CTATCAGGCG
1051 GATGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CCGGCGCGCC
1101 GGTTTCAGAC GGCATGGAAA CCGTGGAAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCC TTcatTGCCT TCGGCAGTAT GGTGCGCACC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTGCGCG ATATGCGCTt
1251 cgtcaaacCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCAcg
1301 accGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGGTCTTGG AAGTGTGTGG GAAACACGGC ATCTGCAAAC CCGTTTGTCT
1401 TTTGGGCGTT GCCGATACCG TAACCGAACA CGGCGATCCG AAAAACTTT
1451 TGGACGATTT GGGTTTGAGT GCCGAAGCGG TGAACGCCG GGTGCGCGAG
1501 TGGCTGCCGG ACCGTGATGC GGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 033.ng>:

**g033.pep**

```

1 MAAADKLLGG DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTIAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDLKDLRSR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKEGGAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVLEA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAT
401 ALAVAEKLNA TVADMRVFKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLLG V ADTVTEHGDP KKLLDDLGLS AEAVERRVRE
501 WLPDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

**m033.seq**

```

1 ATGGCGCGCG CAGACAACT CTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGCGGAC GCGCGCATGA CCGCGGGGCA GCGGTTTGAA GCCTTGAATT
101 GCGCaG.CGA TATGGATGTr GATTTGCTrG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAACGT CCGCGCGCTG CCGAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GCCTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCCGGCGCGA TGGAGTTTGC CCAAAAAGTC
301 GAACACAAAA TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAACAGTC
351 GCTGTCTTTG TTTGAAAAC TCGGCTTCCG CTACACCGGC CCCGTGGACG
401 GACACAACGT CGAAAATCTG GTGGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAAGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCCG TCAAATACCA CGCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAAAATG CCGTCTGAAA AAGAACCCTA GCCCGCGGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAAA TGCTGTGCG ACCGGCGCGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTACCGGT TTTGTTTGCC
901 GTCGACCGCG CGGGCATCGT CCGCGCGGAC GGCCCGACCC ATGCCGGTCT
951 GTACGATTTG AGCTTTTTGC GCTGCGTGCC GAACATGATT GTCGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCTGTGTC TTTGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CCGGCGCGCC
1101 GGTTTCAGAC GGCATGGAAA CCGTGGAAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCGCCCC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTGCGCG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG

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1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGGTGCTGG AAGTATTGGC GAAACACGGC ATCTGCAAAC CCGTTTGTCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTG GGGCTTGAGT GCCGAAGCGG TGGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 033>:

m033.pep

```

1 MAAADKLLGS DRRSVAIIGD GAMTAGQAFE ALNCAXDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTLAE AEHAKQSLSL FENFGFRYT PVDGHNVENL VDVLDLRSR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGK IIRREGKTA FIAFGSMVAP
401 ALAVAELKNA TVADMRVFKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
501 WLSDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

a033.seq

```

1 ATGGCGGCGG CGGACAAACA GTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGGCGAC GCGCGATGA CGGCGGGTCA GCGCTTTGAA GCCTTGAAC
101 GCGCGGGCGA TATGGATGTG GATTGCTGG TCGTCTCAA CGACAACGAA
151 ATGTCGATT CCCCAACGT CGGTGCGTTG CCCAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCCGGCGCGA TGGAGTTTGC CCAAAAAGTC
301 GAACATAAAA TCAAAACCTT TCGCGAAGAA GCCGAACACG CCAAACAGTC
351 ACTGTCTTTG TTTGAAAAC TCGGCTTCCG CTATACCGGC CCCGTGGACG
401 GACACAACGT CGAAAATCTG GTCGATGTAT TGGGAAGACCT GCGCGGACGC
451 AAAGGCCCGC AGCTTCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGATCCCG TCAAATACCA CGCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAAATG CCGTCTGAAA AAGAACCCAA GCCCGCGCGC
601 AAACCGACCT ATACCCAAGT GTTCGGCAA TGGCTGTGCG ACCGGGCGCG
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCG ACCGCTATT CGATGTCGGC
751 ATCGCCGAGC AGCAGCCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAA ACCTGCCCCG TTTGTTTGGC
901 GTCGACCGCG CGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCCGGTTT
951 GTACGATTTA AGCTTTTTC GCTGCATTCC GAATATGATT GTCGCCGCGC
1001 CGAGCGATGA AAATGAATGC CGCCTGCTGC TTTGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCCGTCG CTATCCGCGC GGCACGGGTA CCGGCGTGCC
1101 GGTTTCAGAC GGCATGGAAA CCGTGGAAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCCCCCT
1201 GCATTGGCGG TCGCCGAAA ACTGAACGCC ACCGTCGCGG ATATGCGCTT
1251 CGTCAAAACG ATAGACGAAG AGTTGATTGT CGGCCTTGC CGAAGCCACG
1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCAGC
1351 GCGGTGCTGG AAGTGTGGC GAAACACGGC ATCTGCAAAC CCGTCTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTG GGGCTTGAGT GCCGAAGCGG TGGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 120; ORF 033.a>:

a033.pep

```

1 MAAADKQLGS DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTLAE AEHAKQSLSL FENFGFRYT PVDGHNVENL VDVLEDLRGR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA

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301 VDRAGIVGAD GPTHAGLYDL SFLRCIPNMI VAAPSDENEC RLLSTCYQA  
 351 DAPAAVRYPR GTGTGVPVSD GMETVEIGKG IIRREGCKTA FIAFGSMVAP  
 401 ALAVAGKLNA TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGS  
 451 AVLEVLAKHG ICKPVLLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA  
 501 WLSDRDAAN\*

m033/a033 98.4% identity over a 509 aa overlap

m033.pep	10	20	30	40	50	60
	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISPVGAL					
a033	MAAADKQLGSDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISPVGAL					
	10	20	30	40	50	60
m033.pep	70	80	90	100	110	120
	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
a033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
	70	80	90	100	110	120
m033.pep	130	140	150	160	170	180
	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPLLHVITKKGNGYKLAENDPVKYHAVA					
a033	FENFGFRYTGPVDGHNVENLVDVLEDLRGRKGPLLHVITKKGNGYKLAENDPVKYHAVA					
	130	140	150	160	170	180
m033.pep	190	200	210	220	230	240
	NLPKESAAQMPSEKEPKPAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
a033	NLPKESAAQMPSEKEPKPAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
	190	200	210	220	230	240
m033.pep	250	260	270	280	290	300
	RFPDRYFDVGIAEQHAVTFAGGLACEGMPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
a033	RFPDRYFDVGIAEQHAVTFAGGLACEGMPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
	250	260	270	280	290	300
m033.pep	310	320	330	340	350	360
	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
a033	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
	310	320	330	340	350	360
m033.pep	370	380	390	400	410	420
	GTGTGAPVSDGMETVEIGKGIIRREGCKTAFIAFGSMVAPALAVAEKLNATVADMRFVKP					
a033	GTGTGVPVSDGMETVEIGKGIIRREGCKTAFIAFGSMVAPALAVAGKLNATVADMRFVKP					
	370	380	390	400	410	420
m033.pep	430	440	450	460	470	480
	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTGHGDP					
a033	IDEELIVRLARSHDRIVTLEENAEQGGAGSAGVLEVLAKHGICKPVLLLGVADTVTGHGDP					
	430	440	450	460	470	480
m033.pep	490	500	510			
	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
a033	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
	490	500	510			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 033 shows 98.4% identity over a 509 aa overlap with a predicted ORF (ORF 033.ng)

from *N. gonorrhoeae*:

m033/g033

m033 . pep	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISP NVGAL	60
g033	MAAADKLLGGDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISP NVGAL	60
m033 . pep	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
g033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
m033 . pep	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKG PQLLHVITKKGNGYKLAENDPVKYHAVA	180
g033	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKG PQLLHVITKKGNGYKLAENDPVKYHAVA	180
m033 . pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSR LVAITPAMREGSGLVEFEQ	240
g033	NLPKEGGAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSR LVAITPAMREGSGLVEFEQ	240
m033 . pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA	300
g033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA	300
m033 . pep	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRL LLLSTCYQADAPAAVRYPR	360
g033	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRL LLLSTCYQADAPAAVRYPR	360
m033 . pep	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAGSMVAPAL AVEKLNATVADMR FVKP	420
g033	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAGSMVATAL AVEKLNATVADMR FVKP	420
m033 . pep	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHG ICKPVLLLGVADTVTGHGDP	480
g033	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHG ICKPVLLLGVADTVTEHGDP	480
m033 . pep	KKLLDDLGLSAEAVERRVRWLSDRDAANX	510
g033	KKLLDDLGLSAEAVERRVREWL PDRDAANX	510

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 121>:

g034 . seq

1	ATGAGCCGTT	TATGGTTTTT	TGCCGTAAAA	AACATTATAA	TCCGCCTTAT
51	TTACCTATTG	CCCAAGGAGA	CACAAATGGC	ACTCGTATCC	ATGCGCCAAC
101	TGCTTGACCA	CGCCGCCGAA	AACAGCTACG	GCCTGCCCGC	GTTCAACGTC
151	AACAACCTCG	AACAAATGCG	CGCCATTATG	GAAGCCGCCG	ACCAAGTCAA
201	CGCGCCCGTC	ATCGTACAGG	CGAGCGCAGG	TGCGCGCAAA	TACGcgGCG
251	CGCCGTTTTT	GCGCCACCTG	ATTCTGGCGG	CAGTCGAAGA	ATTTCCGCAC
301	ATCCCCGTCG	TGATGCACCA	AGACCACGGC	GCATCGCCCG	ACGTgtgCCA
351	ACGCTCCATC	CAACTGGGCT	TCTCCTCCGT	GATGATGGAC	GGCTCTTTGC
401	TCGAAGACGG	CAAAACCCCT	TCTTCTTACG	AATACAACGT	CAACGCCACC
451	CGTACCGTCG	TCAACTTCTC	CCACGCCTGC	GGCGTGTCCG	TGAAGGCGA
501	AATCGGCGTA	TTGGGCAACC	TCGAAACCGG	CGAAGCAGGC	GAAGAAGACG
551	GAGTGGGCGC	GGCAGGCAAA	CTCTCACACG	ACCAAATGCT	CACCAGCGTT
601	GAAGATGCCG	TGCGTTTCGT	TAAAGATACC	GGCGTTGACG	CATTGGCGAT
651	TGCCGTCGGC	ACCAGCCACG	GCGCATACAA	ATTCAACCGT	CCGCCACACG



```

701 GCGACGTATT GCGTATCGAC CGCATCAAGG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGGctCCAGC TCCGTTCCGC AAGAatgGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CCGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG CAAAGTCAAC
901 ATCGATACCG ACCTGCGCCT CGCTTCCACC GGCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TTGATCCGCG CAAATACTTG GGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GTTATCTTGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCTGTT TCGTTGGAAA AAATGGCAAG
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 122; ORF 034.ng>:

```

g034.pep
1 MSRLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLEDGKTP SSYEYNVNAT
151 RTVVNFSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAAGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAI AVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWL KVI NEYGNIGET YGVPVEEIVE GIKHGVKRVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL GKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMASRYA KGELNQIVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 123>:

```

m034.seq (partial)
1 ATGAGCTGTT TATGGTTTTT TGCTGTAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA wACAGCTACG GCyTGCCGGC GTTCAACGTC
151 AACAACTCG wACAGATGCG CGCCATCATG GAGGCTGCAG ACCAAGTCGA
201 CGCCCCCGTC ATCGTACAGG CGAGTGCCGG TGCGCGCAA TATGCGGGTG
251 CGCCGTTTTT ACGCCACCTG ATTTTGCGGG CTGTGGAAGT ATTTCCACAC
301 ATCCCCGTCG TCATGCACCA AGACCACGGC GCATCACCCG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TCTCCTCTGT AATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACA
451 CGTACCGTGG TTAACCTTCTC CCACGCTTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGATGCAGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAA CTTTCCACG ACCAAATGCT GACCAGCGTC
601 GAAGATGCCG TATGTTTCGT TAAAGATACC GCGTGTGACG CATTTGGCTAT
651 TGCCGTCGGC ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCCACAG
701 GCGATGTATT ACGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA C...

```

This corresponds to the amino acid sequence <SEQ ID 124; ORF 034>:

```

m034.pep (partial)
1 MSCLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE XSYGLPAFNV
51 NNIXQMRAIM EAADQVDAPV IVQASAGARK YAGAPFLRHL ILAAVEVFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFSHAC GVSVEGEIGV LGNLETGDAG EEDGVGAVGK LSHDQMLTSV
201 EDAVCFVKDT GVDALAI AVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMH...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 125>:

```

a034.seq
1 ATGAGCCGTT TATGGTTTTT TGCCGCAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA AACAGCTACG GCCTGCCCGC GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCCG ACCAAGTCAA
201 CGCGCCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAA TACGCGGGCG
251 CGCCGTTTTT GCGCCACCTG ATTTTGCGGG CTGTGGAAGA ATTTCCGCAC
301 ATCCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TTTCTCCGT GATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTATG AATACAACGT CAACGCCACC

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451 CGTACCGTGG TTAATTTCTC CCACGCCTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAAACTGG CGAAGCCGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCCACG ACCAAATGCT CACCAGCGTC
601 GAAGATGCCG TGC GTTTCGT TAAAGATACC GCGGTTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCACG GCGCGTACAA ATTCAACCGT CCGCCACAG
701 GCGACGTGTT GCGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CCGCTCCAGC TCCGTTCCGC AAGAATGGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG TAAAGTCAAC
901 ATCGATACCG ACTTGCGCCT TGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TCGATCCGCG CAAATATTG AGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCTCGACC GCTACCTCGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCGGTT TCCTTGAAA AAATGGCAAA
1101 CCGTTATGCC AAGGCGGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 126; ORF 034.a>:

```

a034.pep
1  MSRLWFFAAK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51  NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVFNSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAVGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAI AVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV NEYGGNIGET YGVPVEEIVE GIKHGVRKVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL SKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMANRYA KGELNQIVK*

```

m034/a034 96.9% identity over a 257 aa overlap

```

              10      20      30      40      50      60
m034.pep      MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM
              || |||||:|||||
a034           MSRLWFFAAKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAIM
              10      20      30      40      50      60

              70      80      90      100     110     120
m034.pep      EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI
              |||||:|||||
a034           EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI
              70      80      90      100     110     120

              130     140     150     160     170     180
m034.pep      QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVFNSHACGVSVEGEIGVLGNLETGDAG
              |||||:|||||
a034           QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVFNSHACGVSVEGEIGVLGNLETGEAG
              130     140     150     160     170     180

              190     200     210     220     230     240
m034.pep      EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID
              |||||:|||||
a034           EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID
              190     200     210     220     230     240

              250
m034.pep      RIKEIHQALPNTTHIVMH
              |||||
a034           RIKEIHQALPNTTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN
              250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 034 shows 96.5% identity over a 257 aa overlap with a predicted ORF (ORF 034.ng) from *N. gonorrhoeae*:

**m034/g034**

m034 . pep	MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNVLXQMRAIM	60
g034	MSRLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNLEQMRAIM	60
m034 . pep	EAADQVDAPVIVQASAGARKYAGAPFLRLHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI	120
g034	EAADQVNAPVIVQASAGARKYAGAPFLRLHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI	120
m034 . pep	QLGFSSVMDGSLMEDGKTPSSYEYNVNATRTVVNFSSHACGVSVEGEIGVLGNLETGDAG	180
g034	QLGFSSVMDGSLLEDGKTPSSYEYNVNATRTVVNFSSHACGVSVEGEIGVLGNLETGEAG	180
m034 . pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID	240
g034	EEDGVGAAGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID	240
m034 . pep	RIKEIHQALPNTHIVMH	257
g034	RIKEIHQALPNTHIVMHGSSSVQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 127>:

**g036 . seq**

```

1  ATGCTGAAGC CGTGTGTTGGT ATACAGTGCC TGTGCGGCGG cgttgCCTGC
51  GCGGACTTCG AGCAGCAGGC GTTGCGTGCC TTCGGGCAGA TGTGCGTACC
101 AATATTCGAG CAGGGCGGAC GCAACGCCCC GTCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCTGCCGT CTTTTCCTCG AAGGAAAACC TGTTCGGACG
251 GCGAAACAAG CGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGTAT CGAGCGCGGC CAGTGCAGGC CAGTCGGACG GTGAGGCTGG
351 GCGGATGTTC ATGTTTCGTGC CTTCCGTTCC GCCTGTTCTT TGGCAGTCAG
401 GCGGATTTTG TTGCGGACGT AGAGCAGTTC GCGGTGTGCC GCGCCAGTTG
451 CCGGATAGCC GCCGCCGAGG GCGAGCGCGA GAAAATCGGC GCGGTCGGC
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTTCCAGT CGAACGCACT
551 GCCGATGCCG TCTGAAAAGA CGTACCCCTC GGGGAGGGCA ATGTCTGCCG
601 CCCTACCGAC TTGATAATCG CTCAAACGGC GCGGTTTCAG CGTGTGCAAC
651 CACGCATAAA AACTTCGCC CATACGCGCG TCCGAGCGG CGAGTATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGTG GGGATGCCGA
751 TTAAAGGCGT GTCGAACGGC GTTGCCAAAC CTTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 128; ORF 036.ng>:

**g036 . pep**

```

1  MLKPCLVYSA CAAALPARTS SSRRCVPSGR CAYQYSSRAD ATPRRRHSGA
51  VAIRCSSDSS GRFCQTIKAA ILPSFSARKT CSDGETSADS NWRVCVHADGL
101 QTVSSAASAA QSDGEAGRMF MFVPSVPPVL WQSGRFCCGR RAVRRVPRQL
151 RDSRRRGRAR ENRRRSAYRV CLRRADGFPV RTHCRCLRKR RTPRGGQCLP
201 PYRLDNRSNG GGSACRTTHK TLRPYARPQR RVCSFAAAAA RRRHRAWGCR
251 LKACRTALPN LAPRRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 129>:

**m036 . seq**

```

1  ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCCTGC
51  ACGGACTTCG AGCAGCAGGC GTTGCGTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCcg . CGT CTTTTCCTCG AAGGAAAACC TGTTCGGACG
251 GCGAAACCAG TCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGCAGC CAGCTCCTCA CAATCGGCAC AAACGGCACG

```

```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTCT GCCTGTTCTT TGGCAGTCAG
401 GGCGATTTTG TTGCGGACGT AGAGCAAACC GGCGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA AACTTTCGCC CATACGAGCG TCCGTAGCGG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGGGT ATCAAACGGC GTTGCCAAAC CCTGAGCTAC ACCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 130; ORF 036>:

**m036.pep**

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPXSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMR ESRRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*R QGCSFAAAAA RRRHRARVRR
251 LRGYQTALPN PELHRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 131>:

**a036.seq**

```

1 ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCTGTC
51 ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GGCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGCGCGCA ATCCCGCCGT CTTTTCGCG AAGGAAAACC TGTTCCGACG
251 GCGAAACCAG TCGGGAATCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGCAT CGAGCGCGGC GAGTGCAGCG CAATCGGCAT AAACGGCGCG
351 GCGGATGTTT ACAGGCGCGC CCTCCGTTCC GCCTGTTCTT TGGCAGTCAA
401 GGCGATTTTG TTGCGGACGT AGAGCAGCTC GGCGTGTGCC GCAGCGACGG
451 CGGGAAAACC GCCTTCAGCC GCCAGATTGA GGAAGTCGCG GCGGTCGCGC
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTTCCAGCG CGAACGCATT
551 GCCGATGCCG TCTGAAAAGG CGCATCCTTC CGGCAGCCGG ATGTCTGCCG
601 CCCGACCGAC CTGATAATCG CTCAAACGGC GGCGGTTTCA CGTGTGCAAC
651 CATGCATAAA AACTTTCGCC CATACGTGCG TCCGAGCGCG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGAGT ATCAAACGGC GTTGCCAAAC CTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 132; ORF 036.a>:

**a036.pep**

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASAA QSA*TARRMF TGAPSVPPVL WQSRRFCCGR RAARRVPQRR
151 RENRLQPPD* GSRRRSAYRV CLRRADGFPA RTHCRCLKR RILPAAGCLP
201 PDRPDNRSNG GGSACRTMHK TLRPYVRPQR QGCSFAAAAA RRRHRARVRR
251 LKEYQTALPN LAPRRCRYAV P*

```

**m036/a036** 85.6% identity over a 270 aa overlap

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAI PWRHSGAVAIRCSSDSS					
a036	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAI PWRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
m036.pep	GRFCQTIKAAIPXSFSAKRTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
a036	GRFCQTIKAAIPPSFSAKRTCS DGETSADSNWRCVHADGLQTASSAASAAQSAXTARRMF					
	70	80	90	100	110	120

	130	140	150	160	170	180
m036.pep	130	140	150	160	170	180
a036	130	140	150	160	170	180
m036.pep	190	200	210	220	230	240
a036	190	200	210	220	230	240
m036.pep	250	260	270			
a036	250	260	270			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 036 shows 74.9% identity over a 271 aa overlap with a predicted ORF (ORF 036.ng) from *N. gonorrhoeae*:

m036/g036

	10	20	30	40	50	60
m036.pep	10	20	30	40	50	60
g036	10	20	30	40	50	60
m036.pep	70	80	90	100	110	120
g036	70	80	90	100	110	120
m036.pep	130	140	150	160	170	180
g036	130	140	150	160	170	180
m036.pep	190	200	210	220	230	240
g036	190	200	210	220	230	240
m036.pep	250	260	270			
g036	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 133>:

m036-1.seq

```

1  ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGCGG TGTGCTGTC
51  ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTCTT GCCAAACGAT
201 AAAGCGGCA ATCCCGCGT CTTTTCGCGC AAGGAAAACC TGTTCCGACG
251 GCGAAACGAG TCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGGCGC CAGCTCCTCA CAATCGGCAC AAACGGCAGC

```

351 GCGGATGTTT ACAGGGCGCG TCTCGGTTCC GCCTGTTCTT TGGCAGTCAG  
401 GGCgATTtTTG TTGCGGACGT AGAGCAAACC GGCGTGTGCG GCATGGACGG  
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC  
501 ATATCCGGTC TGCTTGAGAA CGCGGGAGCT TCTTCCAGCG CGAAGCGGCT  
551 GCCTATGCGC TCTGAAAAGG CGCATCCCTC CGGACCGCGG ATGTCTGCCG  
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC  
651 CATGCATAAA ACACATTGCGC CATACGAGCG TCCGTAG

This corresponds to the amino acid sequence <SEQ ID 134; ORF 0036-1>:

```
m036-1.pep
1  MLKPCAAYSA CAAVLPARTS SSRCVSSGR CVNQYSSRAD AIPWRRHSGA
51  VAIRCSDSSS GRFCQTIKAA IPPFSARKT CSDGETSADS NWRVCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLFMR ESRRQSAYPK CLRTAEALLP RTRCLCLRLK RIFPAAGCLP
201 PARPDNRNSG GSSAYRTMHK TIRPYERP*
```

**m036-1/g036 76.8% identity in 228 aa overlap**

	10	20	30	40	50	60
m036-1.pep	MLKPCAVYSACA	AVLPARTSSSR	RCVSSGR	CNVQYSS	RADAI	PWRRHSGAV
g036	MLKPCLVYSACA	AALPARTSSSR	RCVPSGR	CAYQYSS	RADAT	PRRRHSGAV
	10	20	30	40	50	60
m036-1.pep	70	80	90	100	110	120
g036	GRFCQTIKAA	IPPSFSARK	TCS	DGETS	ADSNWRC	VHADGLQT
	70	80	90	100	110	120
m036-1.pep	130	140	150	160	170	180
g036	TGALS	VRPVLWQ	SGR	FCCGR	RANRR	VRHGRQD
	130	140	150	160	170	180
m036-1.pep	190	200	210	220	229	
g036	RTRCL	CLRKRR	IPPAAG	CLP	PARPD	NRSNGG
	190	200	210	220	230	240
m036-1.pep	RRR	HRAWG	CR	LRKAC	RTAL	PNLAP
g036	RRR	HRAWG	CR	LRKAC	RTAL	PNLAP

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 135>:

g038.seq

1	ATGACTGATT	TCCGCCAAGA	TTTCCTCAA	TTCTCCCTCG	CCCAAAATGT
51	TTTGAATTC	GGCGAATTTA	CCACCAAAG	CGGACGCGG	TCGCCCTATT
101	TCTTCAATGC	CGGCCTCTTC	AACGACGGCG	CGTCCACGT	GCAACTGGCA
151	AAATTCTATG	CACAATCCAT	CATTGAAAG	GGCATCCGAT	TCGATATGCT
201	GTTCCGCCCC	GCCTACAAG	GCATTATTTT	GGCGGCGGCA	ACCGCGATGA
251	TGCTGC CGGA	AAAGGCGGTG	AACGTCCCTG	TTGCCTACAA	CCGCAAGTAA
301	GCCAAAGACC	GCGGCGAAG	GCGCGTGTG	GTGCGCGCGC	CGCTTAAAGG
351	GCGCGTGTCT	ATTATCGACG	ACGTTGATTC	CGCCGGCCCA	TCGGTACGCG
401	AATCAATCAA	ACTGATTGAA	GCGGAGGTTG	CAACCCCCGC	CGGTGTCGCG
451	ATCGCGCTCG	ACCGCATGGA	AAAAGGCACG	GGTAAATGT	CGCGCGTTCA
501	GGAAGTGGAA	AAACAATACG	GCCTGCCCTG	CGCCCCATCG	GCCAGCCTGA
551	ACGATTTGTT	TATCCTGTTG	CAAAACAACC	CCGAATATCG	ACAGTTCCTC
601	GAACCGTGCT	GCACCTACCG	CCGGCAGTAC	GGCGTAGAAT	AA

This corresponds to the amino acid sequence <SEQ ID 136; ORF 038.ng>:

```
g038.pep
  1  MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGASTLQLA
 51  KFYAQSIIES GIRFDMLFGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDRGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRTYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 137>:

```
m038.seq
  1  ATGACCGATT TCCGCCAAGA TTCTCTCAAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GCGCAATTTA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGTCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451  ATCGCGCTCG ATCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAA AAACAATACG GCTGCCCCG CGCCCCATC GCCAGCCTGA
551  ACGATTGTGT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 138; ORF 038>:

```
m038.pep
  1  MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMLFGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 139>:

```
a038.seq
  1  ATGACCGATT TCCGCCAAGA TTCTCTCAAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GCGCAATTTA CCACCAAGC CGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451  ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAA AAACAATACG GCCTGCCCCG CGCCCCATC GCCAGCCTGA
551  ACGATTGTGT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 140; ORF 038.a>:

```
a038.pep
  1  MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMLFGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

m038/a038 100.0% identity over a 213 aa overlap

```

      10      20      30      40      50      60
m038.pep  MTDFRQDFLKFSLAQNVLFKGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
```

```

|||||
a038      MTDFRQDFLKFSLAQNVLKFGFTTKAGRRSPYFFNAGLFNDGLSTLQLAQFYAQSIIES
          10      20      30      40      50      60

          70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          |||||||
a038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          70      80      90      100     110     120

          130     140     150     160     170     180
m038.pep  IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVKQYGLPVAPI
          |||||||
a038      IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVKQYGLPVAPI
          130     140     150     160     170     180

          190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
          |||||||
a038      ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
          190     200     210

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 038 shows 98.1% identity over a 213 aa overlap with a predicted ORF (ORF 038.ng)

from *N. gonorrhoeae*:

m038/g038

```

          10      20      30      40      50      60
m038.pep  MTDFRQDFLKFSLAQNVLKFGFTTKAGRRSPYFFNAGLFNDGLSTLQLAQFYAQSIIES
          |||||||
g038      MTDFRQDFLKFSLAQNVLKFGFTTKAGRRSPYFFNAGLFNDGASTLQLAQFYAQSIIES
          10      20      30      40      50      60

          70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          |||||||
g038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDRGEGGVLVGAPLKGRVL
          70      80      90      100     110     120

          130     140     150     160     170     180
m038.pep  IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVKQYGLPVAPI
          |||||||
g038      IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGKLSAVQVEVKQYGLPVAPI
          130     140     150     160     170     180

          190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
          |||||||
g038      ASLNDLFILLQNNPEFGQFLEPVRTYRRQYGVEX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 141>:

```

g039.seq
1   ATGCCGTC CG AACCACCTGC CGCTTCAGAC GGCATCAAAC CGACACACAC
51  CGAGAAAACA TCATGCCCGC CTGTTTCTGT CCGCACTGCA AAACCCGCCT
101 CTGGGTCAAA GAAAcccagC TCAAcgtCgC ccaagGCTTC GTCGTCTgcc
151 aaAAAtgcga agGGCTgttt aaAgccaaaG accAtctggc aaGcacGAAA
201 gaacctatat tcaacgattg gcccgaaagt gtttcgggat gTcaaaCTCG

```



```

251 TCcaccgcaT cggcacgcac gccattagca aGAaacagat gtccccgcgac
301 gaaatCgccc atatacctcaa cggcgggtaca acCCTGCACG ATACGCCGCC
351 CGCAACCGCC GCTGCCGCac ctGCCGCCGC ACCGcaggTT TCCGTACCGC
401 CCGCCCGTCA GGAAGGGCTC AACTGGACTA TTGCAACCCT GTTCGCACTT
451 ATCGTCCTCA TTATGCAGCT TTCCTACCTC TTCATCCTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 142; ORF 039.ng>:

```

g039.pep
  1 MPSEPPAASD GIKPTHTEKT SCPPVSVRTA KPASGSKKPS STSPKASSSA
 51 KNAKGCLPKP TIWQARKNLY STIGPKLFRD VKLVHRIGTH AISKKQMSRD
101 EIADILNGGT TLHDTTPATA AAAPAAAPQV SVPPARQEGL NWTIATLFAL
151 IVLIMQLSYL FIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 143>:

```

m039.seq
  1 ATGCCGTCCG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
 51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCCGTCT
101 CTGGGTCAAA GAAACCCAAC TCAATGTCGC CGnnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnCCC GAGGCTGTTT
251 CGGATGTCAA ACTCGTTCAC CGTATCGGCA CGCGCGCCAT CGGCAAGAAA
301 CAGATTTCCT GTGACGAAAT CGCCGGCATC CTCAACGGCG GTACAACCCA
351 GCCCGATATT CCGCCCGCAA CCGCCGCCAC CCCTGCTGCC GCACCGCAGG
401 TTACCGTACC GCCCGCCGCG CCGCCCGGTC AGGATGGGTT CAACTGGACG
451 ATTGCAACCC TGTTTGCCCT TATCGTCCTC ATTATGCAGC TTCCTACCT
501 CGTCATCCTA TGA

```

This corresponds to the amino acid sequence <SEQ ID 144; ORF 039>:

```

m039.pep
  1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPPXXXXXX
 51 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXP EAVSDVKLVH RIGTRAIGKK
101 QISRDEIAGI LNGGTTPDI PPATAATPAA APQVTVPPAA PARQDGFNWT
151 IATLFLALIVL IMQLSYLVIL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 145>:

```

a039.seq
  1 ATGCCGTCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
 51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCCGTCT
101 CTGGGTCAAA GAAACCCAAC TCAATGTCGC CCAAGGCTTC GTCGTCTGCC
151 AAAAATGCGA AGGAATGTTT AAAGCCAAAG ACCATCTGGC AAGCACGAAA
201 GAACCCATAT TCAACGATT. TGCCCGAAGC TGTTTCGGAT GTCAAACCTCG
251 TTCACCGCAT CGGCACGAGC GCCATCGGCA AGAAACAGAT TTCCCGTGAC
301 GAAATCGCCG GCATCCTCAA CGGCGGCACA ACCCAGCCCG ATATTCCGCC
351 CGCAACCGCC GCCACCCCTG CTGCCGCACC GCAGGTACC GTACCGCCCG
401 CCGCGCCCGC CCGTCAGGAT GGGTTCAACT GGACGATTGC AACCTGTTT
451 GCCCTTATCG TCCTCATTAT GCAGCTTCC TACCTCGTCA TCCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 146; ORF 039.a>:

```

a039.pep
  1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPKASSSA
 51 KNAKECLPKP TIWQARKNPY STIXPEAVSD VKLVHRIGTS AIGKKQISRD
101 EIAGILNGGT TQPDIPPATA ATPAAAPQVT VPPAAPARQD GFNWTIATLF
151 ALIVLIMQLS YLVIL*

```

m039/a039 79.4% identity over a 170 aa overlap

```

              10      20      30      40      50      60
m039.pep      MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNMSMPXXXXXXXXXXXXXXXX
               |||
a039           MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNMSMPKASSSAKNAKECLPKP

```

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	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPDI				
a039	TIWQARKNPYSTIX----	PEAVSDVKLVHRIGTSAIGKKQISRDEIAGILNGGTTQPDI				
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAATPAAAPQVTVP	PPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
a039	PPATAATPAAAPQVTVP	PPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
	120	130	140	150	160	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 039 shows 60.8% identity over a 171 aa overlap with a predicted ORF (ORF 039.ng) from *N. gonorrhoeae*:

m039/g039

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPD	THEEIPC	PPVSAPTAKPV	SGSKKPN	SMPXXXXXXXXXXXXXXXXX	
			:		:	
g039	MPSEPPAASDGIKPT	HTTEKTS	CPVSVRTAKP	PASGSKKPS	STSPKASSAKNAKGCLKPK	
	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPDI				
	:	:	:			
g039	TIWQARKNLYSTIG----	PKLFRDVKLVHRIGTHAISKQMSRDEIADILNGGTTLHDT				
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAAT-PAAAPQVTVP	PPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
g039	PPATAAAAPAAAPQVSV	PPA---RQEGLNWTIATLFALIVLIMQLSYLFILX				
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 147>:

g040.seq

```

1  ATGAACGCGC CCGACAGCTT TGTCGCCCAC TTCCGCGAAG CCGCCCCCTA
51  CATCCGCCAA ATGCGCGGCA CGACACTGGT CGCCGGCATA GAcggCCGCC
101 TGCTCGAAGG CGGCACCTTA AATAAGCTCG CCGCCGACAT CGGGCTGTG
151 TCGCAACTGG GCATCCGACT CGTCCTCATC CACGGCGCGT ACCACTTCCT
201 CGAccgCCTC GCCGCCGCGC AAGgccGCAC GCCGCATTAT TGCCGgggtt
251 tGCGCGTTAC CGACGaAACc tcGctcgGAC AGGCGCAGCA GtttGCCGGC
301 AccgTCCGCA GCCGTTTGA agcCGCATTG tgcggcagCG tttcaggatt
351 cgcgCGCGCG CCTTCCGTCC CGCTCGTAtc gggcaacttc ctgacCGCCC
401 GTCcgatggg cgtgattgac ggaACCGata tggaatacgc ggggggttatc
451 cgcaaaaccg ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGATG CCGCCGCTCG GGCATTCTTA CGGCGGCAAA ACCTTCAATC
551 TCGATATGGT GCAGGCCGCC GCTTCCGTCT CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTT ACCTGACCC TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGCCAGCGA AACCCGACGA CTGATTTCGT CCGCCGTGTC CGCGCTCGAA
751 GCGCGCGTGC ATCGCGTCCA AATCCTCAAC GGGGCCGCCG ACGGCAGCCT
801 GCTGCAAGAA CTCTTACCC GCAACGGCAT CGGCACGTCC ATTGCCAAG
851 AAGCCTTCGT CTCCATCCGG CAGGCGCACA GCGGCGACAT CCCGCACATC
901 GCCGCCCTCA TCCGCCCGCT GGAAGAACAG GCGGTCCTAT TGCACCGCAG
951 CCGGAATAC CTCGAAAACC ACATTTCGGA ATTTTCATC CTCGAACACG

```

```

1001 ACGGCGACCT GTACGGCTGT GCCGCACTCA AAACCTTTGC CGAAGCCGAT
1051 TCGGCGGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGg
1101 ctACGGCGAA CGCCTGCTTG CCCACATTAT CGATAAGGCG CGCGGCATAG
1151 GCATAAGCAG GCTGTTTCGA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGCTGCCCG AAACGCGGCG
1251 CAAAGACTAC CGCAGCAACG GACGAAACCC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 148; ORF 040.ng>:

**g040.pep**

```

1 MNAPDSFVAH FREAAPYIRQ MRGTTLVAGI DGRLLGGTL NKLAADIGLL
51 SQLGIRLVLI HGAYHFLDRL AAAQGRTPHY CRGLRVTDET SLGQAQQFAG
101 TVRSRFEAL CGSVSGFARA PSVPLVSGNF LTARPMGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWM PPLGHSYGGK TFNLDMVQAA ASVAVSLQAE
201 KLVYLTLSDG ISRPDGTAE TLSAQEAQSL AEHAASETRR LISSAVAAL
251 GGVHRVQILN GAADGSLQLE LFTRNGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GVLLHRSREY LENHISEFSI LEHGDGDLGC AALKTFAEAD
351 CGEIACLAVS PQAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNGRNPHIL VRRLLHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 149>:

**m040.seq**

```

1 ATGAGCGCGC CCGACCTCTT TGTGCCCCAC TTCCGCGAAG CCGTCCCCTA
51 CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAAGCTCG CCGCCGACAT CGGGCTGTTG
151 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCCGCTC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TCGCGGTAC CGACGAAACC TCGCTCGAAC AGGCGCagCA GTTTGCCGGC
301 ACCGTCCGCA GCCGTTTGA AGCCGCATTG TGCGGCAGCG TTTCCGGGTT
351 CGCGCGCGCG CCTTCCGTCC CGCTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGAATACGC GGGCGTTATC
451 CGCAAAACCG ACACCGCCGC CCTCCGTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCCGCTCG GACATTCTTA CAGCGGCAAG ACCTTCTATC
551 TCGATATGCT TCAAACCGCC GCCTCCGCG CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTT ACCTGACCTT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG CGGGAACAGC
701 CCGGCGGGCA AACCGGACGG CTGATTTCTG CCGCCGAAC CTTCACCCGC
751 AACGGCATCG GCACGTCCAT TGCCAAAGAA GCCTTCGTCT CCATCCGGCA
801 rGCGCAywgG G.CGACATCC CGCACATCGC CGCCCTCATC CGCCCGCTGG
851 AAGAACAGGG CATCTGCTG CACCGCAs.c GCGAATACCT CGAAAACCAC
901 ATTTCCGAAT TTCCATCCT CGAACACGAC GGCAACCTGT ACGGTTGCCG
951 CGCCCTGAAA ACCTTTGCCG AAGCCGATTG CGGCGAAATC GCCTGCCTTG
1001 CCGTCTCGCC GCag.cACAG GACGGCGGCT ACGGCGAACG CnTGCTTGCC
1051 CACATTATCG ATAAGGCGCG CGGCATAGGC ATAAGCAGCG TGTTGCGACT
1101 GTCCACAAAT ACCGGCGAAT GGTTCGCCGA ACGCGGCTTT CAGACGGCAT
1151 CGGAAGACGA GTTGCCCGAA ACGCGGCGCA AAGACTACCG CAGCAACGGA
1201 CGGAACTCGC ATATTCTGGT ACGTCGCTG CACCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 150; ORF 040>:

**m040.pep**

```

1 MSAPDLFVAH FREAVPYIRQ MRGKTLVAGI DDRLLEGDTL NKLAADIGLL
51 SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFYLDMLQTA ASAAVSLQAE
201 KLVYLTLSDG ISRPDGTAE TLSAQEAQSL AEHAGGQTRR LISSAEFLTR
251 NIGTSLIAKE AFSIRQAHX XDIPHIAALI RPLEEQILL HRXREYLENH
301 ISEFSILEHD GNLYGCAALK TFAEADCGEI ACLAVSPQXQ DGGYGERXLA
351 HIIDKARGIG ISRLFALSTN TGEWFAERGF QTASEDELPE TRRKDYRSNG
401 RNSHILVRRL HR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 151>:

**a040.seq**

```

1  ATGATCGTGC CCGACCTCTT TGTGCCCCAC TTCCGCGAAG CCGCCCCCTA
51  CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAAGTTCG CCGCCGACAT CCGGCTTTTG
151 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCGCGC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TCGCGGTTAC CGACGAAACC TCGCTCGAAC AGGCGCAGCA GTTTGCCGGC
301 ACCGTCCGCA GCCGTTTTGA AGCCGCATTG TCGCGCAGCG TTTCCGGGTT
351 CGCGCGCGCG CCTTCCGTCC CGTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGGAAATACG GGGCGTTATC
451 CGCAAAACCG ACACCGCCGC CCTCCGTTC CAACTCGACG CCGGCAATAT
501 CGTCTGGCTG CCGCCGCTCG GACATTCCTA CAGCGGCAAG ACCTTCCATC
551 TCGATATGCT TCAAACCGCC GCCTCCGTG CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTT ACCTGACCCT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGTA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGGCGGCGA AACGCGACGG CTGATTTCTG CCGCCGTTGC CGCGCTCGAA
751 GCGCGGCTGC ATCGCGTCCA AATCCTCAAC GGAGCCGCGG ACGGCAGCCT
801 GCTGCAAGAA CTCTTCAACC GCAACGGCAT CGGCACGTCC ATTGCCAAAG
851 AAGCCTTCGT CTCCATCCGG CAGGCGCACA GCGGCGACAT CCGGCACATT
901 GCCGCCCTCA TCCGCCCGCT GGAAGAACAG GGCATCCTGC TGCACCGCAG
951 CCGCGAATAC CTGAAAACC ACATTTCCGA ATTTTCCATC CTGAAACACG
1001 ACGGCAACCT GTACGGTTGC GCGGCCCTGA AAACCTTTGC CGAAGCCGAT
1051 TCGGCGGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGG
1101 CTACGGCGAA CGCTGCTTG CCCACATTAT CGATAAGCGG CGCGGCATAG
1151 GCATAAGCAG GCTGTTGCA CTGTCCACAA ATACCGGCGA ATGTTTGGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGTTGCCCG AAACGCGGCG
1251 CAAAGACTAC CGCAGCAACG GACGGAATC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 152; ORF 040.a>:

a040.pep

```

1  MIVPDLFVAH FREAAPYIRQ MRKTLVAGI DDRLLEGDTL NKFAADIGLL
51  SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFHLDMLQTA ASVAVSLQAE
201 KLVYLTSLDG ISRPDGTLAV TLSAQEAQSL AEHAGGETRR LISSAVAAL
251 GGVHRVQILN GAADGSLLOE LFTRNGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GILLHRSREY LENHISEFSI LEHDGNLYGC AALKTFEAD
351 CGEIACLAVS POAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNRNSHIL VRRLHR*

```

m040/a040 91.5% identity in 436 aa overlap

	10	20	30	40	50	60
m040.pep	MSAPDLFVAHFREAVPYIRQMRKTLVAGIDDRLLEGDTLKNKLAADIGLLSQLGIRLVLI					
a040	MIVPDLFVAHFREAAPYIRQMRKTLVAGIDDRLLEGDTLKNKFAADIGLLSQLGIRLVLI					
	10	20	30	40	50	60
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEALCGSVSGFARA					
a040	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEALCGSVSGFARA					
	70	80	90	100	110	120
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEALCGSVSGFARA					
a040	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEALCGSVSGFARA					
	70	80	90	100	110	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPLGHSYSGK					
a040	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPLGHSYSGK					
	130	140	150	160	170	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTSLDGISRDPDGTLAETLSAQEAQSLAEHAGGQTRR					
a040	TFHLDMLQTAASVAVSLQAEKLVYLTSLDGISRDPDGTLAVTSLAQEAQSLAEHAGGETRR					
	190	200	210	220	230	240

229

	190	200	210	220	230	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI					
a040	LISSAVAALGGVHRVQILNGAADGSLLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI					
	250	260	270	280	290	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS					
a040	AALIRPLEEQGILLHRSREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS					
	310	320	330	340	350	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY					
a040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY					
	370	380	390	400	410	420
m040.pep	RSNGRNSHILVRRLRHX					
a040	RSNGRNSHILVRRLRHX					
	430					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 040 shows 88.3% identity over a 436 aa overlap with a predicted ORF (ORF 040.ng) from *N. gonorrhoeae*:

m040/g040

m040.pep	MSAPDLFVAHFREAVPYIROMRGKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI	60
g040	MNAPDSFVAHFREAAPIYIOMRGTTLVAGIDGRLLGGTLNKLAAADIGLLSQLGIRLVLI	60
m040.pep	HGARHFLDRHAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA	120
g040	HGAYHFLDRLAAAQGRTPHYCRGLRVTDETSLGQAQQFAGTVRSRFEAALCGSVSGFARA	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK	180
g040	PSVPLVSGNFLTARPMGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWMPPLGHSYGGK	180
m040.pep	TFYLDMLQTAASAASVSLQAEKLVYLTLSDGISRDPDGTLAETLSAQEAQSLAEHAGGQTRR	240
g040	TFNLDMVQAAASVAVSLQAEKLVYLTLSDGISRDPDGTLAETLSAQEAQSLAEHAASETRR	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI	276
g040	LISSAVAALGGVHRVQILNGAADGSLLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS	336
g040	AALIRPLEEQGVLLHRSREYLENHISEFSILEHDGDLYGCAALKTFAEADCGEIACLAVS	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	396
g040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	420
m040.pep	RSNGRNSHILVRRLRHX	413
g040	RSNGRNPILVRRLRHX	437

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 153>:

```
g041.seq
1  ATGAGTTCGC CCAAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGGCCT
51  GATTACCGCC GCCGCTTCG TCGCGAACC GCAAAGCATC GGTGCGCTGG
101 TGTGCGAAGT ACCGCTGACC GATATGATCC GTTATCCGCT GCTGTCCGCC
151 GGTTCAGTT GGACGGACGA ATACGGCAAT CCGCAGAAAT ACGAAGCCTG
201 CAAACGCCGG CTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCGCGCTC ATTACCACCA GCCTCAGCGA CGACCGCGTC
301 CATCCCGCCC ACGCGCTCAA ATTCTACGCC AAATGCGCG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCCAACGCGA ATCCGCCGAC AAATCGCCT GCGTGTGCT GTTTTGTAAA
451 GAATTTTGG GATAA
```

This corresponds to the amino acid sequence <SEQ ID 154; ORF 041.ng>:

```
g041.pep
1  MSSPKHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEACKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQRESAD KLACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 155>:

```
m041.seq
1  ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGGACT
51  GATTACTGCC GCCGCTTCG TCGCGAACC GCAAAGCATC GGC GCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGTT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAATGCGCG AAACCTCCGC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCCAACGCGA ATCCGCCGAC GAATCGCCT GCGTCTTGCT GTTTTGTAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 156; ORF 041>:

```
m041.pep
1  ISSPEHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEVCRRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYSPDGGGHT GNGTQRESAD ELACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 157>:

```
a041.seq
1  ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGGACT
51  GATTACTGCC GCCGCTTCG TCGCGAACC GCAAAGCATA GGC GCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGCT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAATGCGCG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CGCAGCGCGA AGCCGCCGAC GAATCGCCT GCGTGTGCT GTTTTGTAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 158; ORF 041.a>:

```
a041.pep
1  ISSPEHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEVCRRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQREAAD ELACVLLFLK
```

151 EFLG\*

m041/a041 98.7% identity over a 154 aa overlap

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
a041	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRLGELSPYHNLSDGIDYPPALITTSLSDDRHPAHALKFYAKLRETSQSW					
a041	PQKYEVCKRRLGELSPYHNLSDGIDYPPALITTSLSDDRHPAHALKFYAKLRETSQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
a041	LYSPDGGGHTGNGTQREAADELACVLLFLKEFLGX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 041 shows 96.8% identity over a 154 aa overlap with a predicted ORF (ORF 041.ng) from *N. gonorrhoeae*:

m041/g041

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
g041	MSSPKHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRLGELSPYHNLSDGIDYPPALITTSLSDDRHPAHALKFYAKLRETSQSW					
g041	PQKYEACKRRLGELSPYHNLSDGIDYPPALITTSLSDDRHPAHALKFYAKLRETSQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
g041	LYSPDGGGHTGNGTQRESADKLACVLLFLKEFLGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 159>:

g041-1.seq

```

1  ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCG CGCGCACTTT CAGACGGCAT TTTGAATCAA
151 ATGCAGGACA CGCGGCAGAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAGAAATG CGGAATATCC GAAGGGCGTG TACCGCATGT
251 GTACGGCGGC GACCTACCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTCGATGA GTTGCTCGGC GACGATGTGT ATTTGGGCGG
351 CGTGTCGCAC TTGGTGGAGC AGCCCAACCG CGCGCTGCTG ACTTTGAACA
401 AATCGGGCGG CGATACGGCG TATACGCTGG AAGTGGATTT GGAAGCAGGG
451 GAATTGGTAG AGGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAAG TGTGGCTGGT GGAACGCGGC

```

```

601 AAGAGTTTCG AGGAAAGCCT GCCGGCGTAC CAAATCGATA AAGGCGCGAT
651 GATGGTAAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AGACGTATTT GCAGGTGTCG
751 TCCGAAGGCG GGGCGAAACC GTTGAACCTG CCTAATGATT GCGATGTGGT
801 CGGCTATCTG GCGGGACATC TTTTGCTGAC GCTGCGCAAG GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCGT TGGTGGCGGT GAAACTGAAT
901 CCGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCAAGCCTGC
1001 TGGAGAATGT ACAAGGCCGT CTGAAAGCGT GGCGGTTTGC CGACAGCAAA
1051 TGGCAGGAAG CCGAGTTGCC GCACCTGCCC TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGCGGCG ACCTGGTTTA TCTTGCCGCC AGCGATTTC A
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAC TGACC
1201 GTCATGCGCC TCCAGCCGCA GCAGTTTGTT TCAGACGGCA TCGAAGTGC
1251 GCAGTTTGGG GCGGTGTCGT CCGACGGCGA ACGATTTCCT TATTTCCACG
1301 TCGGCAAAAA CGCGCGCCC GACACGCCGA CCTAGTCTA TGCTTACGGA
1351 GGTTCGGCA TTCTGAATT GCCGATTAT CTGGGCAGCG TCGGCAAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTGTATT GGCAACATC CGCGGCGGCG
1451 GAGAATTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAAACAC
1501 AAAAGCGTTG ATGATTTGTT GGCAGTCGTG CGTGATTTGT CCGAACGCGG
1551 CATGAGTTCG CCCAAACACA TCGGCTTGCA GGGCGGCAGC AACGCGGCGC
1601 TGATTACCGC CGCCGCTTC GTGCGCGAAC CGCAAAGCAT CGGTGCGCTG
1651 GTGTGCGAAG TACCGCTGAC CGATATGATC CGTTATCCG TGCTGTCCG
1701 CGGTTCAAGT TGGACGGACG AATACGGCAA TCCGAGAAA TACGAAGCCT
1751 GCAAACGCCG GCTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCACT CATTACCACC AGCCTCAGCG ACGACCGCGT
1851 CCATCCCGCC CACGCGCTCA AATTCTACGC CAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CAACTCGCC TCGGTGTTGC TGTTTTGA
2001 AGAATTTTG GGATAA

```

This corresponds to the amino acid sequence <SEQ ID 160; ORF 041-1.ng>:

g041-1.pep

```

1 MKSYDPYRHH FENLDSAEQ NFAAEANAET RARFLNNDKA RALSDGILNQ
51 MQDTRQIPFC QEHRARMYHF HQNAEYPKGV YRMCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLNKSGGDTA YTLEVDLEAG
151 ELVEGGFHFH AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPAY QIDKGAMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 SEGGAAPLNL PNDGDVVGYL AGHLLLTLRK DWHRANQSYR SGALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADSK
351 WQEAELPHLP SGALEMTDQF WGGDVVYLA SDFTTPLTLF ALDLNVMELT
401 VMRLQPQQFV SDGIEVRQFW AVSSDGERIP YFHVGNNAAP DTPTLVYAYG
451 GFGIPELPHY LGSVGKYWLE EGNFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV RDLSEGRMSS PKHIGLQGG NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEACKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSFQSWLYS PDGGGHTGNG
651 TQRESADKLA CVLLFLKEFL G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 161>:

m041-1.seq

```

1 ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAGAAAA CGACAAGGCG CGCGCGCTTT CAGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAGAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAGGACG CGGAGTATCC GAAGGGCGTG TACCGCGTGT
251 GTACCGCGGC GACGTATCGT TCCGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTGACGCA ATTGCTTGGC GACGATGTGT ATTTGGGCGG
351 CGTGTGCGAC TTGGTGGAAC AGCCCAACCG CGGTTGTTA ACTGAGCA
401 AATTGGGCAG CGATACGGCG TACACGCTGG AAGTGGATT TGAAGCAGGG
451 GAGTTGGTCG AAGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG AACGAACGCC
551 AGTTGACCCA ATCGGGCTAT CCGCGCGAAG TATGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCTGTGTAT CAAATCGGCG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ATCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AAACCTATTT GCGGGTCTCA

```



```

751  GCCGAAGGCG AGGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTGGT
801  CCGCTATCTG GCGGGGCATC TTTTGCTGAC GCTGCGCAAG GACTGGAACC
851  GCGCGAACCA AAGCTATCCG AGCGGCGCGC TGGTGGCGGT GAAGCTGAAT
901  CCGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951  GGCATTGGAA AGCGTGGAAG CGACCAAGCG TTTTGTGGTG GCGAGCCTGT
1001 TGGAGAACGT ACAAGGCCGT CTGAAAGCAT GGCGGTTTGC CGACGGCAAA
1051 TGGCAGGAAG TCGAATTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCT TGGGGCGGCG ACGTGGTTTA CCTTGCCGCC AGCGATTTCa
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAGTGACC
1201 GTCATGCGCC GCCAGCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCCGAATT GCCGATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GGCGAACATC CGCGCGCGCG
1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAACAT
1501 AAAAGCGTTG ATGATTATT GGCAGTCGTG CGCGATTTGT CCGAACGCGG
1551 TATCAGTTCC CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT CGCGCGCGTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCGG GTTGGGCGAA TTGTCGCGCT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCCG
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CGAACTCGCC TGCGTCTTGC TGTTTTTGAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 162; ORF 041-1>:

**m041-1.pep**

```

1  MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLENDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKGV YRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TSLKLGSDTA YTLEVDLEAG
151 ELVEGGFHFH AGKNHVSWRD ENSVWVCPAW NERQLTQSGY PREVWLVERG
201 KSFEESLPVY QIGEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLRVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRK DWNRRANQSY SGALVAVKLN
301 RGE LGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADGK
351 WQEVLPRLP SGALEMTDQP WGGDVVYLAA SDFTPPLTLF ALDLNVMELT
401 VMRRQPQFQ SDGINVQFQW TTSADGERIP YFHVGNKNAAP DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLANI RGGGFEFGRW HQAAQGISKH
501 KSVDDLLAVV RDLSEGRIS PEHIGLQGS NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDRVHPA HALKFYAKLR ETSAQSWLYS PDGGGHTGNG
651 TQRESADELA CVLLFLKEFL G*

```

**m041-1/g041-1** 94.6% identity in 671 aa overlap

	10	20	30	40	50	60
m041-1.pep	MKSYPDPYRHFENLDSAETQNFAAEANAETRARFLENDKARALSDGILAQ LQDTRQIPFC					
g041-1	MKSYPDPYRHFENLDSAETQNFAAEANAETRARFLNNDKARALSDGILNQMQDTRQIPFC					
	10	20	30	40	50	60
m041-1.pep	QEHRARMYHFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
g041-1	QEHRARMYHFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
	70	80	90	100	110	120
m041-1.pep	LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHFHAGKNHVSWRDENSVMVCPAW					
g041-1	LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHFHAGKNHVSWRDENSVMVCPAW					
	130	140	150	160	170	180
m041-1.pep	NERQLTQSGYPREVWLVERGKSFEEESLPVYQIGEDGMMVNARWRYLDPQGS PIDLIEASDG					
g041-1	NERQLTQSGYPREVWLVERGKSFEEESLPVYQIGEDGMMVNARWRYLDPQGS PIDLIEASDG					
	190	200	210	220	230	240

g041-1	DERQLTESGYPREVWLVERGKSFEESLPAYQIDKGAMMVNAWRYLDPQGSPIDLIEASDG
	190 200 210 220 230 240
m041-1.pep	250 260 270 280 290 300
	FYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLTLRKDWNRRANQSYPSGALVAVKLN
g041-1	: : :
	FYTKTYLQVSSEGGAKPLNLPNDCDVVGYLAGHLLTLRKDWHRRANQSYPSGALVAVKLN
	250 260 270 280 290 300
m041-1.pep	310 320 330 340 350 360
	RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRKAWRFADGKWQEVELPRLP
g041-1	: : :
	RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRKAWRFADSKWQEAELPHLP
	310 320 330 340 350 360
m041-1.pep	370 380 390 400 410 420
	SGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTVMRRQFQQFSDGINVQQFW
g041-1	: : :
	SGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTVMRLQFQQFVSDGIEVRQFW
	370 380 390 400 410 420
m041-1.pep	430 440 450 460 470 480
	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI
g041-1	::: : : :
	AVSSDGERIPYFHVGNKNAAPDPTLVYAYGGFGIPELPHYLGSVGKYWLEEGNAFVLANI
	430 440 450 460 470 480
m041-1.pep	490 500 510 520 530 540
	RGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSESGISSPEHIGLQGGSGNGGLITAAAF
g041-1	: : :
	RGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSESGMSSPKHIGLQGGSGNGGLITAAAF
	490 500 510 520 530 540
m041-1.pep	550 560 570 580 590 600
	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG
g041-1	: : :
	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYACKRRLGELSPYHNLSDG
	550 560 570 580 590 600
m041-1.pep	610 620 630 640 650 660
	IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADELA
g041-1	: : :
	IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADKLA
	610 620 630 640 650 660
m041-1.pep	670
	CVLLFLKEFLGX
g041-1	: : :
	CVLLFLKEFLGX
	670

## m041-1/P55577

sp|P55577|Y4NA\_RHISN PROBABLE PEPTIDASE Y4NA >gi|2182536 (AE000086) Y4na [Rhizobium sp. NGR234] Length = 726

Score = 370 bits (940), Expect = e-101

Identities = 217/682 (31%), Positives = 331/682 (47%), Gaps = 22/682 (3%)

Query: 2 KSYDPYRHFENLDSAEQNFAAEANAETRARFLENDKARALSDGILAQDTRQIPFCQ 61  
K DP + +D + + N T + ++ + L LQ T +I  
Sbjct: 42 KDASDPRAYLNEIDGDKAMTWVEAHNLSTVDKLSKDPYSEYQADALTILQATDRIASPS 101

Query: 62 EHRARMY-HFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH 120  
R M +F QD + +G++R T +YRSG P+W+ + V + G G  
Sbjct: 102 FARDGMIDNFWQDGHVQGLWRRITWESYRSGNPQWRTILDVDALSKAEGKTWVFEGGDC 161

Query: 121 LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHPAGKNHVSWRDENSVVWCPAW 180  
L N L+ LS G D E D+ GE V+ GF P GK V+W DEN++V W

Sbjct: 162 LPPTSNLCLIRLSDGGKDADVVREFDIAKGEFVKEGFVLPEGKQSVTVVDENTIIYVTREW 221

Query: 181 NERQLTQSGYPREVWLVERGKSFEESLPVYQ-----IGEDGMM--VNAWRYLDPOGSPI 232  
 ++T SGY +V+RG+S ++++ +++ E G++ ++ +D +

Sbjct: 222 TPGEVTS SGYAYVTKVVRGQSLDQAVEIFRGQKQKDVSAERGLRDIDGKYVMDTSYRGL 281

Query: 233 DLIEASDGFYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLTLRKDWNANQS-YPS 291  
 D FY + + L LP GY G + L+ DW A + + +

Sbjct: 282 DFENTEALAFYPNGH---PDTRKVVLPPLTTAVFSGYKQQAIIYWLKSDWTSAGKTVFHN 337

Query: 292 GALVAVKLNRGELGAAQL----LFAPDETQALESVETTKRFVVASLLENVQGRKAWRFA 347  
 GA++A L A++ LF P+E Q++ TK +V S+L NV ++++ F

Sbjct: 338 GAIIAFDLKAALADPARVEPLVLFMPNEHQSVAGTTQTKNRLVLSILSNVTSEVRSFDFG 397

Query: 348 DGKWQVEVLPRLPSGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQ 407  
 G W +L + L +T D +++ + F P TLF D ++ + P

Sbjct: 398 KGGWSSFKLALPENSTLSLTSSDDESQDLFVFESEGFLEPSTLFCADAATGQVEKITSTPA 457

Query: 408 QFDSGGINVQQFWTTSADGERIPYFHVGNKNAAP---DMPTLVYAYGGFGIPELPHYLGSI 464  
 +FD+ G+ QQFW TS DG ++PYF V + PT++YAYGGF IP P Y +

Sbjct: 458 RFDAGGLQAQQFWATSKDGTKVPYFLVARKDVKLDGNTPTILYAYGGFQIPMQPSYSAVL 517

Query: 465 GKYWLEEGNAFVLANIRGGGEFGPRWHQAAQGISKHSVDLLAVVRDLSEGGISSPEHI 524  
 GK WLE+G A+ LANIRGGGEFGP+WH A ++ + DD AV +DL + ++S H+

Sbjct: 518 GKLWLEKGGAYALANIRGGGEFGPKWHADAGLKTNRQRYDDFQAVAQDLIAKKVTSTPHL 577

Query: 525 GLQGSNGGLITAAAFVREPOSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEV 584  
 G+ GGSNGGL+ ++ P A+V +VPL DM+ + +SAG+SW EYG+P V

Sbjct: 578 GIMGGSNGGLLMGVQMIQRPDLDNNAVVIQVPLDMVNFTRMSAGASWQAEYGSPPD-PVE 636

Query: 585 KRRLGELSPYHNLSDGIDYPPALITTSLSDDRHPAHALKFYAKLRETSASQSWLYSPDGG 644  
 L +SPYHN+ G+ YP TS DDRV P HA K A + + Y G

Sbjct: 637 GAFLRSISPYHNKAGVAYPEFFETSTKDDRVGPVHARKMAALFEDMGLPFYYENIEG 696

Query: 645 GHTGNGTQRESADELACVLLFL 666  
 GH +E A A +++

Sbjct: 697 GHAAAANLQEHARRYALEYIYM 718

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 163>:

a041-1.seq

```

1 ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCA CGCGCATTTGT CTGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAAAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAAGATG CGGAATATCC GAAAGGCGTG TACCGCGTGT
251 GTACCGCGGC GACTTACCGT TCGGGCTATC CTGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTTCGACGA ATTGCTCGGT GACGATGTAT ATCTAGGCGG
351 CGTGTCGCAC CTGGTGGAAAC AGCCCAACCG CGCGTTGTTA ACACTGAGCA
401 AATCGGGCGG CGATACCGCG TACACGCTGG AAGTGGATTT GGAAGCAGGG
451 GAGTTGGTAG AAGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAGG TGTGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCGGTGTAC CAAATTGCTG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCTGACGGT TTTTACACCA AAACCTATTT GCAGGTCTCA
751 GCCGAAGGCG AAGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTAGT
801 CGGCTATCTG GCCGGACATC TTTTGTGAC CTTGCGTAAA GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCAT TGGTAGCAGT AAAATTAAAC
901 CGCGGCGAAT TGGGCGCGGC GCAGCTTTTG TTTGCGCCCA ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTCTGT GCGAGCCTGC
1001 TGGAAAACGT ACAGGGTCGT CTGAAAGCGT GCGCTTTTAC TGATGGCAAA
1051 TGGCAGGAAA CCGAGTTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGGGGCG ACGTAGTTTA CCTTGCCGCC AGCGATTTC
1151 CCACGCCGCT GACGCTGTTT GCATTGGATT TGAACGTGAT GGAAGTACC
1201 GTCATGCGCC GCCAGCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCCGAATT GCCGCATTAT CTGGGCAGCA TTGGCAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GCGCAACATC CGCGGCGGCG

```

```

1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTTATT GGCAGTCGTG AGCGATTTGT CCGAACGCGG
1551 TATCAGTTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT AGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCGG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGCTT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACGCAGCGCG AAGCCGCCGA CGAACTCGCC TGCGTGTTCG TGTTTTGTAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 164; ORF 041-1.a>:

a041-1.pep

```

1  MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKG VYRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLSKSGGDTA YTLEVDLEAG
151 ELVEGGFHFH AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPVY QIAEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 AEGEAKPLNL PNDQDVVGYL AGHLLTLRK DWHRANQSY SGALVAVKLN
301 RGELGAAQLL FAPNETQALE SVETTKRFV ASLLENVQGR LKAWRFTDGK
351 WQETELPRLP SGALEMTDQP WGGDVVYLAA SDFTPLTLF ALDLNVMELT
401 VMRRQPPQFD SDGINVQQFW TTSADGERIP YFHVGNKNAAP DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAPVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV SDSLSEGISS PEHIGLQGS NGGLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQREAADELA CVLLFLKEFL G*

```

a041-1/m041-1 97.9% identity in 671 aa overlap

	10	20	30	40	50	60
a041-1.pep	MKSYPDPYRHFENLDSAETQNFAAEANAETRARFLNNDKARALSDGILAQ					
	:					
m041-1	MKSYPDPYRHFENLDSAETQNFAAEANAETRARFLNNDKARALSDGILAQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a041-1.pep	QEHRARMYHFHQDAEYPKG VYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
	:					
m041-1	QEHRARMYHFHQDAEYPKG VYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a041-1.pep	LVEQPNRALLTLSKSGGDTAYTLEVDLEAGELVEGGFHFAPAGKNHVSWRDENS					
	:					
m041-1	LVEQPNRALLTLSKSGGDTAYTLEVDLEAGELVEGGFHFAPAGKNHVSWRDENS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a041-1.pep	DERQLTESGYPREVWLVERGKSFEEESLPVYQIAEDGMMVNAWRYLDPQGS					
	:     :					
m041-1	NERQLTQSGYPREVWLVERGKSFEEESLPVYQIGEDGMMVNAWRYLDPQGS					
	190	200	210	220	230	240
	250	260	270	280	290	300
a041-1.pep	FYTKTYLQVSAEAEKPLNLPNDQDVVGYLAGHLLTLRKDWHRANQSYPSGALVAVKLN					
	:					
m041-1	FYTKTYLQVSAEAEKPLNLPNDQDVVGYLAGHLLTLRKDWHRANQSYPSGALVAVKLN					
	250	260	270	280	290	300
	310	320	330	340	350	360
a041-1.pep	RGELGAAQLLFAPNETQALESVETTKRFVVASLLENVQGRKAWRFTDGK					
	:					
m041-1	RGELGAAQLLFAPNETQALESVETTKRFVVASLLENVQGRKAWRFTDGK					
	310	320	330	340	350	360

	370	380	390	400	410	420
a041-1.pep	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW					
m041-1	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW					
	370	380	390	400	410	420
	430	440	450	460	470	480
a041-1.pep	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
m041-1	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
	430	440	450	460	470	480
	490	500	510	520	530	540
a041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDDLAVVSDLSESGISSPEHIGLQGGSNGLITAAAF					
m041-1	RGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF					
	490	500	510	520	530	540
	550	560	570	580	590	600
a041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG					
m041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a041-1.pep	IDYPPALITTSLSDDRVHPAHALKFYAKLRETSPQSWLYSPDGGGHTGNGTQREAADELA					
m041-1	IDYPPALITTSLSDDRVHPAHALKFYAKLRETSAQSWLYSPDGGGHTGNGTQRESADELA					
	610	620	630	640	650	660
	670					
a041-1.pep	CVLLFLKEFLGX					
m041-1	CVLLFLKEFLGX					
	670					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 165>:

**g042.seq**

```

1  ATGACGATGA TTTGCTTGCG CTTCCAagcG TTCGTGCCGC ATACCAGCGC
51  GTTATCCAAC ACTTCCACGG CAGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TCGGTCGAT  GATGAAATC CAGCCGGGGT TTTTCTCTTT GATGTATTCT
151 AAGGAAACGG GCTGCCCGTG CCCTTCGTTG CGTAAAGATT CGTCCACGGG
201 CGGCAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GATTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCTGTAACCG ACAGCACCAG CCCGCGTCTC
301 TTGCCTTTGG cggCTTCGCG CTTTGGGCG AACAGCGCGT CAATCTGCGC
351 ATTCAATTCC GCCACGCGCG CTTCTTACC GAAAATCCGC GACAGGGTCT
401 CCATCTGCTT CTCGCCGCTG GTGCGGATAT TGCGGTTGTC CACCGTCAAA
451 TCTATGgtgG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCACCCGG
501 CCCGCCGGTA ATGACAAACT GCGGATTGTG GCGGTGCAGG GATTGCGCAAT
551 CGGGCTCAAA CAGCGTCCCC ACCGTTGCCG CTTGTCAAA TGCAGGCTGC
601 AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 166; ORF 042.ng>:

**g042.pep**

```

1  MTMICLRFQA FVPHTSALSN TSTAAGPSCP MAAVRSMMKI QPGFFSLMYS
51  KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTSRP
101 LPLAASREFA NSASICAFNS ATRASLPKIR DRVSICFSPL VRILPLSTVK
151 SMVVAFFANC SYASAGPPV MTNCGLWRCR DSQSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 167>:

## m042.seq

```

1   ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAmT ACTTCGACAG CCGcCGGCCy TTCyTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTGTGC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 168; ORF 042>:

## m042.pep

```

1   MTMICLRFOA FVPRTSALSX TSTAAGXSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTSXGLXRCR ASXSGSNSVP TVAALSNAG
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 169>:

## a042.seq

```

1   ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCC ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTGTGC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 170; ORF 042.a>:

## a042.pep

```

1   MTMICLRFOA FVPRTSALSX TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*GL*RCR AS*SGSNSVP TVAALSNAG
201 K*

```

m042/a042 99.0% identity over a 201 aa overlap

	10	20	30	40	50	60
m042.pep	MTMICLRFOAFVPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVDSTSPRPLPLAASRVWANSASICAFNS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVDSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
a042	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
	130	140	150	160	170	180

```

a042      |||||
          AARASLPKIRAKVSICFSPVLRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          130      140      150      160      170      180

          190      200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          |||||
a042      ASXSGSNSVPTVAALSNAGCKX
          190      200

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 042 shows 93.0% identity over a 201 aa overlap with a predicted ORF (ORF 042.ng) from *N. gonorrhoeae*:

m042/g042

```

          10      20      30      40      50      60
m042.pep  MTMICLRFAQFVPRTSALSXTSTAAGXSCPMMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
          |||||:|||||
g042      MTMICLRFAQFVPHTSALSNTSTAAGPSCPMMAAVRSMMKIQPGFFSLMYSKETGCPCPSL
          10      20      30      40      50      60

          70      80      90      100     110     120
m042.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRVWANSASICAFNS
          |||||
g042      RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRFWANSASICAFNS
          70      80      90      100     110     120

          130     140     150     160     170     180
m042.pep  AARASLPKIRAKVSICFSPVLRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          |:|||||:|||||:|||||:|||||:|||||: |||||
g042      ATRASLPKIRDVSICFSPVLRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR
          130     140     150     160     170     180

          190     200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          | |||||
g042      DSQSGSNSVPTVAALSNAGCKX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 171>:

m042-1.seq

```

1   ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGTA A

```

This corresponds to the amino acid sequence <SEQ ID 172; ORF 042-1>:

m042-1.pep

```

1   MTMICLRFAQ FVPRTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPV VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/g042 95.4% identity in 173 aa overlap

240

```

              10      20      30      40      50      60
m042-1.pep  MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
              |||||:|||||:|||||:|||||:|||||:|||||
g042         MTMICLRFQAFVPRHSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPCPSL
              10      20      30      40      50      60

              70      80      90      100     110     120
m042-1.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRVWANSASICAFNS
              |||||:|||||:|||||:|||||:|||||:|||||
g042         RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRFWANSASICAFNS
              70      80      90      100     110     120

              130     140     150     160     170
m042-1.pep  AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX
              |:|||||:|||||:|||||:|||||:|||||:
g042         ATRASLPKIRDRVSICFSPLVRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR
              130     140     150     160     170     180

g042         DSQSGSNSVPTVAALSNAGCKX
              190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 173>:

```

a042-1.seq
1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCC
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGTA A

```

This corresponds to the amino acid sequence <SEQ ID 174; ORF 042-1.a>:

```

a042-1.pep
1  MTMICLRFOA FVPRTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMY
51 KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCPKADTLL PVTDSTSPR
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/a042-1 100.0% identity in 173 aa overlap

```

              10      20      30      40      50      60
m042-1.pep  MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
              |||||:|||||:|||||:|||||:|||||:|||||
a042-1       MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
              10      20      30      40      50      60

              70      80      90      100     110     120
m042-1.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRVWANSASICAFNS
              |||||:|||||:|||||:|||||:|||||:|||||
a042-1       RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRVWANSASICAFNS
              70      80      90      100     110     120

              130     140     150     160     170
m042-1.pep  AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX
              |||||:|||||:|||||:|||||:|||||:
a042-1       AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX
              130     140     150     160     170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 175>:



```

g043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GTCGGCCCAT CAGCACTTTT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GCCTGAACGC TTCgttgaAC
101 CGTCCCGCGT ggcggtagcc gcAAAAGTGC ATcGCGGCTT GGATGGTGCT
151 GCCCGATTTCG ATGAGGGcga gcGCGTGTTT CAGCCGCAGG CGGCGCAGGC
201 GTCCGGCGAC GGTTCGCGG GTTTGCCTT TGAATAGCG TTTCAGGTAG
251 CATTCGTTCA GCCCACGCG GCGGGCGATT TCGGCGATGG TCAGCGGGCG
301 GGCGAATTCG CTGTTCAAAA TATCGGCGGC TTCGTCTATG CGCCGGCGGC
351 GGTAGCCGTT GTCGTGGCGG CGGAAGGTGA AGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 176; ORF 043.ng>:

```

g043.pep
1  MVVSNQNIYA VGPSALFHIR RQKSVMPER FVEPSRVAVA AKVHRGLDGA
51  ARFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQPD AAGDFGDGQRA
101 GEFVQNIIGG FVYAPAAVAV VVAAEGEA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 177>:

```

m043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCCCT CAGCACTTCT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT
151 GCCCGATTTCG ATGAGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCAgGC
201 ATCCGGCGAC GGTTCGCGG GTTTGCCTT TGAATAGCG TTTCAGGTAG
251 CATTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTCAGGA TGTGCGCGC TTCGTCTATG CGCCGACGGC
351 GGTAAACGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 178; ORF 043>:

```

m043.pep
1  MVVSNQNIYA AGPSALLHIR RQKSVMPSE FVEPSRVAVA AKVHGGLDGA
51  AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AAGDFGDGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 043 shows 89.8% identity over a 128 aa overlap with a predicted ORF (ORF043.a) from *N. gonorrhoeae*:

m043/g043

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
g043	MVVSNQNIYAVGPSALFHIRRQKSVMPSERFVEPSRVAVAAKVHRLDGAARFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
g043	QPQAAQASGDGFAGLRFEIAFQVAFVQPDAGDFGDGQRTAGEFAVQNIIGGFVYAPAAVAV					
	70	80	90	100	110	120
	130					
m043.pep	VVAAEGEAQX					
g043	VVAAEGEAXX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 179>:

```

a043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCCCT CAGCACTTCT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT

```

```

151 GCCGGATTCTG ATGAGGGCGA GCGCGTGTTC CAGCCGCAGG CCGCGCAGGC
201 ATCCGGCGGAC GGTTCGCGCG GTTTCGCGTT TGAATAGCG TTTCAGGTAG
251 CATTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GCGGAATTCTG TGTTCAGGA TGTGCGCGGC TTCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 180; ORF 043.a>:

```

a043.pep
1  MVVSNQNIYA AGPSALLHIR RQKSVMPSER FVEPSRVAVA AKVHGGLDGA
51  AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

m043/a043 100.0% identity in 129 aa overlap

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
a043	MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	70	80	90	100	110	120
	130					
m043.pep	VVAAEGEAQX					
a043	VVAAEGEAQX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 181>:

```

g044.seq
1  ATGCTGCCCG ACCAGAGCGT CGAGTTCTTG CCACAAGTCG TCGTTTTTGA
51  CGGGCTGTTT GGCGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
101 CAGTTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTCAGCCC TCGATAACG GCGGTCAGCT
201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTTCG
251 CGGCTGCCGT AGCGCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 182; ORF 044.ng>:

```

g044.pep
1  MLPDQSVEFL PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
51  GAAAFERFQP FDNGGQLHAV VGGLRFAAEK FFFAAVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 183>:

```

m044.seq
1  ATGCCGTCCG ACTAGAGCGT CGAGTTCTTT CCAGAAGTCG TCGTTTTTGA
51  CGGGCTGTTT GGAGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
101 CAGTTTTTCCA TGCCATTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTCAGTCC TCGATGACG GCAGTCAGTT
201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTTCG
251 TGGCTACCGT AGCGCAyTaa

```

This corresponds to the amino acid sequence <SEQ ID 184; ORF 044>:

```

m044.pep
1  MPSDXSVEFF PEVVVFDGLF GGGFPAVALP TVYPVFHAI F DVLRVGADDD
51  GAAAFERFQS FDDGSQPHAV VGGLRFAAEK FFFVATVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 185>:

```
a044.seq
  1 GTGCCGTCGG ACCAGCGCGT CGAGTTCTTT CCACAAGTCG TCGTTTTTGA
 51 CGGGCTGTTT GGCAGCGGTT TTCCAGCCGT TGCCTTCCA ACCGTGTATC
101 CAGTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTGAGCG ATTTCAGTCC TTCGATGACG GCGGTCAGTT
201 CCATACGGTT GTTGGTGGTT TGCCTTCGC CGCCGAAAAG TTCTTTTTCG
251 TGGCTGCCGT AGCGCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 186; ORF 044.a>:

```
a044.pep
  1 VPSDQRVEFF PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
 51 GAAAFERFQS FDDGGQFHTV VGGLRFAAEK FFFVAVAH*
```

m044/a044 91.0% identity over a 89 aa overlap

	10	20	30	40	50	60
m044.pep	MPSDXSVEFFPEVVVFDGLFGGGFPVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS					
a044	VPSDQRVEFFPQVVVFDGLFGGGFPVALPTVYPVFHAVFDVLRVGADDDGAAAFERFQS					
	10	20	30	40	50	60
	70	80	90			
m044.pep	FDDGSQFHAVVGGLRFAAEKFFVATVAHX					
a044	FDDGGQFHTVVGGLRFAAEKFFVAVAHX					
	70	80	90			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 044 shows 86.5% identity over a 89 aa overlap with a predicted ORF (ORF 044.ng) from *N. gonorrhoeae*:

m044/g044

	10	20	30	40	50	60
m044.pep	MPSDXSVEFFPEVVVFDGLFGGGFPVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS					
g044	MLPDQSVEFLPQVVVFDGLFGGGFPVALPTVYPVFHAVFDVLRVGADDDGAAAFERFQP					
	10	20	30	40	50	60
	70	80	90			
m044.pep	FDDGSQFHAVVGGLRFAAEKFFVATVAHX					
g044	FDNGGQLHAVVGGLRFAAEKFFFAA VAHX					
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 187>:

```
g046.seq
  1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGC CCGCCGCGcc gCGCCTGTAT
 51 GATGACCATC CGCACGCGGT CGTCTGCAA ACCTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC gaATATGGAA AGGCTGCCGt TTTcGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TtcgctGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGTCGCG GGagaGCGCG AGcagcaagt cggcatcttC
351 CgcgccggcG Cgttataatg tgAAGGGGGA TCGCccgttg ccgaAAACGG
401 TTTGGacatc gaggcggctg CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAAcg TTACGTCGTT GTTGGTGATG GCGGCAAGGT TTTGCGCGAC
```

501 GGTAGAACCT ACCTGCCCCG TGCCTAAAAT GAGGATTTTC ACGGTATGGG  
551 TCGCCGGGTG A

This corresponds to the amino acid sequence <SEQ ID 188; ORF 046.ng>:

g046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG  
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT  
101 MLVSSLRESA SSKSASSAPA RYNVKGDAPL PKTVWTSRRL PVSCNAFSSM  
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 189>:

m046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAaT CCGC.r.sGC gCGcCTGTAT  
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC  
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG  
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT  
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG  
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG  
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC  
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCCCGTTG CCGAAAACGG  
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG  
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC  
501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG  
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 190; ORF 046>:

m046.pep

1 MSAMLRPTSX PXXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG  
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT  
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM  
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 191>:

a046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGT CCGCCGCGCC GCGCCTGTAT  
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC  
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG  
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT  
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG  
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG  
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC  
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCCCGTTG CCGAAAACGG  
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG  
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC  
501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG  
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 192; ORF 046.a>:

a046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG  
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT  
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM  
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAE\*

m046/a046 98.4% identity over a 186 aa overlap

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSGLMVSVMPNME					
a046	MSAMLRPTSSPPRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSGLMVSVMPNME					

245

	10	20	30	40	50	60
	70	80	90	100	110	120
m046.pep	RLPFSLFSSSLGLRYSRYSLERTRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
a046	RLPFSLFSSSLGLRYSRYSLERTRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m046.pep	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
a046	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
a046	TVWVAEX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 046 shows 97.3% identity over a 185 aa overlap with a predicted ORF (ORF 046.ng) from *N. gonorrhoeae*:

m046/g046

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTIRTRSSAKRKTCTNAPGQSIRPASC SVTSCSGLMVSVMPNME					
g046	MSAMLRPTSPPPRRACMMTIRTRSSAKRKTCTNAPGQSIRPASC SVTSCSGLMVSVMPNME					
	10	20	30	40	50	60
	70	80	90	100	110	120
m046.pep	RLPFSLFSSSLGLRYSRYSLERTRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
g046	RLPFSLFSSSLGLRYSRYSLERTRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m046.pep	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
g046	RYNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLVMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
g046	TVWVAGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 193>:

g047.seq

1	ATGGTCATCA	TACAGGCGcg	gcGCGGCGGG	CTGCTTGTCG	GACGCAGCAT
51	TGCCGACATC	GCCCAAGATT	TGCCCGACGG	GGCCGACTGC	CAAATCTGCG
101	CCGTTTACCG	CAACAACCGC	CTCATCGTCC	CCGCGCCGCA	AACCGTCATC
151	ATCGAAGGCG	ACGAAATCCT	GTTTGCCGCC	GCCGCCGAAA	ACATCGGGGC
201	GGTCATACCc	gaATTGCGCC	CCAAAGAAAC	CAGCACCCGC	CGCATCATGA
251	TTGCCGCGCG	CGGCAACATc	tgctACCGCC	TCGCCAAGCA	GCTCGAACAC

```

301 GCATAcacG TCAAAATCAT CGAATGCCGG CCGCGCcggtg ccgaATGGAT
351 AGCCGAAAAC ctcgAcaaCA CCCTCGTCCT GCAAGGTTTCG Gcaaccgacg
401 aAaccctgct cgAcaacgaa tacatcgacg aaatcgaCGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTAtg tCCGCCCTTT TGGCGAAAAA
501 CCTcggcgCG AAGCgcgtca teggCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCGCACG
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCGGTC GTCCGCGCCG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGTGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAAC TGAAGAACTC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 194; ORF 047.ng>:

```

g047.pep
1 MVIIQARRGG LLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGNI CYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLLDNE YIDEIDVFCA
151 LTNDDESIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS AIIIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRIILNELEKL
301 IQVKMGFFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 195>:

```

m047.seq
1 ATGGTCATCA TACAGCGCG C...syGCGGA sTGCTTGTCG GACGCAGCAT
51 TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCCTCATC
151 ATCGAAGCGC ACGAAATCCT ATTGCGCCG CCGCGCGAAA ACATCGGCGC
201 GGTCATACCC GAATTGCGCC CCAAAGAAAC CCAAAGAAAC CAGCcCmgmm
251 GcATCATGAT TkCGGCGGC GGCAACATCG GCTACCGTCT CGCCAAGCAG
301 CTCGAACACG CATACAACGT yAAAATCATC GAATGCCGCG CGCGCCGTGC
351 CGAATGGATA GCCGAAAACC TCGACAACAC CCTCGTCyTG CAAGGTTCCG
401 CAACCGACGA AACCTGTCT GACAACGAAT ACATCGACGA AATCGACGTA
451 TTCTGCGCCC TGACCAACGA CGACGAAAGC AACATTATGT CCGCCCTTTT
501 GGCGAAaAAC CTCGGCGCGA AGCGCGTCAT CGGCATCGTC AACCGCTCAA
551 GCTACGTCGA TTTGCTCGAA GGCAACAAAA TCGACATCGT CGTCTCCCCC
601 CACCTCATCA CCATCGGCTC GATACTCGCC CACATCCGCG CGGCGGACAT
651 CGTTGCCGTC CACCCATCC GCGCGGCGAC GGCGGAAGCC ATCGAAGTCG
701 TCGCACACGG CGACAAAAAA ACTCCGCA TCATCGGCAG GCGCATCAGC
751 GGCATCAAAT GGCCGAAGG CTGCCACATT GCGCGCGTCG TCCGCGCCG
801 AACCGGCGAA ACCATTATG GACACCATAC CGAAACCGTC ATCCAAGACG
851 GCGACCAT CATCTTTTTC GTCTCGCGCC GCGCATCCT GAACGAACG
901 GAAAACTCA TCCAGGTCAA AATGGGCTTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 196; ORF 047>:

```

m047.pep
1 MVIIQARXXG XLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETQRN QPXXIMIXGG GNIGYRLAKQ
101 LEHAYNVKII ECRPRRAEWI AENLDNTLV LQGSATDETL DNEYIDEIDV
151 FCALTNDDES NIMSALLAKN LGAKRVIGIV NRSSYVDLLE GNKIDIVVSP
201 HLITIGSILA HIRRGDIVAV HPIRRGTAE AIEVVAHGD KKTSAIIGRRIS
251 GIKWPEGCHI AAVVRAGTGE TIMGHHTETV IQDGDHIIFF VSRRLILNEL
301 EKLIQVKMGF FG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 197>:

```

a047.seq
1 ATGGTCATCA TACAGGCGCG GCGCGGCGGA CTGCTTGTCG GACGCAGCAT

```

```
51  TGCCGACATC  GCCAAGATT  TGCCCGACGG  GGCCGACTGC  CAAATCTGCG
101 CCGTTTACCG  CAACAACCGC  CTCATCGTCC  CCGCGCCGCA  AACCGTCATC
151 ATCGAAGGCG  ACGAAATCCT  ATTTGCCGCC  GCCGCCGAAA  ACATCGGCGC
201 GGTCATACCC  GAATTGCGCC  CCAAAGAAAC  CAGCACCCGC  CGCATCATGA
251 TTGCCGCGCG  CGGCAACATC  GGCTACCGTC  TCGCCAAGCA  GCTCGAACAC
301 GCATACAACG  TCAAAATCAT  CGAATGCCGG  CCGCGCCGTG  CCGAATGGAT
351 AGCCGAAAAC  CTCGACAACA  CCCTCGTCCT  GCAAGGTTCT  GCAACCGACG
401 AAACCCGTCT  CGACAACGAA  TACATCGACG  AAATCGACGT  ATTCTGCGCC
451 CTGACCAACG  ACGACGAAAG  CAACATTATG  TCCGCCCTTT  TGCGCAAAAA
501 CCTCGGCGCG  AAGCGCGTCA  TCGGCATCGT  CAACCGCTCA  AGCTACGTCG
551 ATTTGCTCGA  AGGCAACAAA  ATCGACATCG  TCGTCTCCCC  CCACCTCATC
601 ACCATCGGCT  CGATACTCGC  CCACATCCGG  CGCGGCGACA  TCGTTGCCGT
651 CCACCCCATC  CGGCGCGGCA  CGCGGAAGC  CATCGAAGTC  GTCGCACACG
701 GCGACAAAAA  AACTTCCGCC  ATCATCGGCA  GCGGCATCAG  CGGCATCAAA
751 TGGCCCGAAG  GCTGCCACAT  TGCCGCCGTC  GTCCGCGCCG  GAACCGGCGA
801 AACCATTATG  GGACACCATA  CCGAAACCGT  CATCCAAGAC  GCGGACCACA
851 TCATCTTTT  CGTCTCGCGC  CGGCGCATCC  TGAACGAAC  T  GAAAAACTC
901 ATCCAAGTCA  AAATGGGCTT  TTTCGGATAA
```

This corresponds to the amino acid sequence <SEQ ID 198; ORF 047.a>:

```
m047.pep
1  MVIIQARRGG  LLVGRSIADI  AQDLPGADC  QICAVYRNNR  LIVPAPQTVI
51  IEGDEILFAA  AAENIGAVIP  ELRPKETSTR  RIMIAGGNI  GYRLAKQLEH
101 AYNVKIIECR  PRRAEWIAEN  LDNTLVLQGS  ATDETLLDNE  YIDEIDVFCA
151 LTNDDESIM  SALLAKNLGA  KRVIGIVNRS  SYVDLLEGNK  IDIVVSPHLI
201 TIGSILAHIR  RGDIVAVHPI  RRGTAEAIEV  VAHGDKKTS  IIGRRISGIK
251 WPEGCHIAAV  VRAGTGETIM  GHHTETVIQD  GDHIIFFVSR  RRIILNELEK
301 IQVKMGFFG*
```

m047/a047 96.5% identity over a 312 aa overlap

```

      10      20      30      40      50      60
m047.pep  MVIIQARXXGLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA
||||||| | ||||||| ||||||| ||||||| ||||||| |||||||
a047      MVIIQARRGGLLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA
      10      20      30      40      50      60

      70      80      90     100     110     120
m047.pep  AAENIGAVIPELRPKETQRNPXXIMIXGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
||||||| : ||| ||||||| ||||||| ||||||| ||||||| |||||||
a047      AAENIGAVIPELRPKETSTR---IMIAGGNIYRLAKQLEHAYNVKIIIECRPRRAEWI
      70      80      90     100     110

      130     140     150     160     170     180
m047.pep  AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESIMISALLAKNLGAKRVIGIV
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a047      AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESIMISALLAKNLGAKRVIGIV
      120     130     140     150     160     170

      190     200     210     220     230     240
m047.pep  NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a047      NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK
      180     190     200     210     220     230

      250     260     270     280     290     300
m047.pep  TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRIILNEL
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a047      TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRIILNEL
      240     250     260     270     280     290

      310
m047.pep  EKLIQVKMGFFGX
|||||||
```

a047            EKLIQVKMGFFGX  
                 300            310

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 047 shows 96.2% identity over a 312 aa overlap with a predicted ORF (ORF 047.ng) from *N. gonorrhoeae*:

m047/g045

m047.pep	MVIIQARXXGXLVGRSIADIAQDLPDGADCQICAVYRNRLIVPAPQTVIIEGDEILFAA	60
g047	MVIIQARRGGLLVGRSIADIAQDLPDGADCQICAVYRNRLIVPAPQTVIIEGDEILFAA	60
m047.pep	AAENIGAVIPELRPKETQRNQPPXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI	120
g047	AAENIGAVIPELRPKETSTR---IMIAGGNICYRLAKQLEHAYNVKIIIECRPRRAEWI	117
m047.pep	AENLDNTLVLQGSATDETLDDNEYIDEIDVFCALTNDDES NIMSALLAKNLGAKRVIGIV	180
g047	AENLDNTLVLQGSATDETLDDNEYIDEIDVFCALTNDDES NIMSALLAKNLGAKRVIGIV	177
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	240
g047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	237
m047.pep	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIINEL	300
g047	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIINEL	297
m047.pep	EKLIQVKMGFFGX    313	
g047	EKLIQVKMGFFGX    310	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 199>:

g048.seq

```

1  ATGCTCGACA AAGGCGAGGA GTTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTA CTACGTc ggcCCcgTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG
101 CAGGTCCGAC CACAGCCACC CGCATGGACA AATTTACCCG CCAAATGCTC
151 AAACAAACCG GCCTCTTGGG CATGATCGGC AAATCCGagc gcgGcgcggc
201 cacctGCGAA GCcatCGCCG ACAACAAGGC CGTG TACCTC ATGGCAGTCG
251 GCGGCGCGGC ATACCTCGTG GCAAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCGG AATTGGGTAT GGAAGCCGTT TACGAATTG AAGTCAAAGA
351 TATGCCCCTA ACCGTCGCCG TGGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAGTCT
451 TGA

```

This corresponds to the amino acid sequence <SEQ ID 200; ORF 048.ng>:

g048.pep

```

1  MLDKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51  KQTGLLMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAV YEFVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 201>:

m048.seq

```

1  ATGCTCAACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTA CTACGTc GGCCCCGTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCGG

```



```

101 CAGGTCCGAC CACAGCCACC CGCATGGACA AATTCACCCG CCAAATGCTC
151 GAACAAACCG ACCTCTTGGG CATGATCGGC AAATCCGAGC GCGGCGTGGC
201 CACCTGCGAA GCCATCGCCG ACAACAAAGC CGTGTACCTC ATGGCAGTCG
251 GCGGCGCGGC GTATCTCGTG GCAAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCGG AATTGGGCAT GGAAGCCATT TACGAATTG AAGTCAAAGA
351 CATGCCCGTA ACCGTCGCCG TAGATAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCG CAAATGGCAG GCGAAATCG GCATCATCCC CGTCGAATCT
451 TGA

```

This corresponds to the amino acid sequence <SEQ ID 202; ORF 048>:

```

m048.pep
  1 MLNKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
  51 EQTDLLGMIG KSERGVATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPGLGMEAI YEFVKGMPV TVAVDSKGES IHATAPRWQ AKIGIIPVES
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 203>:

```

a048.seq
  1 ATGCTCGACA AAGGCGAAGA ATTGCCGTC GATTTCACCA ACCGCCTGAT
  51 TTAACACGTC GCGCCCGTCG ATCCGGTCGG CGACGAAATC GTCGGCCAG
101 CAGGTCCGAC CACCGCCACC CGCATGGACA AATTCACCCG CCAAATGCTC
151 GAACAAACCG ACCTCTTGGG CATGATCGGC AAATCCGAGC GCGGCGCGGC
201 CACCTGCGAA GCCATCGCCG ACAACAAAGC CGTGTACCTC ATGGCAGTCG
251 GCGGCGCGGC GTATCTCGTG GCAAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCGG AATTGGGCAT GGAAGCCATT TACGAATTG AAGTCAAAGA
351 CATGCCCGTA ACCGTCGCCG TAGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCC CCAATGGCAG GCGAAATCG GCATCATCCC CGTCAAATCT
451 TGA

```

This corresponds to the amino acid sequence <SEQ ID 204; ORF 048.a>:

```

a048.pep
  1 MLDKGEELPV DFTNRLIYYV GPVDPVGDEI VGPAGPTTAT RMDKFTRQML
  51 EQTDLLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPGLGMEAI YEFVKGMPV TVAVDSKGES IHATAPQWQ AKIGIIPVKS
151 *

```

m048/a048 96.0% identity over a 150 aa overlap

	10	20	30	40	50	60
m048.pep	MLNKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML EQTDLLGMIG					
a048	MLDKGEELPV DFTNRLIYYV GPVDPVGDEI VGPAGPTTAT RMDKFTRQML EQTDLLGMIG					
	10	20	30	40	50	60
m048.pep	KSERGVATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL AFPGLGMEAI YEFVKGMPV					
a048	KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL AFPGLGMEAI YEFVKGMPV					
	70	80	90	100	110	120
m048.pep	TVAVDSKGES IHATAPRWQ AKIGIIPVESX					
a048	TVAVDSKGES IHATAPQWQ AKIGIIPVKSX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 048 shows 96.4% identity over a 150 aa overlap with a predicted ORF (ORF 048.ng) from *N. gonorrhoeae*:



m048/q048

	10	20	30	40	50	60
m048.pep	MLNKGEELPVDF	TNRLIYYVGP	VPDVPVGDEV	VGPA	PTTATRMDK	FTQRMLEQTDLLGMIG
	:					
g048	MLDKGEELPVDF	TNRLIYYVGP	VPDVPVGDEV	VGPA	PTTATRMDK	FTQRMQLKQTGLLGMIG
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAI	ADNKAVYLM	AVGGAAYLV	AKAIKSSK	VLAFPEL	GMEAIYEF
	:					
g048	KSERGAATCEAI	ADNKAVYLM	AVGGAAYLV	AKAIKSSK	VLAFPEL	GMEAVYEF
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESI	HATAPRKWQ	AKIGIIP	VESX		
g048	TVAVDSKGESI	HATAPRKWQ	AKIGIIP	VESX		
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 205>:

g049.seq

```
1 ATGCGGGCGC AGGCGTTTGA TCAACCGTTC GGTCAGCTCC TGTTCCGACA
51 GGCAGAACAC TTCGCGCCGG TTGACGGCTT TCGGGTTACG GATATTGATT
101 TGGACGGGCA TCAACGCGCT TCCGCAACCG CCTTCGCGCT TTTCCGCAAC
151 CCCGTCTGCC GCCGTACCGG ATTCGTGCCG ATCGCGGTTT TCCCCGCCCT
201 CAATCTGTGC GGTTTCAAAT TCGGCACTGT CTTTTTTGGC ATCGAACCGG
251 ATTCTCCGCC GCGATTGAT GTGTTTTTCC GAAAccggca tTTGCAGGGA
301 AGCCTgcgcg TTGAGCCAGT TTTCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCGc tGTTGTGTTC TTCCTGCCAT
401 TTCTTCAGAT ACGCCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 206; ORF 049.ng>:

g049 . pep

```
1  MRAQAFDQPF  GQLLFQAEH  FAPVDGFRVQ  DIDLDGHQRL  FRTAFAVFRN
51  PVCRRTGFCR  IGVFPALNLC  GFKFGTVFFG  IEPDSPPRFD  VFFRNRHLQG
101 SLRVEPVFLK  DDHRVGFDL  AAIGNGAVVF  FLPFLQIRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 207>:

```
m049.seq (partial)
      1 ATGCGGGCGC AGGCGTTTGA TCAGCCGTTC GGTCAGCTCC TGTTCGGACA
     51 GGCAGAACAC TTCGCGCCGG TTGACGGCTT TCGGGTTTCA GATATTGATT
    101 TGGACAGGGCA TCAACGTTTC TTCGCAATCG TTTTCCCGGT TTCCCGAAAC
    151 CGCCGCGCTCA TTCGTGCCGG ATTCGTGCCTC GTCGCGGGTT TCCCGCGTTT
    201 CAATCTGTCC GGTTTCAAAT TCGACACTGT CTTTTTTGGT ATCAAACCGG
    251 ATTCTCCGCC GCGATTCGAT GTGTTTTTCC GAAACCGACA TTTGCAGGGA
    301 AGCCTGCGCG TTGAGCCAGT TTTCTGAAG GACGATCATC GGGTCGGTTT
    351 CGACTTCCTC GCCGCAATCG GCAACGGCGG CATTGTGTTC CTCCTGCCAT
    401 TTTTTCACTG ACGCCTT...
```

This corresponds to the amino acid sequence <SEQ ID 208; ORF 049>:

m049.pep (partial)

1	MRAQAFDQPF	QQLLFGQAEH	FAPVDGFRVQ	DIDLGDGHRF	FRIVFPVFRN
51	RRLLRAGFCL	VGVPFAPNLS	GFKFDTVFEG	IKPDSPPRFD	VFFRNRLHQQ
101	SLRVEPVFLK	DDHRVGFDFL	AAIGNGGIVF	LLPFFQIRL...	

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 209>:

a049.seq

1	ATGCGGGCGC	AGGCGTTTGA	TCAGCCGTTC	GGTCAGCTCC	TGTTCCGACA
51	GGCAGAACAC	TTCGCGCCGG	TTGACGGCTT	TCGGGTTTCA	AATATTGATT
101	TGGACGGGCA	TCAACGCTTC	TTCCGCACCG	CCTTCGCGCT	TTTCCGCAAC
151	CCCGTCTGCC	GCCGTACCCG	ATTCTGCCGC	ATCGGCGCTT	TCCCGCCCTT
201	CAATCTGTCC	GGTTTCAAAT	TCGGCACTGT	CTTTTTTGCC	ATCAAAACCG
251	ATTCTCCGCC	GCGATTCGAT	GTGTTTTTCC	GAACCGGACA	TTTGCAGGGA
301	AGCCTGCGCG	TTGAGCCAGT	TTTCTGAAG	GACGATCATC	GGGTCGGTTT
351	CGACTTCCTC	GCCGCAATCG	GCAACGGCGG	CATTGTGTTC	CTCCTGCCAT
401	TTTTTCCAT	ACGCGCTT			

This corresponds to the amino acid sequence <SEQ ID 210; ORF 049.a>:

a049.pep

1	MRAQAFDQPF	QQLLFGQAEH	FAPVDGFRVQ	NIDLGHQRF	FRTAFAVERN
51	PVCRRTFR	IGVFAPNLS	GFKFGTVFFG	IKPDSPPRF	VFERNRHLQG
101	SLRVEPVFLK	DDHRVGDFEL	AAIGNGGIVE	LLPFFOIRL	

**m049/a049** 90.6% identity over a 139 aa overlap

		10	20	30	40	50	60
m049.pep		MRAQAFDQPFQGQLLFGQAEHFAPVDGFRVQDIDLGDGHQRFRRIVFPVFRNRRLIRAGFCL					
a049		MRAQAFDQPFQGQLLFGQAEHFAPVDGFRVQNIIDLGDGHQRFRRITAFAVFRNPVCRRTRECFR					
		10	20	30	40	50	60
		70	80	90	100	110	120
m049.pep		VGVFPAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLQGSLRVEPVFLKDDHRVGFDFL					
		:					
a049		IGVFPAFNLSGFKFETVFFGIKPDSPPRFDVFFRNRLQGSLRVEPVFLKDDHRVGFDFL					
		70	80	90	100	110	120
		130	139				
m049.pep		AAIGNGGIVFLLPFFQIRL					
a049		AAIGNGGIVFLLPFFQIRL					
		130					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 049 shows 86.3% identity over a 139 aa overlap with a predicted ORF (ORF 049.ng) from *N. gonorrhoeae*:

m049/g049

		10	20	30	40	50	60
m049.pep		MRAQAFDQPFQGQLLFGQAEHFAPVDGFRVQDIDL	DGHQRF	FRIVFPVFRNRRL	IRAGFCL		
g049		MRAQAFDQPFQGQLLFGQAEHFAPVDGFRVQDIDL	DGHQRL	FR	TAF	AVFRNP	VCRRTGFCR
		10	20	30	40	50	60
		70	80	90	100	110	120
m049.pep		VGVFPAFNLSGFKFDTVFFGIKPDSPPRFDV	FRNRHLQ	GS	LRVEPVFLKDD	HRVGFDFL	
		:         :					
g049		IGVFPAFNLSGFKFDTVFFGIKPDSPPRFDV	FRNRHLQ	GS	LRVEPVFLKDD	HRVGFDFL	
		70	80	90	100	110	120
		130	139				
m049.pep		AAIGNGGIVFLLPFFQIRL					
		:           :					
g049		AAIGNGAVVFFLPFLQIRLX					
		130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 211>:

g050.seq

```

1   atgggCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
51  caccGcGAA AAAGccgtgt TGATGGcaaa AGAATCCCTG ATGAGCCACA
101 TCGAcAtCca aGaATTGCAG GAAAAAGCCG CGTccggggc ggaattgtcc
151 accaccgaAG ccCTGCGCCT cGAACTCTTT GAAAAGGTCA ACGCGCTGGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAT GCCGCCTCCA AACCGATTGC CATGATTCCC
301 AACTGTGCcg ccacCCGcca cgtcgAATTT GAATTGgACG GCTCAGgtcc
351 TGTCGAactc acgccGCcgc gtgtCGAAGA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 212; ORF 050.ng>:

g050.pep

```

1   MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVED*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 213>:

m050.seq

```

1   ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGTATCG GCATCGGCGG
51  C..agCCgAA AAAGCCGTGC TGATGGCAAA AGAGTCCCTG ATGAGCCACA
101 TCGACATTCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GgAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTGGG
201 CATCGGCGCA CAAGGCTTGG GCGGACTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA TCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCC
351 TGTCGAACTC ACGCCGCCG GCGTCGAAGA TGGCCCGATT TGA

```

This corresponds to the amino acid sequence <SEQ ID 214; ORF 050>:

m050.pep

```

1   MGAGWCPPGI LGIGIGGXAE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDGPI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 215>:

a050.seq

```

1   ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
51  TACGCCCCGAA AAAGCCGTGT TGATGGCGAA AGAATCCCTG ATGAGCCACA
101 TCGACATCCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GGAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTAGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCC
351 TGTCGAACTC ACGCCGCCG GCGTCGAAGA CTGGCCC

```

This corresponds to the amino acid sequence <SEQ ID 216; ORF 050.a>:

a050.pep

```

1   MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDWP

```

m050/a050 97.7% identity over a 129 aa overlap

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF					
	:					
a050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF					

253

	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYP	THAASKPIAMIPNCAATRHVEFELDGSGPVEL				
a050	EKVNALGIGAQGLGGLTTVLDVKILDYP	THAASKPIAMIPNCAATRHVEFELDGSGPVEL				
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
a050	TPPRVEDWP					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 050 shows 98.4% identity over a 127 aa overlap with a predicted ORF (ORF 050.ng) from *N. gonorrhoeae*:

m050/g050

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLM	SHIDIQELQEKAASGAELSTTEALRLELF				
g050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLM	SHIDIQELQEKAASGAELSTTEALRLELF				
	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYP	THAASKPIAMIPNCAATRHVEFELDGSGPVEL				
g050	EKVNALGIGAQGLGGLTTVLDVKILDYP	THAASKPIAMIPNCAATRHVEFELDGSGPVEL				
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
g050	TPPRVEDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 217>:

g050-1.seq

```
1  ATGACCGTTA TCAAGCAAGA AGACTTTATT CAAAGTATCT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCAAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCCGAA AACACCGGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG GATGTGCAAT
251 GGGATGCGGA CATGAGCGTG GAAAAGATGG TTAACGAAGG CGTACGCCGC
301 GCCTACACTT GGAAGGCAA CACCCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCACA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GCGGGCTCTG AAAACAAATC CAAACTCGCT ATGCTCAACC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACGATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTTGGGC ATCGGCATCG GCGGCACgcc CGAAAAAGCC
601 GTGTTGATGG cgaAAGAATC CCTGATGAG CACATCGACA TCCAAGAATT
651 GCAGGAAAAA GCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAGG GTCAACGCGC TGGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTACCCGAC
801 CCATGCCGCC TCCAAACCGA TTGCCATGAT TCCCAACTGT GCCGCCACCC
851 GCCACGTCGA ATTGAATTG GACGGCTCAG GTCCTGTCGA ACTCACGCCG
901 CCGCGCGTCG AAGACTGACC CGATCTGACT TACAGCCCGC ACAACGGCAA
951 ACGCGTCGAT GTCGATAAGC TGACCAAGA AGAAGTGGCA AGCTGGAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCGG CCGCGATGCC
1051 GCGCACAAAC GCCTCGTCAA TATGCTCGAC AAAGGCGAGG AGTTGCCCGT
1101 CGATTTACAC AACCGCCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCG
1151 GCGATGAAGT CGTCGGTCCC GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTTACCC GCCAAATGCT CAAACAAACC GGCCTCTTGG GCATGATCGG
```

```

1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAGG
1301 CCGTGACTAC CATGGCAGTC GCGGCGCGG CATACCTCGT GGCAAAAGCC
1351 ATCAATCTT CCAAAGTCTT GCGGTTCCCG GAATTGGGTA TGGAGCCCGT
1401 TTACGAATTT GAAGTCAAAG ATATGCCCCG AACCGTCGCC GTGGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCCGC GCAAATGGCA GCGGAAAATC
1501 GGCATCATCC CCGTCGAGTC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 218; ORF 050-1.ng>:

g050-1.pap

```

1  MTVIKQEDFI  QSICDAFQFI  SYHHPKDYID  ALYKAWQKEE  NPAAKDAMTQ
51  ILVNSRMCAE  NNRPICQDTG  IATVFLKVGM  DVQWDADMSV  EKMVNEGVR
101  AYTWEENTLR  ASVLADPAGK  RQNTKDNTPA  VIHMSIVPGG  KVEVTCAAKG
151  GGSSENKSLA  MLNPSDNIVD  WVLKTIPTMG  AGWCPPGILG  IGIGGTPEKA
201  VLMAKESLMS  HIDIQELQEK  AASGAELSTT  EALRLELFEK  VNALGIGAQG
251  LGGLTTVLVD  KILDYPHAA  SKPIAMIPNC  AATRHVEFEL  DSGSPVELTP
301  PRVED*PDLT  YSPDNGKRVD  VDKLTKEEVA  SWKTGDVLL  NGKILTGRDA
351  AHKRLVNMLD  KGEELPVDF  NRIYVVGVP  DPVGDEVVGP  AGPTTATRMD
401  KFTRQMLKQT  GLLGMIGKSE  RGAATCEAIA  DNKAVYLM  AV  GGAAYLVAKA
451  IKSSKVLAF  ELGMEAVYEF  EVKDMPTVTA  VDSKGESHA  TAPRKWQAKI
501  GIIPVES*

```

g050-1/p14407

```

sp|P14407|FUMB_ECOLI FUMARATE HYDRATASE CLASS I, ANAEROBIC (FUMARASE)
>gi|280063|pir|B44511 fumarate hydratase (EC 4.2.1.2) fumb, iron-dependent - Escherichia coli
>gi|146048 (M27058) anaerobic class I fumarase (EC 4.2.1.2) [Escherichia coli] Length = 548
Score = 172 bits (432), Expect = 4e-42
Identities = 138/488 (28%), Positives = 216/488 (43%), Gaps = 22/488 (4%)

```

```

Query: 11  QSICDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAENNRPICQDTG 70
      Q+  DA  +  H K  L+  E +  K  Q L NS + A+  P CQDTG
Sbjct: 53  QAFHDASFMLRPAHQKQVAAILHDPEASEND---KYVALQFLRNSEIAAKGVLPCTCQDTG 109

```

```

Query: 71  IATVFLKVGMVDVQWDADMSVEKMVNEGVRRAAYTWEENTLRASVLADPAGKRQNTKDNTPA 130
      A + K G V W  E+ +++GV Y E N + A  K NT N PA
Sbjct: 110 TAIIVGKKGQRV-WTGGGD-EETLSKGVNTYI-EDNLRYSQNAALDMYKEVNTGTNLPA 166

```

```

Query: 131  VIHMSIVPGGKVEVTCAAKGGGSENKSKL-----AMNPSDNIVDWVLKTIPTMGAGWCP 185
      I + V G + + C AKGGGS NK+ L  A+L P + +++++ + T+G  CP
Sbjct: 167 QIDLYAVDGDDEYKFLCVARGGGSANKTYLYQETKALLTPG-KLKNFLVEKMRTLGTAAAC 225

```

```

Query: 186  PXXXXXXXXTPEKAVLMAKESLMSHIDIQELQEKAAASGAELSTTEALRLELFEKVNNXX 245
      P  T + L + +H  EL + +  L  EL E+
Sbjct: 226 PYHIAFVIGGTSAETNLKTVKLASAHY-YDELPTGNEHGQAFRDVQLEQELLEAAQKLG 284

```

```

Query: 246  XXXXXXXXXXTTVDKILDPYTHAASKPIAMIPNCAATRHVEFELDGGSG---PVELTP 301
      D++++ P H AS P+ M +C+A R+++ +++ G  +E P
Sbjct: 285 LGAQFGGKYFAH-DIRVIRLPRHGASCPVGMGVSCADRNIAKINREGIWIKEHNP 343

```

```

Query: 302  RVEDXPDLTYSPDNGKRVDVDKLTKE---EVASWKTGDVLLNGKILTGRDAAHKRLVNM 358
      +  +VD+++ KE  +++ +  L L G I+ GRD AH +L +
Sbjct: 344 QYIPQELRQAGEGEAVKVDLNRPMKEILQLSQPVSTRSLTGTIIVGRDIAHAKL 403

```

```

Query: 359  LDKGEELPVDFNRIYXXXXXXXXXXXXXXXXXXTTATRMDKFTRQMLKQTGLLGMIGK 418
      +D G+ELP + IYY  TTA RMD + +  G + M+ K
Sbjct: 404 IDAGKELPQYIKDHPYIYAGPAKTPAGYPSGSLGPTTAGRMDSYVDLLQSHGGSMIMLAK 463

```

```

Query: 419  SERGAATCEAIADNKAVYLMVGG-AAYLVAKAIKSSKVLAFPELGMEAVYEFVVKDMPV 477
      R  +A +  YL ++GG AA L ++IK + +A+PELGMEA+++ EV+D P
Sbjct: 464 GNRSQQVTDACHKHGGFYLGSIIGGPAVLAQQSIKHLECVAYPELGMEAIVKIEVEDFPA 523

```

```

Query: 478  TVAVDSKG 485
      + VD KG

```

```

Sbjct: 524 FIIVDDKG 531

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 219>:

m050-1.seq

```

1  ATAGCCGTC ACAAACAGGA AGACTTTATC CAAAGCATTT GCGATGCCTT
51  CCAATTCATC AGCTACTATC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101  AGGCGTGCCA GAAGGAAGAA AATCTGCGCG CCAAAGACGC GATGACGCAG
151  ATTTTGGTCA ACAGCCGTAT GTGTGCGGAA AACAACCGCC CCATCTGCCA
201  AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG AACGTCCAAT
251  GGGATGCGGA CATGAGCGTG GAAGAGATGG TTAACGAAGG CGTACGCCGC

```

301	GCCTACACTT	GGGAAGGCAA	TACGCTGCGC	GCTTCCTGTC	TCGCCGATCC
351	GGCCGGCACA	CGCCAAAAAC	CCAAAGACAA	CACCCCGCGC	GTCATCCATA
401	TGAGCATCTG	CGCGGGCGAT	AAAGTCGAAG	TAACCTGCGC	GTCCAAAGGC
451	GGCGGCTCTG	AAACAAATCT	CAAACTCGCC	ATGCTCAATC	CTTCCGACAA
501	CATCGTCGAT	TGGGTATTGA	AAACCATCCC	GACCATGGGC	GCGGGCTGGT
551	GTCCTCCCGC	CATCTTGGGT	ATCGGCATGC	GCGGCACCGC	CGAAAAAGCC
601	GTGCTGATGG	CAAAAGAGTC	CCTGATGAGC	CACATCGACA	TTCAAGAATT
651	CGAGGAAGAAG	CGCGGCTCGC	GC CGGAATT	GTCACACCAC	GAAGCCCTGC
701	GCCTCGAACT	CTTTGAAAAA	GTCAACGCGC	TGGGCATCGG	CGCACAAAGC
751	TTGGGCGGAC	TGACACCCTG	GTTGGACGTG	AAAATCCTCG	ATTATCCGAC
801	CCAGCGCGCC	TCCAACCGTA	TTCGCAATGT	TCCGAACATG	GCGCCGACCC
851	GCCACGTCGA	ATTTGAATTG	GACGGCTCAG	GCCCTGTCGA	ACTCACGCGC
901	CGCGCGCTCG	AGACTGTGGC	CGATTGACTG	TACAGCCCCG	ACAACGCGCA
951	ACGCGTCGAT	GTCGACAAGT	TGACCAAGA	AGAAGTGGCA	AGCTGGAAAA
1001	CGCGGCGAGT	ATTGCTGTG	ACCGCAAAAA	TCCTCACCGG	CGCGCATGCC
1051	GCACATCAAC	GCCTCGTCGA	TATGCTCAAC	AAAGCGGAAG	AATTGCGCGT
1101	CGATTTACAC	AACCGCTGTA	TTTACTACGT	CGGCCCGCTC	GATCCGGTCT
1151	CGGATGAAGT	GCTGGCTCGC	GCAAGTCCGA	CCACAGCCAC	CCGATGGAC
1201	AAATTCAACC	GCCAAATGCT	CGAACAAACC	GACCTCTTGG	GCATGATCGG
1251	CAAAATCCGAG	CGCGCGGTGG	CCACCTGCGA	AGCCATCGCC	GACACAAAGC
1301	CGGTGTACCT	CATGGCAGTG	GGCGGCGGCG	CGTATCTCGT	GCGAAAGACC
1351	ATCAAAATCTT	CCAAAGTCTT	GGCGTTCCCC	GAATTGGGCA	TGGAAGCCAT
1401	TTACGAATTT	GAAGTCAAAG	ACATGCCCCG	AACCGTCGCC	GTAGATAGCA
1451	AAGGCGAATC	CATCCACGCC	ACCGCCCCGC	GCAATGGCA	GGCGAAAAATC
1501	GGCATCATCC	CGGTGCAATC	TTGA		

This corresponds to the amino acid sequence <SEQ ID 220; ORF 050-1>:

m050-1.pap

1	MTVIKQEDFI	QSICDAFQFI	SYYPKDYID	ALYKAWQKEE	NPAAKDAMTQ
51	ILVNSRMCAE	NNRPICQDTG	IATVFLKVG	NVQWDADMSV	EEMVNEGVR
101	AYTWEGNTLR	ASVLADDPKG	RQNTKDNTPA	VIHMSIVPGG	KVEVTCAAKG
151	GGSSEKSKLA	MNLPNSDNI	WVLTITPTMG	AGWCPPGILG	IGIGGTPEKA
201	VLMAKESLMS	HIDIQELQEK	AASGAELSTT	EALRLELFEK	VNALGIGAQQ
251	LGGLTTVLVD	KILDPHPHAA	SKPTAMINPC	AATHRFVPEL	DGSGPVELTP
301	PRVEDWPDLT	YSPDNKRKVD	VDKLTKEEVA	SWTKGDVLL	NGKILTRDA
351	AHKRLVDMLN	KGEEPLVDFT	NRLIYYGPGV	PDGDEVVPG	AGPTTATRMD
401	KFTRQMLEQT	DLLGMIGKSE	RGVATCEAIA	DNKAVYLMV	GGAYVLVAKA
451	IKSSKVLAPF	ELGMEAIYEF	EVKDMPVTVA	VDSKGESIHA	TAPRKWQAKI
501	GIIPVES*				

m050-1/q050-1 98.2% identity in 507 aa overlap

	10	20	30	40	50	60
m050-1.pep	MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
g050-1	MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
	10	20	30	40	50	60
m050-1.pep	70	80	90	100	110	120
g050-1	NNRPICQDGTGIATVFLKVGMMNVQWDADMSVEEMVNEGVRRAYTWEGNTLRASVLADPAGK					
	70	80	90	100	110	120
m050-1.pep	130	140	150	160	170	180
g050-1	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG					
	130	140	150	160	170	180
m050-1.pep	190	200	210	220	230	240
g050-1	AGWCPPGILGIGIGGTPEKAVLMAKESLMSHIDIQELQEKAASGAELSTTEALRLELFEK					
	190	200	210	220	230	240
m050-1.pep	250	260	270	280	290	300
g050-1	VNALGIGAQGLGGLTTVLVDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGS GPVELTP					
	250	260	270	280	290	300

	310	320	330	340	350	360
m050-1.pep	PRVEDWPDLTYS	PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLN				
g050-1	PRVEDXPDLTYS	PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVNMLD				
	310	320	330	340	350	360
	370	380	390	400	410	420
m050-1.pep	KGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE					
g050-1	KGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLKQTGLLMIGKSE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m050-1.pep	RGVATCEAIADNKAVYLMVAVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPVTVA					
g050-1	RGAATCEAIADNKAVYLMVAVGGAAYLVAKAIKSSKVLAFPELGMEAVYEFVVKDMPVTVA					
	430	440	450	460	470	480
	490	500				
m050-1.pep	VDSKGESIHATAPRKWQAKIGIIPVESX					
g050-1	VDSKGESIHATAPRKWQAKIGIIPVESX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 221>:

a050-1.seq

```

1   ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AACCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCGCAT GTGTGCCGAA AACAACCGCC CCATCTGCCA
201 AGATACCGGT ATCGCGACCG TGTTTTGTAA AGTCGGTATG GATGTGCAAT
251 GGGATGCAGA CATGAGCGTC GAAGAGATGG TTAACGAAGG CGTGCGCCGC
301 GCCTACACTT GGGAAAGCAA TACGCTGCGC GCTTCCGTC TCGCCGACCC
351 CGCCGGCAAA CGCCAAAATA CCAAGACAA CACGCCGCCG GTCATCCATA
401 TGAGCATCGT GCCGGCGGAC AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GCGGTTCTG AAAACAAATC CAACTCGCC ATGCTCAACC CTTCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATTC GACCATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTGGGC ATCGGCATCG GCGGTACGCC CGAAAAGCC
601 GTGTTGATGG CGAAGAATC CCTGATGAGC CACATCGACA TCCAGAATT
651 GCAGGAAAAA GCCGCGTCCG GCGCGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAATC CTTTGAAAAA GTCAACGCGC TAGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGACGTG AAAATCCTCG ATTACCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCCGAATGCG GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTGCG ACTCACGCCG
901 CCGCGCGTCG AAGACTGGCC CGATTGACT TACAGCCCGC ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAAGA AGAAGTGCGA AGCTGGAATA
1001 CCGCGACGAT ATTGCTGTTG AACGGCAAAA TCCTACCGCG CCGCGATGCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCGAC AAAGCGCAAG AATTGCCCGT
1101 CGATTTACAC AACCGCCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCG
1151 GCGACGAAAT CGTCGGCCCA GCAGGTCCGA CCACGCCCAC CCGCATGGAC
1201 AAATTCACCC GCCAATGCT CGAACAACCC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAG
1301 CCGTGTAACCT CATGGCAGTC GGCGGCGCGG CGTATCTCGT GGCAAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GGCGTTCCCC GAATTGGGCA TGGAAAGCCAT
1401 TTACGAATTT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGC CCCAATGGCA GCGGAAAAATC
1501 GGCATCATCC CCGTCAAATC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 222; ORF 050-1.a>:

a050-1.pep

```

1   MTVIKQEDFI QSIDAFQFI SYHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVMG DVQWDADMSV EEMVNEGVR
101 AYTWEGNLRL ASVLADPAGK RQNTKDNTFA VIHMSIVPGD KVEVTCAAKG
151 GGSNKSRLA MLNPSDNIVD WVLKTIPTMG AGWCPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQG
251 LGGLTTVLVD KILDYPHTAA SKPIAMIPNC AATRHVEFEL DGSGPVELTP
301 PRVEDWPDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVDMLD KGEELPVDFN NRLIYYVGPV DPGDEIVGP AGPTTATRMD
401 KFTRQMLEQT DLLGMIGKSE RGAATCEAIA DNKAVYLMVAV GGAAYLVAKA
451 IKSSKVLAFV ELGMEAIYEF EVKDMPTVTA VDSKGESIHA TAPPQWQAKI
501 GIIPVKS*

```



a050-1/m050-1 98.4% identity in 507 aa overlap

	10	20	30	40	50	60
a050-1.pep	MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
m050-1	MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a050-1.pep	NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAITWEGNTLRASVLADPAGK					
m050-1	NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAITWEGNTLRASVLADPAGK					
	70	80	90	100	110	120
	130	140	150	160	170	180
a050-1.pep	RQNTKDNTPAVIHMSIVPGDKVEVTC AAKGGGSENKSKLAMLNPSDNIVDWLKTIP TMG					
m050-1	RQNTKDNTPAVIHMSIVPGDKVEVTC AAKGGGSENKSKLAMLNPSDNIVDWLKTIP TMG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a050-1.pep	AGWCPPGILGIGIGGTPEKAVLMKESLM SHIDIQELQEKAASGAELSTTEALRLELF EK					
m050-1	AGWCPPGILGIGIGGTPEKAVLMKESLM SHIDIQELQEKAASGAELSTTEALRLELF EK					
	190	200	210	220	230	240
	250	260	270	280	290	300
a050-1.pep	VNALGIGAQQGLGGLTTVL DVKILDYP THAASKPIAMIPNCAATRHVEFELDGSGPVELTP					
m050-1	VNALGIGAQQGLGGLTTVL DVKILDYP THAASKPIAMIPNCAATRHVEFELDGSGPVELTP					
	250	260	270	280	290	300
	310	320	330	340	350	360
a050-1.pep	PRVEDWPDLTYS PDNGKRV DDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLD					
m050-1	PRVEDWPDLTYS PDNGKRV DDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLN					
	310	320	330	340	350	360
	370	380	390	400	410	420
a050-1.pep	KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE					
m050-1	KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE					
	370	380	390	400	410	420
	430	440	450	460	470	480
a050-1.pep	RGAATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFVKDMPVTVA					
m050-1	RGVATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFVKDMPVTVA					
	430	440	450	460	470	480
	490	500				
a050-1.pep	VDSKGESIHATAPPQWQAKIGIIPVKSX					
m050-1	VDSKGESIHATAPRKWQAKIGIIPVESX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 223>:

g052.seq

```

1  ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
51  CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
201 GCGCGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA
251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 224; ORF 052.ng>:

g052.pep

```

1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
101 RLRLETTWSP ACRKVKNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 225>:

```

m052.seq
1 ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTCAAAGG
51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA
251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 226; ORF 052>:

```

m052.pep
1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
101 RLRLETTWSP ACRKVKNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 227>:

```

a052.seq
1 ATGGCTTTGG TCGCGGAGGA AACGGAAATA TCCGCGCCGT GTTCAAAGG
51 CTGAGAGCCG ACAGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCTCCC
151 AAGGGATTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
201 GGCGGCTTTC CATTTCGTTA TATCAGTCGG CGACACGTGA CTCACTTCGA
251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAATCAC ATGGTCGCCC GCCTGCAAAA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 228; ORF 052.a>:

```

a052.pep
1 MALVAEETEI SAPCFKG*EP TGDSRLLSTT KSAPMPCANS AKASKSATSP
51 KGLDGVSKNS SLVLALTAAF HSFISVGD* LTSMPLNVTM LLIKPTVVPN
101 RLRLEITWSP ACKKVKNAA*

```

m052/a052 95.8% identity over a 119 aa overlap

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP KGLDGVSKNS					
a052	MALVAEETEI SAPCFKGXEP TGDSRLLSTT KSAPMPCANS AKASKSATSP KGLDGVSKNS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m052.pep	SLVLALTAAF HSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX					
a052	SLVLALTAAF HSFISVGDXTLTSMPLNVTMLLIKPTVVPNRLRLEITWSPACKKVKNAA					
	70	80	90	100	110	120

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 052 shows 95.8% identity over a 119 aa overlap with a predicted ORF (ORF 052.ng) from *N. gonorrhoeae*:

m052/g052

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP KGLDGVSKNS					

```

g052      MALVAEETEISAPCFKGCEPTGDSRLSTTKSAPMPCANSASAKSKSATSPKGLDGVSKNS
           10      20      30      40      50      60

           70      80      90      100     110     120
m052.pep  SLVLALTAAFHSFISVGDTWLTSMPLATMLLIKPTVVPNRLRLLEITWSPACKKVNAAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g052      SLVLALTAAFHSFISVGDTRLTLPMPNLVTMLLIKPTVVPNRLRLLETTWSPACRKVKNAAX
           70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 229>:

```

g073.seq
1  ATGTGTATGC CATACGCAAT AAGGGTTTCA GACGGCATCT GCCGCATTTT
51  TCCGCCGATG CCGTCTGAAA CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AGTCCGGGGC GGatacCGGC GCGAGTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT TGGTGATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAAAAGAGT TCCACGACTT TCCACGCGGC TGCTTGGTCG
301 GCGACTTCAA AACCGATGAC GATGCCGCGC CCGTTTGTCT GTTTCGGGAT
351 AAGCTCCGCC TCGGATGGT CGGCAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 230; ORF 073.ng>:

```

g073.pep
1  MCMPIAIRVS DGICRIFPPM PSETRNQRAS ACFKSSIKSP TYSKPTDRRT
51  SPGRIPAASF SSGCILPCVV VHGLVMVERT SPRLAVREKS STTFHAAAWS
101 ATSKPMTMPP PFCCLRISSA CGWSGNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 231>:

```

m073.seq
1  ATGTGTATGC CATATAAGAT AAGGGTTTCA GACGGCATCT GCTGTCCAAT
51  GCCGTCTGAA ACACGCAATC AGCGTGCGAG TGCCTGTTTC AAATCGTCAA
101 TCAAATCGCC AACATATTCC AAACCGACCG ACAGGCGCAC CAATCCGGGG
151 CGGATGTTGG CCGCGAGTTT TTCTTCGGGC TGCATCCTGC CGTGCGTGGT
201 TGTCCACGGG TGGGTAATGG TCGAGCGCAC GTCACCGAGG TTGGCGGTGC
251 GGGAAAAGAG TTCCACGCCG TCCACAACCT TCCACGCCGC TTCTTGATCG
301 GCAACTTCAA AGCCGATGAC GATGCCGCGC CCGTTTGTCT GTTTCGGGAT
351 AAGCGCCGCC TGAGGATGGT CGGACAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 232; ORF 073>:

```

m073.pep
1  MCMPIKIRVS DGICCPMPSE TRNQRASACF KSSIKSPTYS KPTDRRTNPG
51  RMLAASFSSG CILPCVVVHG WVMVERTSPR LAVREKSSTP STTFHAASKS
101 ATSKPMTMPP PFCCLRISAA XGWSNPNV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 233>:

```

a073.seq
1  ACGTGTATGT CATATAAGAT AAGGGTTTCA GACGGCATTT GCGGTGTTTT
51  TCCGCCGATG CCGTCTGAA. CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AATCCGGGGC GGATGTTGGC GCGAGTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT GGGTAATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAGAAAAGT TCGACGCCGT CCACGACTTT CCACGCGGCT
301 GCTTGGTCGG CCACTTCAAA GCCGATGACG ATGCCGCCGC CGTTTGTCTG
351 TTTGCGGATA AGCTCCGCCT GAGGATGGTC GGGTAATCCG GTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 234; ORF 073.a>:

```

a073.pep
1  TCMSYKIRVS DGICGVFPPM PSEXNRQRAS ACFKSSIKSP TYSKPTDRRT
51  NPGRMLAASF SSGCILPCVV VHGWVMVERT SPRLAVREKS STPSTTFHAA
101 AWSATSKPMT MPPFPCLRI SSA*GWSGNP V*

```

m073/a073 92.3% identity over a 130 aa overlap

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICCC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
a073	TCMSYKIRVSDGICGVFPMPSEXRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCCCLRI				
a073	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAAAWSATSKPMTMPPPFCCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNDNPVX				
a073	SSAXGWSGNPVX				
		130			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 073 shows 87.0% identity over a 131 aa overlap with a predicted ORF (ORF 073.ng) from *N. gonorrhoeae*:

m073/g073

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICCC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
g073	MCMPIKIRVSDGICRIFPMPSETRNQRASACFKSSIKSPTYSKPTDRRTSPGRIPAAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCCCLRI				
g073	SSGCILPCVVVHGLVVERTSPRLAVREKSST---TFHAAAWSATSKPMTMPPPFCCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNDNPVX				
g073	SSACGWSGNPVX				
		120			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 235>:

g075.seq

```

1  ATGCCGCCTT ACTTCATCAC CCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GGCAGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCCGTTCGG GCAACGCTGC GTTTCCTGT
151  GCCGCCAAAG CCAGCGGGGC GGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201  TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTT ACGAAATTTT
251  TAAAAAATG TGTTCGCGG CTTGTGAAG GTTTAGAGA CCGCTGCCG
301  GGCCTCTTAA ACTTAATCTT CTTTTCGTA GAATCCGAAA ATTACAAATT
351  CCCCCTAT CTCTCCAAT GCCGAGCTAA AAGCGTCTTC ATAGCTGTCA
401  TATTTACCGG CTGA

```

This corresponds to the amino acid sequence <SEQ ID 236; ORF 075.ng>:

g075.pep

```

1  MPPYFILLT MENTKSAKT PTTIQPASIP SAFAASKAFF AVSGNAAFAC
51  AAKASGAAVT TASFAPYLQ VLINFMIFS TKFLKKCVCG LCEGFRDLRP
101  GLLNLIFFV ESENYKFPAY LFQCRKSVF IAVIFTG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 237>:

```
m075.seq
1  ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GCGGAAAATG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CCGCTTCCAA AGCGTTTTTT GCCGTATCGG GCAACGTTGC ATTTGCATGT
151 GCGGCCAAAG CCAGGGGAGC AGCTGTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTC AAAAAAGTGT
251 TGGCGGTAAT GGATGGAGCG TTTTTCAGAC GACCGCCGAA CATCCGAAAA
301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
351 CTTCCAAACC TGCCTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 238; ORF 075>:

```
m075.pep
1  MPSYFITLLT MENTKSAAKM PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51  AAKARGAAVT TASFAPYLQ VLINFMIFSF KKCLAVMDGA FFRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVE IIGIGD*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 075 shows 65.7% identity over a 137 aa overlap with a predicted ORF (ORF 075.ng) from *N. gonorrhoeae*:

m075/g075

	10	20	30	40	50	60
m075.pep	MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
g075	MPPYFITLLTMENTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAAKASGAVT					
	10	20	30	40	50	60
	70	80	90	100	110	
m075.pep	TASFAPYLQVVLINFMIFSF---KKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVAD					
g075	TASFAPYLQVVLINFMIFSFTKFLKKVCGLCEGFRDRLPGLLNLIFFVESENYKFPAY					
	70	80	90	100	110	120
	120	130				
m075.pep	FFQTCVNRFFEVEIIGIGDX					
	:    ::   :  :					
g075	LFQCRKSVFIAVIFTGX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 239>:

```
a075.seq
1  ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAAGA CAAAAAGCGC
51  GCGGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CCGCTTCCAA AGCGTTTTTT GCTGTATCGG GCAACGTTGC ATTTGCATGT
151 GCGGCCAAAG CCAGGGGAGC AGCTGTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTC AAAAAAGTGT
251 TGGCGGTAAT GGATGGAGCG TTTTTCAGAC GACCGCCGAA CATCCGAAAA
301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
351 CTTCCAAACC TGCCTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 240; ORF 075.a>:

```
a075.pep
1  MPSYFITLLT MEKTKSAKT PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51  AAKARGAAVT TASFAPYLQ VLINFMIFSF KKCLAVMDGA FFRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVE IIGIGD*
```

m075/a075 98.5% identity over a 136 aa overlap

	10	20	30	40	50	60
m075.pep	MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
a075	MPSYFITLLTMEKTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
	10	20	30	40	50	60
m075.pep	TASFAPYLRQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLRQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
m075.pep	TASFAPYLRQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLRQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
m075.pep	CVNRFFEVEIIGIGDX					
a075	CVNRFFEVEIIGIGDX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 241>:

g080.seq

1	ATGTGGGATA	ATGCCGAAGC	GATGGAACGG	CTGACGCGCT	GGCTGCTTGT
51	CATGATGGCG	ATGCTGCTTG	CTGCGTCCGG	GCTGGTTTGG	TTTTACAATT
101	CGAATCATCT	GCCCGTCAAG	CAGGTGTCGC	TGAAGGGCAA	CCTGGTTTAT
151	TCCGATAAGA	AGGCATTGGG	CAGTTTGGCG	AAAGAATACA	TCCATGGGAA
201	TATTTTGAGG	ACGGACATCA	ATGGCGCACA	GGAAGCCTAC	CGCCGGTATC
251	CGTGGATTGC	GTCGGTCATG	GTGCGCCGCC	GTTTTCCTCGA	TACGGTTGAG
301	GTCGTCTCTGA	CCGAGCGCAA	GCCGGTTGCA	CGTTGGGGCG	ACCATGCCTT
351	GGTGGACGGC	GAAGGCAATG	TTTTTGAAGC	CCGCTTGGAC	AGACCCGGAA
401	TGCCGGTATT	CAGAGGCGCG	GAAGGAACGT	CTGCCGAAAT	GCTCCGCCGT
451	TATGACGAAT	TTTCGACTGT	TTTGGCAAAA	CAGGGTTTGG	GCATCAAAGA
501	GATGACCTAT	ACGGCACGTT	CGGCGTGGAA	TGTCGTTTTG	GACAACGGCA
551	TCACCGTCAG	GCTCGGACGG	GAAAACgAGA	TGAAACGCCT	CCgGCTTTTT
601	ACcgAAGCGT	GGCAGCATCT	gttgcGTAAG	AATAAAAATC	GGTTATCCTA
651	TGTGGATATG	Aggtataagg	acggatttTC	agtcccccat	gctCCCGACG
701	GTTTACCCGA	AAAAGAATcc	gAAGAAATatt	gggaacaggt	ttgggacata
751	ttacggcctg	gcgtcggaaa	cggttcgacg	caaatttcaa	tcagttataAA
801	GGGCAGacga	acaatggaac	AGcagtaa		

This corresponds to the amino acid sequence <SEQ ID 242; ORF 080.ng>:

g080.pep

1	MWDNAEAMER	LTRWLLVMMMA	MLLAASGLVW	FYNSNHLPVK	QVSLKGNLVY
51	SDKKALGSLA	KEYIHGNILR	TDINGAQEAY	RRYPWIASVM	VRRRFPDIVE
101	VVLTERKPVA	RWGDHALVDG	EGNVFEARLD	RPMPVFRGA	EGTSAEMLRR
151	YDEFSTVLAK	QGLGIKEMTY	TARSAWNVVL	DNGITVRLGR	ENEMKRLRLF
201	TEAWQHLLRK	NKNRLSYVDM	RYKDGFSVPH	APDGLPEKES	EEYWEQVWDI
251	LRPGVNGST	QISISYKRR	TMEQQ*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 243>:

m080.seq

1	ATGTGGGATA	ATGCCGAAGC	GATGGAACGG	CTGACGCGCT	GGCTGCTTGT
51	CATGATGGCG	ATGCTGCTTG	CTGCGTCCGG	GCTGGTTTGG	TTTTACAATT
101	CGAATCATCT	GCCCGTCAAG	CAGGTGTCGC	TGAAGGGCAA	CCTGGTTTAT
151	TCCGATAAGA	AGACATTGGG	CAGTTTGGCG	AAAGAATACA	TCCATGGGAA
201	TATTTTGAGG	ACGGACATCA	ATGGCGCACA	GGAGCCTAC	CGCCGGTATC
251	CGTGGATTGC	GTCGGTCATG	GTGCGCCGCC	GTTTTCCTCGA	CACGGTTGAG
301	GTCGTCTCTGA	CCGAGCGCAA	GCCGGTCCGG	CGTTGGGGCG	ACCATGCCTT
351	GGTGGACGGC	GAAGGCAATG	TTTTTGAAGC	CCGCTTGGAC	AGACCCGGAA
401	TGCCGGTATT	CAGAGGCGCG	GAAGGAACGT	CTGCCGAAAT	GCTCCGCCGT
451	TATGACGAAT	TTTCGACTGT	TTTGGCAAAA	CAGGGTTTGG	GCATCAAAGA
501	GATGACCTAT	ACGGCACGTT	CGGCGTGGAT	TGTCGTTTTG	GACAACGGCA
551	TCACCGTCAG	GCTCGGACGG	GAAAACGAGA	TGAAACGCCT	CCGGCTTTTT

601 ACCGAAGCGT GGCAGCATCT GTTGCCTAAA AATAAAATC GGTTATCCTA  
 651 TGTGGATATG AGGTATAAGG ACGGATTTC AGTCCGCTAT GCTTCCGACG  
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 2441; ORF 080>:

m080.pep  
 1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNSNHLVPK QVSLKGNLVY  
 51 SDKKTLGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE  
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR  
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF  
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES EE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 080 shows 97.9% identity over a 242 aa overlap with a predicted ORF (ORF 080.ng) from *N. gonorrhoeae*:

m080/g080

m080.pep	10	20	30	40	50	60
	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKTLGSLA					
080	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKALGSLA					
	10	20	30	40	50	60
m080.pep	70	80	90	100	110	120
	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTEVVLTERRKPVARWGDHALVDG					
080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTEVVLTERRKPVARWGDHALVDG					
	70	80	90	100	110	120
m080.pep	130	140	150	160	170	180
	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
080	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSANNVVL					
	130	140	150	160	170	180
m080.pep	190	200	210	220	230	240
	DNGITVRLGRENMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYASDGLPEKES					
080	DNGITVRLGRENMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVPHAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
080	EEYWEQVWDILRPGVNGSTQISISYKGRRTMEQQX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 245>:

a080.seq  
 1 ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT  
 51 CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT  
 101 CGAATCATCT GCGGCTCAAG CAGGTGTCGC TGAAGGGCAA CCTAGTTTAT  
 151 TCCGATAAGA AAGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA  
 201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC  
 251 CGTGGATTGC GTCGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG  
 301 GTCGTCCTGA CCGAGCGCAA GCCGCTCGCG CGTTGGGGCG ACCATGCCTT  
 351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGTTTGAC AGACCCGGAA  
 401 TGCCGGTATT CAGAGCGCGG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT  
 451 TATGACGAAT TTTGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA  
 501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTGG GACAACGGCA

```

551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
601 ACCGAAGCGT GGCAACATCT GTTGCCTAAA AATAAAAAATC GGTATCCTA
651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTCCCGACG
701 GTTTACCGA AAAAGATCC GAAGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 246; ORF 080.a>:

a080.pep

```

1 MWDNAEAMER LTRWLLVMMA MLLAASGLVW FYNSNHLPVK QVSLKGNLVY
51 SDKKALGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE
101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RGPMPVFRGA EGTSAEMLRR
151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY APDGLPEKES EE*

```

m080/a080 99.2% identity over a 242 aa overlap

	10	20	30	40	50	60
m080.pep	MWDNAEAMERLTRWLLVMMA MLLAASGLVWFYNSNHLPVKQVSLKGNLVYSDKKTLGSLA					
a080	MWDNAEAMERLTRWLLVMMA MLLAASGLVWFYNSNHLPVKQVSLKGNLVYSDKKALGSLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m080.pep	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTEVVVLTERKPVARWGDHALVDG					
a080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTEVVVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m080.pep	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
a080	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m080.pep	DNGITVRLGREMKNRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYASDGLPEKES					
a080	DNGITVRLGREMKNRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
a080	EEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 247>:

g081.seq

```

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AACAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGATA
101 TTCGGGAAGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGACGCG
151 CATGATTTTG TTGGAGGCGT ATTGTCTGCG GGCGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGCGG CTTTGGGCGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC GTTGCAAACG TTGGCGAAGG CGTGGCGCGA TAATGTGAAC
301 CCGTTTGTGT TCGGCATTAC CGGTTGCGGC GGCAAGACGA CGGTGAAGGA
351 GATGCTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATGAT GCCGTTTCGG
401 CGACGGCAGG CAACTTCAAC AACCACatcg gaTTGCCGCT GACTTTATTG
451 AAATtaaaAcg aAAAAACCCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTTGGcgaa ctggcggtTt taacgcaaat CGCCAAACCC GATGCCGCTT
551 TGGtcaACAA CGCCTGCGC GCCCATGTGC GATGCGGTTt cgacggagtg
601 GGCATATTG CCAAAGcgaa aagcGAGATT TatgcagGct tATGTTCAGA
651 CGGCATGGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGTT TAATTTGAAT ACGTGCACTT TCGGCGTCGA TAGCGCGGAT
751 GTCCGCGCGG AAAATATCGT GCTGAAACCT TTGTCGTGCG AATTGATTT

```



265

```

801 GGTGTGCGGC GACGAGCGCA CTGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG CAAGGCTTCA GCAACATCAA
951 AGGCCGTCTG AACGTCAAAG CCGGCATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAATCCC GACAGTATGA AAGCCGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG CATTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAGGAc gaAGCCGCCG CCATGCACGC CGAagt cggc GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGcggaAA AATTTGGCGC GGACGGTTTG TGGTTCGCGC CCAAAGACCC
1251 GTTGATTCAA GTGTTGAGCC ACGATTGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGAtggAAG AAGTGTCTGA GGCATTGGAG
1351 GATAAGTga

```

This corresponds to the amino acid sequence <SEQ ID 248; ORF 081.ng>:

g081.pep

```

1 MKPLDLNFIC QALKLPMPSE NKPVSRIVTD SRDIREGDVF FALAGGRFDA
51 HDFVGGVLSA GAAAVVVSRE DCAALGGALK VDDTLAALQT LAKAWRDNVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVSATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNALR AHVGCDFDGV
201 GDIKAKSEI YAGLCSDGMA LIPQEDANMA VFKTATFNLN TCTFGVDSGD
251 VRAENIVLKP LSCEFDLVCG DERTAVVLPV PGRHNVHNAA AAAALALAAG
301 LSLNDVAEGL QGFSNIKGR LNVKAGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMMGELGED EAAAMHAEVG AYARDQGIEA AYFVGDNVSVE
401 AAEKFGADGL WFAAKDPLIQ VLSHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 249>:

m081.seq

```

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGAGCG GTTTGACGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCT GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGTGCTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC ATTGCAAACG CTGGCAAAGG CGTGGCGTGA AAATGTGAAT
301 CCGTTTGTGT TCGGCATTAC CGGTTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGCTGGCT GCGGTATTGC GCCgCCGTTT CGGCGATGAT GCCGTGTTGG
401 CGACGGCAGG CAACTTCAAC AACCATATCG GATTGCCGCT GACTTGTGTT
451 AAGTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTGCGCGAA CTGGCGGTTT TAACGCAMAT CGCCAAACCA AATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GGCATATTG CCAAGCGGAA AAGCGAGATT TACCAAGGTT TATGTTTCTG
651 CGGCATTGCA CTGATTCTTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTGAAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTTACGCGG AAAATATTGT GCTGAAACCG TTGTCGTGCG AATTGATTAT
801 GGTGTGCGGC GATGAGCGCG CCGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCT GACAGCATGA AAGCTGCGAT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAACTG GCGGAGGACG AAGCCGCCGC TATGCACGCC GAAGTCGGCG
1151 CGTATGCCCC CGACCAAGGC ATCGAAGCGG CTTATTTTGT CGGCGACAAC
1201 AGCGTCGAAG CGGCGGAAAA ATTTGGCGCG GACGGTTTGT GGTTCGCGCG
1251 CAAAGACCCG TTGATTCAAG TGTTGCGCCA CGATTGCCC GAACGCGCCA
1301 CCGTGTGGT GAAAGGTTTC CGCTTTATGC AGATGGAAGA AGTGTGCGAG
1351 GCATTGGAGG ATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 250; ORF 081>:

m081.pep

```

1 MKPLDLNFIC QALKLPMPSE SKPVSRIVTD SRDIRAGDVF FALAGERFDA
51 HDFVEDVLAA GAAAVVVSRE DCAAMDGALK VDDTLAALQT LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTXIAKP NAALVNNAMR AHVGCDFDGV

```

```

201  GDIKAKSEI YQGLCSGIA LIQEDANMA VFKTATLNLN TRTFGIDSGD
251  VHAENIVLKP LSCEFDLVCG DERAADVLPV PGRHNVHNAA AAAALALAAG
301  LSLNDVAEGL KGFSNIKGR LNVKSGIKGAT LIDDTYNANP DSMKAAIDVL
351  ARMPAPRIFV MGD MGELGEL GEDEAAAMHA EVGAYARDQG IEAAYFVGDN
401  SVEAAEKFGA DGLWFAAKDP LIQVLRHDLR ERATVLVKGS RFMQMEEVVE
451  ALEDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 081 shows 94.1% identity over a 455 aa overlap with a predicted ORF (ORF 081.ng) from *N. gonorrhoeae*:

m081/g081

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLPMPSESKPVSRIVTDSRDIRAGDVFFALAGERFDAHDFVEDVLAA					
g081	MKPLDLNFICQALKLPMPSENKPVSRIVTDSRDI REGDVFFALAGGRFDAHDFVGGVLSA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
g081	GAAAVVVSREDCAALGGALKVDDTLAALQTLAKAWRDNVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNKHYAVIEMGMNHFGE LAVLTXIAKP					
g081	AVLRRRFGDDAVSATAGNFNNHIGLPLTLLKLNKHYAVIEMGMNHFGE LAVLTQIAKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVCGFDGVGDIKAKSEIYQGLCSGIALIPQEDANMAVFKTATLNLN					
	:					
g081	DAALVNNALRAHVCGFDGVGDIKAKSEIYAGLCSDGMALIPQEDANMAVFKTATFNLN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAADVLPV PGRHNVHNAAAAAALALAAG					
g081	TCTFGVDSGDVRAENIVLKPLSCEFDLVCGDERTAVVLPV PGRHNVHNAAAAAALALAAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGFSNIKGR LNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
g081	LSLNDVAEGLQGFSNIKGR LNVKAGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
g081	MGDMGELGE---DEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGS RFMQMEEVVEALEDKX					
g081	LIQVLSHDLPERATVLVKGS RFMQMEEVVEALEDKX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 251>:

```
a081.seq
1   ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51  GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGATGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCG GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGTTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTACCGC GTTGCAAATG TTGGCGAAGG CGTGGCGCGA GAATGTGAAC
301 CCGTTTGTGT TCGGTATTAC CGGCTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATAAT GCCGTTTGG
401 CGACGGCAGG CAACTTCAAC AACCACATCG GATTGCCGTT GACTTTGTTG
451 AAATTAAACG AAAAAACCCG CTATGCCGTG ATTGAAATGG GTATGAACCA
501 TTTTGGCGAA CTGGCGGTTT TGACACAAAT CGCCAAACCC GATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTGC GCTGCGGTTT CGACGGAGTG
601 GCGCATATTG CCAAAGCGAA AAGCGAGATT TATCAAGGCT TATGTTCAGA
651 CGGCATGGCG CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTGGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTCCACGCGG AAAATATCGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC AACGAGTGCG CAGCCGTGGT TCTGCCCGTT CCCGCCGCC
851 ACAATGTCCA CAACGCCGCC GCCGCCGCCG CGCTGTCTTT GGCTGCAGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGCTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCTT GACAGCATGA AAGCTGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGTGAGGAC GAAGCCGCCG CCATGCACGC CGAAGTCGGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGCGGAAA AATTTGCGCG GGACGTTTGT TGGTTCGCGG CCAAAGACCC
1251 GTTGATTCAA GTGTTGCGCC ACGATTGGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAGGTTT CCGCTTTATG CAGATGGAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTGA
```

This corresponds to the amino acid sequence <SEQ ID 252; ORF 081.a>:

```
a081.pep
1   MKPLDLNFIC QALKLMPSE SKPVSRIVTD SRDIRAGDVF FALAGGRFDA
51  HDFVEDVLAA GAAAVVVSRE DCVAMDGALK VDDTLTALQM LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDN AVLATAGNFN NHIGLPLTLL
151 KLNKHHRYAV IEMGMNHFG E LAVLTQIAKP DAALVNNAMR AHVCGGFDGV
201 GDIKAKSEI YQGLCSDGMA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
251 VHAENIVLKP LSCEFDLVCG NECAAVVLPV PGRHNVHNA AAAAAAALAA
301 LSLNDVAEGL KGFSNIKGR L NVKSGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMLGELG E EAAAMHAEVG AYARDQGIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLIQ VLRHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*
```

m081/a081 96.7% identity over a 455 aa overlap

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLMPSESKPVSRIVTDSDIRAGDVFFALAGERFDAHDFVEDVLAA					
a081	MKPLDLNFICQALKLMPSESKPVSRIVTDSDIRAGDVFFALAGGRFDAHDFVEDVLAA					
	10	20	30	40	50	60
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	130	140	150	160	170	180
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNKHHRYAVIEMGMNHFGELAVLTQIAKP					
a081	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNKHHRYAVIEMGMNHFGELAVLTQIAKP					

268

	130	140	150	160	170	180
m081.pep	190	200	210	220	230	240
a081	190	200	210	220	230	240
m081.pep	250	260	270	280	290	300
a081	250	260	270	280	290	300
m081.pep	310	320	330	340	350	360
a081	310	320	330	340	350	360
m081.pep	370	380	390	400	410	420
a081	370	380	390	400	410	
m081.pep	430	440	450			
a081	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 253>:

g082.seq

```

1  aTGTGGTTGT TGAAGTTGCC TGCCGTCGCC GAAACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATCTC CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAACGGGT TCACATTATC GCGCCACGCC
151 TTCGCCAAGC TTTGCAACGC GGCAAGCGTG TCATCGACTT TCAACGCGCC
201 GCCCAAAGCC GCGCAATCTT CGCGCGAAAC CACAACGCC GCCGCGCCG
251 CAGACAATAC GCCTCCAACA AAATCATGCG CGTCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC TTCCCGAATA TCGCGGTGT CGGTTACGAT
351 GCGCGACACG GGTTTGT TTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTCATAT TTGCTTTCGT TAATATTCGG
451 CCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGTGT
501 GGTAAACAC AGATTATTTT CCCATTCTCA TTCGGCATTT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGCCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGACT GTCTGTGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCGGCAC ATCGGGGACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 254; ORF 082.ng>:

g082.pep

```

1  MWLLKLPAVA ETASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTLSRHA
51  FANVCNAASV SSTFNAPPKA AQSSRETTTA AAPADNTPPT KSCASNRPAA
101 NAKNTSPSRI SRLSVTMRDT GLFSDGIGSL RAWQMKFRSS GFIFAFVNIR
151 AADTSVAADF FIACFAVVKH RLFSSHSAF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGLSVD KGKVIARH IGDIPPKIIA VIGQLVGFD TPTAESA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 255>:

m082.seq

```

1  ATGnnGTTGT TGAAGTTGCC TGCCGTCGCC AACACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATTTT CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAACGGAT TCACATTTTC ACGCCACGCC
151 TTTGCCAGCG TTTGCAATGC GGCAAGCGTG TCATCGACTT TCAACGCGCC

```

201	ATCCATTGCA	GCACAACTCT	CGCGCGAAAC	CACAACCGCC	GCCGCACCAG
251	CAGCCAAATAC	GTCTTCAACA	AAATCATGCG	CGTCAAACCG	CTCGCCCGCC
301	AATGCGAAAA	ACACATCGCC	CGCGCGGAT	TCGCGGCTGT	CGGTTACGAT
351	CGCGCAGCAG	GGTTTGTCTT	GAGTCGGCAT	CGGAAGCTTG	AGGGTTTGGC
401	AGATGAAATT	TAGGTCACGT	CGGTTTCATAT	TTACTTTCGT	TAAATTTGCG
451	GCGGCGGACA	CATCGGTAGC	GGCTGATTTT	TTTATCGCCT	GTTTTGCTGT
501	GGTAAAACAC	AGATTATTTT	CCCATTCTCA	TTCGG <sub>s</sub> ATT	TTTCTGTACG
551	TATCATTTTT	TAGACGTATT	TTTAGTCGAT	TTGCCTTTTC	CCGCATACCA
601	CGGCGCGGGG	TCGTCGGGCA	GTCCGTCGAT	AAAGGCAAGG	TTATTGCCTT
651	CGCCCTGTCAC	ATCGGGGAACA	TTC <sub>s</sub> CCCCAAA	AATCATAGCC	GTATCGGGC
701	AACTCGTCGG	TTTCGATACC	CGTCCAAC <sub>s</sub> CTG	CCGAATCCGC	GTAA

This corresponds to the amino acid sequence <SEQ ID 256; ORF 082>:

```
m082.pep
1  MXLLKLPAVA NTASSPKRRR NTAASISFTV VLPPEPVMPT TNGFTFSRHA
51  FASVCNAASV SSTFNAPSIA AQSSRETTTA AAPAANTSST KSCASNRSRA
101 NAKNTSPARM SRLSVTMRDT GLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSSHSHXFL FLYVSFFRRI FSRFAFSRIP
201 RRGVVGQSD KGKVIAFALH IGNIPPKIIA VIGQLVGFDI RPTAESA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 082 shows 92.7% identity over a 247 aa overlap with a predicted ORF (ORF 082.ng) from *N. gonorrhoeae*:

m082/g082

		10	20	30	40	50	60
m082.pep		MXLLKLPAVANTASSPKRRRNTAASISFTVVLPPPEPVMPTNGFTFSRHAFASVCNAA	SV				
		:					
g082		MWLLKLPAVAETASSPKRRRNTAASISFTVVLPPPEPVMPTNGFTLSRHAFANVCNAA	SV				
		10	20	30	40	50	60
		70	80	90	100	110	120
m082.pep		SSTFNAPSIAAQSSRETTTAAAPAAANTSSTKSCASNRS PANAKNTSPARMSRLSVTMR	DT				
		:					
g082		SSTFNAPPKAAQSSRETTTAAAPADNTPPTKSCASNRP PANAKNTSPSRISRLSVTMR	DT				
		70	80	90	100	110	120
		130	140	150	160	170	180
m082.pep		GLLSDGIGISLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSH	SXF				
		:					
g082		GLFSDGIGISLRAWQMKFRSSGFIFAFVNIRAADTSVAADFFIACFAVVKHRLFSHSH	SAF				
		130	140	150	160	170	180
		190	200	210	220	230	240
m082.pep		FLYVSFFRRIFSRFAFSRIPRRGVVGQSVDKGVIAFALHIGNIPPKIIAIVIGQLVG	FDT				
		:					
g082		FLYVSFFRRIFSRFAFSRIPRRGVVGLSVDKGVIAFARHIGDIPPKIIAIVIGQLVG	FDT				
		190	200	210	220	230	240
m082.pep		RPTAESAX					
g082		RPTAESAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 257>:

**a082.seq**

1 ATGTGGTTGT TGAAGTTGCC TGCCGTCGCC AAAACGGCAT TATCGCCGAA  
51 ACGGCGGGCG AATACCGCAG CCAACATTTT CTTACCGTC GTCTTGCCGC

```

101 CCGAGCCGGT AATACCGAAC ACAAACGGGT TCACATTCTC GCGCCACGCC
151 TTCGCCAACA TTGCAACGC GGTAAAGCGTG TCATCGACTT TCAACGCGCC
201 ATCCATTGCA ACGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCCG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CATCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTCGCTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTCATAT TACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTT TTTATCGCCT GTTTGCTGT
501 GGTAAACAC AGATTATTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGG TCGTCGGGCA GTCGTCGAT AAAGGCAAGG TTATGTCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTCGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 258; ORF 082.a>:

**a082.pep**

```

1 MWLLKLPAPA KTALSPKRRR NTAANISFTV VLPPEVPVNP TNGFTFSRHA
51 FANICNAVSV SSTFNAPSIA TQSSRETTA AAPAANTSST KSCASNPPA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVKH RLFSSHSAF FLYVSFFRRI FSRFAFSRIP
201 RRGVVQSV D KGVIAFALH IGNIPPKIIA VIGQLVGFD T RPTAESAX*

```

**m082/a082** 95.5% identity over a 247 aa overlap

	10	20	30	40	50	60
m082.pep	MXLLKLPVAVANTASSPKRRRNTAASISFTVVLPPEVMPNTNGFTFSRHAFAVCNAASV					
a082	MWLLKLPVAKTALSPKRRRNTAANISFTVVLPPEVPVNPNTNGFTFSRHAFAVICNAVSV					
	10	20	30	40	50	60
m082.pep	70	80	90	100	110	120
a082	SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRPANAKNTSPARMSRLSVTMRDT					
	70	80	90	100	110	120
m082.pep	130	140	150	160	170	180
a082	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVKHRLFSHSHSXF					
	130	140	150	160	170	180
m082.pep	190	200	210	220	230	240
a082	FLYVSFFRRIFSRFAFSRIPRRGVVQSV D KGVIAFALHIGNIPPKIIAVIGQLVGFD T					
	190	200	210	220	230	240
m082.pep	RPTAESAX					
a082	RPTAESAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 259>:

**g084.seq**

```

1 ATGAAacaAT CCGcccgaat aAAAAATATG GATCAGACAT TAAAAAATAC
51 attgggcatt tGCGCGcttt tagcctTTTG TTTTggcgcG gccatCGCAT
101 CAGGTTATCA CTGGAATAT GAATACGGCT ACCGTTATTG TGCCGTGGGC
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GCTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCCTT CTTATCAGAT AGTCGGTTTCG
301 ATATTGAAA GCAATCCTGC CGAGGCGCGT GAATTGTGCG GCAATCTTCC
351 CGGGTCGCTT TATTTGTGTC AGGCATTATT TTTTATTTT GGCTTGACAG

```

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401 TTTGGAAATA TTGTGTATCT GTGGGGGTAT TTGCTGACGT AAAAACTAT  
 451 AAACGTCGCA GCAAAATATG GCTGACCATA TTATTGACTT TGATTTTGTG  
 501 CTGCGCGGTG ATGGAGAAAA TCGccggcga taaAGATTGG CGAGaacctg  
 551 atgccggcct gttgttgaat ATTTTcgacc tgtattaCga cttggctttc  
 601 cgcgccggca cAATATGCCG CCAAGCGCGC CCACattttg gaagCagcaa  
 651 aaaaagcgtC AACATGGCAt atccgccaac ttgcgcccaa gTataa

This corresponds to the amino acid sequence <SEQ ID 260; ORF 084.ng>:

g084.pep

1 MKQSARIKNM DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSVAVG  
 51 ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVWGLY GAPSYQIVGS  
 101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS VGVFADVKNY  
 151 KRRSKIWLTI LLTLILSCAV MEKIDGDKDW REPDAGLLN IFDLYYDLAF  
 201 RAGTICRQAR PHFGSSKKSVMAYPPTCAQ V\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 261>:

m084.seq

1 ATGAAACAAT CCGCCcGAAT AAAa.ATATG AATCAGACAT TACTTTATAC  
 51 ATTGGGCATT TGCGCGCTTT TAACCTTTnn nnnnnnnnnnn nnnnnnnnnnn  
 101 nnnnnTATCA CCCnGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGT  
 151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG  
 201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT  
 251 TGCCGTCGG CTGGCTGTAT GGTGCGCGT CTTATCAGAT AGTCGTTTCG  
 301 ATATTGGAAG GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC  
 351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTCATTTT GGCTTGACAG  
 401 TTTGGAAATA TTGTGTATCG GGGGGGGTAT TTGCTGACGT AAAAACTAT  
 451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTG  
 501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG  
 551 ATGCCGCGCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTGGCT.TC  
 601 CGCGCCGCGA CAATATGCCG CCAAGCGCGC CCACATTTG GAAGCAGCAA  
 651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

This corresponds to the amino acid sequence <SEQ ID 262; ORF 084>:

m084.pep

1 MKQSARIKXM NQTLTYTLGI CALLTFXXXX XXXXXYHPEY EYGYRYSVAVG  
 51 ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVWGLY GAPSYQIVGS  
 101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS GGVFADVKNY  
 151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLN IFDLYYDLAX  
 201 RAGTICRQAR PHFGSSKKSVMAYPSCCAQ V\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 084 shows 90.5% identity over a 231 aa overlap with a predicted ORF (ORF 084.ng) from *N. gonorrhoeae*:

m084/g084

	10	20	30	40	50
m084.pep	MKQSARIKXMNQTLTYTLGICALLTF-----YHPEYEGYRYSVAVGALASVVFLLL				
	:          :				
g084	MKQSARIKNMDQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSVAVGALASVVFLLL				
	10	20	30	40	50
	60	70	80	90	100
m084.pep	LARGFPRVSSVLLIYVGTALYLPVWGLYGAPSYQIVGSILESNPAEAREFVGNLPGSL				
g084	LARGFPRVSSVLLIYVGTALYLPVWGLYGAPSYQIVGSILESNPAEAREFVGNLPGSL				
	70	80	90	100	110
	120	130	140	150	160
m084.pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL				
g084	YFVQALFFIFGLTVWKYCVSVGVFADVKNYKRRSKIWLTI LLTLILSCAVMEKIDGDKDW				
	130	140	150	160	170
	130	140	150	160	170

	180	190	200	210	220
m084 . pep	REPDAGLLLNIFDLYDLAXRAGTICRQARPHFGSSSKSVNMAYPSCCAQVX				
g084	REPDAGLLLNIFDLYDLAFRAGTICRQARPHFGSSSKSVNMAYPPTCAQVX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 263>:

## a084 . seq

```

1  ATGAAACAAT CCGCCCGAAT AAAAAATATG GATCAGACAT TAAAAAATAC
51  ATTGGGCATT TGC GCGCTTT TAGCCTTTTG TTTTGGCGCG GCCATCGCAT
101 CAGGTATATCA CTTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCAGCGG GTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGTCGCG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTCG
301 ATATTGGAAT GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTT GGCTTGACAG
401 TTTTGAGATA TTGTGTATCG GGGGGGGTAT TTGCTGACGT AAAAAACTAT
451 AAACGCCGCA GCAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCTTCC
601 .GCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTG GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 264; ORF 084.a>:

## a084 . pep

```

1  MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51  ALASVVFLLL LARGFPRVSS VVLLIYVGT ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWRYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLN IFDLYYDLAS
201 XAGTICRQAR PHFGSSSKSV NMAYPSCCAQ V*

```

m084/a084 92.2% identity over a 231 aa overlap

	10	20	30	40	50	60
m084 . pep	MKQSARIKXMQNTLLTYTLGICALLTFXXXXXXXHYHPEY EYGYRYSAVGALASVVFLLL					
a084	MKQSARIKMDQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVGALASVVFLLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m084 . pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGS ILESNPAEAREFVGNLPGSL					
a084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGS ILESNPAEAREFVGNLPGSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
	190	200	210	220	230	
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSSKSVNMAYPSCCAQVX					
a084	REPDAGLLLNIFDLYYDLASXAGTICRQARPHFGSSSKSVNMAYPSCCAQVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 265>:

## g085 . seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGACGCGT TGAAAGATAA

```



```

51  GGCAAAGGC GTGTCCTGA TCGGCGTCGA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AACCTGACCG ACTGCGTCAC TTTGGAAGAG
151 GCGGTTTCAGA CGGCATACGC CCAAGCCGAA GCGGGCGATA TTGTCTTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT tatCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 266; ORF 085.ng>:

**g085.pep**

```

1  MGKGQDFTPL RDALKDKAKG VFLIGVDAPO IRRDLGCGGL NLTDCVTLEE
51  AVQTAYAQAQ AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 267>:

**m085.seq**

```

1  ATGGGTAAAG GGCAGGACTT CACGCCCCTG CGCGATGCAC TGGTAGGCAA
51  GGCAAAGGC GTGTCCTGA TTGGTGTCGA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AATATGACCG ACTGCGCCAC TTTGGGAGAA
151 GCCGTTTCAGA CGGCATATGC CCAAGCCGAA GCAGGCGATA TTGTGTTGCT
201 CAGCCCCGCC TCGCGGAGCT TTGATATGTT CAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT TATCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 268; ORF 085>:

**m085.pep**

```

1  MGKGQDFTPL RDALVGKAKG VFLIGVDAPO IRRDLGCGGL NMTDCATLGE
51  AVQTAYAQAQ AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 085 shows 94.7% identity over a 94 aa overlap with a predicted ORF (ORF 085.ng) from *N. gonorrhoeae*:

**m085/g085**

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGGLNMTDCATLGEAVQTAYAQAQ					
g085	MGKGQDFTPLRDALKDKAKGVFLIGVDAPOIRRDLGCGGLNLTDCVTLEEAQTAYAQAQ					
	10	20	30	40	50	60
	70	80	90			
m085.pep	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
g085	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 269>:

**a085.seq**

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCCTG CGGACGCGC TTGCCGGCAA
51  GGCAAAGGC GTGTCCTGA TCGGTGTCGA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGATCTG AATATGACCG ACTGCGCCAC TTTGGAAGAA
151 GCGGTTTCAGA AGGCATATGC CCAAGCCGAA GCGGGCGATA TCGTCTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT TATCGGGGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 270; ORF 085.a>:

**a085.pep**

```

1  MGKGQDFTPL RDALAGKAKG VFLIGVDAPO IRRDLGCDL NMTDCATLEE
51  AVQKAYAQAQ AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

**m085/a085** 94.7% identity over a 94 aa overlap

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGGLNMTDCATLGEAVQTAYAQAQ					

```

|||||
a085  MGKGQDFTPLRDALAGKAKGVFLIGVDAPQIRRDLDGCDLNMTDCATLEEAQKAYAQAE
      10      20      30      40      50      60
      70      80      90
m085.ppep AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX
|||||
a085  AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX
      70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 271>:

```

g086.seq
1  ATGGTGGTGC TGATGACGGC GTTCGGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTC GCATCGAAGG AAGCGGCGA TCAGTTTTTC TATTGACCA
101 GGCAGGCGGG GTTCGTCGTT GCCGGCCTTA TAGCGAGCGG TTTTATATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201 CTTATCCGGC CTGTTGCTGG TAGCCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCa AGCTGGCAGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAAG TTTGGGTTGG CAGTCGATTT
401 GGCAGGGGAC GGCCAACCTG ATTATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAAACAT TAGAAATGTA CGgcCGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTTCG
551 GTTCGTTTGT CGTCATTACC GTCATTACCG TTGGAATGCT GTTCTCGGCA
601 GGATTGCCGT GGAATATTT TTTTGTCTCG GTAGGCAGCG TCTTGGGTGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CCGGTAGTGG
701 CATTTTGGAA CCCGTGGAAA GACCCGACAG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TGCGAGTTTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGTCCAT CATCGCTGAA GAATTCGGCT TCTTCGGGAT GTCGGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGtttgA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CGGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGctgCcg tTGATGTCCT ATGGcggTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTTG CGTATCGATT
1151 ATGAAAACCG CCAGAAAATG CGCGTTTACC GGGTGGAGTA AA

```

This corresponds to the amino acid sequence <SEQ ID 272; ORF 086.ng>:

```

g086.ppep
1  MVVLMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGFLW
51  FLCRMRTWRR LVPWIFALSG LLLVAVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTTRREE VLRSMESLGW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VITVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFLDPWK DPQGAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGWLVRV AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGNVIG
351 ALPTKGLTLP LMSYGGSSVF FMLISMMLLL RIDYENRQKM RGYRVE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 273>:

```

m086.seq
1  ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTC GCATCAAAAG AAGCGGCGA TCAGTTTTTC TATTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCCTTA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201 CCTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCa AGCTGGCAGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGcGCA GCATGGAAAG TTTGGGTTGG CAGTCGATTT
401 GGCAGGGGAC GGCCAATCTG ATCATGTCCG CCACCAATCC GCAGrCACGT
451 CGTGAAaACAT TAGAAATGTA CGGCGGTWTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTTCG

```

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```

551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGGAATGCT GTTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCTCCTG GTAGGCAGCG TCTTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTTGA CCCGTGGAAA GACCCGCAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TGCAGAGTTG AGCAAACGCG GCTTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTGGAT CGGkrTCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA mCAAAGyCT GACGCGGCCG Tg.AtGTCCw ATGGCGGTTT
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTkG CGTATAGATT
1151 ATGAAACCG CCGGAAATG CCGGTTATC GGGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 274; ORF 086>:

m086.pep

```

1  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTRREE VLRSMESLGW QSIWRGTANL IMSATNPQXR
151 RETLEMYGRX RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFLDPWK DPQAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGLVVR AFSIGKQSRD LGLTFNAYIA SGIGIWGXQ SFFNIGVNIG
351 ALPXKGLTXP XMSXGGSSVF FMLISMMLLX RIDYENRRKM RGYRVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 086 shows 96.7% identity over a 396 aa overlap with a predicted ORF (ORF 086.ng)

from *N. gonorrhoeae*:

m086/g086

	10	20	30	40	50	60
m086.pep	MVVLMTAFSLLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
	:     :     :     :     :					
g086	MVVLMTAFGLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLWFLCRMRTWRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m086.pep	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTRREE					
	:     :     :     :     :					
g086	LVPWIFALSGLLLVAVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTRREE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m086.pep	VLRSMESLGWQSIWRGTANLIMSATNPQXRRETLEMYGRXRRAILPIMLVAFGLVLIMVQ					
	:     :     :     :     :					
g086	VLRSMESLGWQSIWRGTANLIMSATNPQARRETLEMYGRFRAILPIMLVAFGLVLIMVQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m086.pep	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQVVAFLDPWK					
	:     :     :     :     :					
g086	PDFGSFVVITVITVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQVVAFLDPWK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m086.pep	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEEFGFFGMCVL					
	:     :     :     :     :					
g086	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEEFGFFGMCVL					
	250	260	270	280	290	300
	310	320	330	340	350	360

276

```

m086.pep      IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFNIGVNIGALPKGLTXP
               |||||||||||||||||||||||||||||||||||||||||:|||||
g086          IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFNIGVNIGALPTKGLTLP
               310      320      330      340      350      360

               370      380      390
m086.pep      XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX
               |||||||||||||||||||:|||||||||
g086          LMSYGGSSVFFMLISMMLLLRIDYENRQKMRGYRVEX
               370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 275>:

```

a086.seq
1  ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCCGGCTTC
51  TGTGTATTGG GCATCAAAAG AAGCGGGCGA TCAGTTTTTC TATTTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCTTGA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTTGA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTGC
201 CCTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCGGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAAG TTTGGGTTGG CAGTCGATTT
401 GGCGGGGGAC GGCCAATCTG ATCATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAAACAT TAGAAATGTA CGGCCGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTTC
551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCTCCTG GTAGGCAGCG TCTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTTGGA CCCGTGGAAA GACCCGAGG GTGCCGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TCGGAGTTTG AGCAAACGCG GCTTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGTCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGAT CGGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGCTGCCG TTGATGTCTT ATGGCGGTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTTG CGTATAGATT
1151 ATGAAAACCG CCGGAAAATG CGCGGTTACC GGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 276; ORF 086.a>:

```

a086.pep
1  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTTRREE VLRSMESLGW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDLPWK DPQGAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFQFFGMCVL
301 IFCYGWLVVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGVNIG
351 ALPTKGLTLP LMSYGGSSVF FMLISMMLLL RIDYENRRKM RGYRVE*

```

m086/a086 98.0% identity over a 396 aa overlap

```

               10      20      30      40      50      60
m086.pep      MVVLMTAFSLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR
               |||||||||||||||||||||||||||||||||||||||||
a086          MVVLMTAFSLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR
               10      20      30      40      50      60

               70      80      90      100     110     120
m086.pep      LVPWIFALSGLLLVVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTTRREE
               |||||||||||||||||||||||||||||||||||||||||
a086          LVPWIFALSGLLLVVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTTRREE

```

277

	70	80	90	100	110	120
m086.pep	130	140	150	160	170	180
	VLRSMESLQWQSIWRGTANLIMSATNPQXRRETLEMYGRXRAIILPIMLVAFGLVLMVQ					
a086	VLRSMESLQWQSIWRGTANLIMSATNPQARRETLEMYGRFRAIILPIMLVAFGLVLMVQ					
	130	140	150	160	170	180
m086.pep	190	200	210	220	230	240
	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
a086	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	190	200	210	220	230	240
m086.pep	250	260	270	280	290	300
	DPQGAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
a086	DPQGAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
	250	260	270	280	290	300
m086.pep	310	320	330	340	350	360
	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFNIGVNIGALPKXGLTXP					
a086	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFNIGVNIGALPTKGLTLP					
	310	320	330	340	350	360
m086.pep	370	380	390			
	XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX					
a086	LMSYGGSSVFFMLISMMLLLRIDYENRRKMRGYRVEX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 277>:

g087.seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GGCGGAACGG GCGGACACAT
51  TTTCCAGCT CTGGCTGTGG CGGATTCAAT GCGCGTGCGC GGTCAATCATG
101 TAATTGGCT GGGCAGCAAG GATTTCGATG AAGAGCGCAT CGTGCCGCAA
151 TACGGCATA GCTTGGAAC GCTGGCGATT AAAGGAATAC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TTCCGTTTAC TCTGTACAAA ACCGTCCGCG
251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCGT CATCGGCTTC
301 GCGGTTTTG TTACCTTTCC CGGCGTCTG GCGGCGAAAC TCTTGGGCGT
351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGCTTG TCCAACCGCC
401 AccTGTCGCG ctGGGCGAAA CGGGTGTGT ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGTTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGCGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCAGT TTGGGTGCGG ACGTTTTGAA CAAAACCGTA
601 CCGCAGGCGT TGGCACTGCT GCCTGAAGAG GTGCGCCCGC AGATGTACCA
651 CCAGTCGGGG CGTAACAAGC TGGGCAATCT TCAGGCGGAT TATGACGCGT
701 TGGGCGTGAA AGCGGAATGC GTGGAATTTA TTACCGACAT GGTGTCCGCC
751 TACCGTGATG CCGATTGGT GATTTGCCGT GCCGGCGCGC TGACGATTGC
801 CGAGTTGACG GCGGCGGGGC TGGGCGCGTT GTTAGTGCCG TATCCTCAGC
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTCATGGT GCAGGCAGAA
901 GCGGGGCTGC TGTTGCCGCA AACCAGTTG ACGGCGGAAA AACTCGCCGA
951 AATCCTCGGC AGCCTCAACC GCGAAAATG CCTCAAATGG GCGGAAAACG
1001 CCCGTACGTT GGCATTGCCG CACAGCGCGG ATGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAAA

```

This corresponds to the amino acid sequence <SEQ ID 278; ORF 087.ng>:

g087.pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRVR GHVVIWLGSK DSMEERIVPQ
51  YGIRLET Lai KGIRNGIKR KLMLPFTLYK TVREAQRIIR KHRVECVIGF
101 GGFVTFPGGL AAKLLGVPIV IHEQNAVAGL SNRHLSRWAK RVLVAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKTV

```

201 PQALALLPEE VRPQMYHQSG RNKLGNLQAD YDALGVKAEC VEFITDMVSA  
251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE  
301 AGLLLPQTQL TAEKLAETLG SLNREKCLKW AENARTLALP HSADDVAEEA  
351 IACAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 279>:

```
m087.seq
1  ATGGGCGGTA  AAACCTTTAT  GCTGAwkkCG  GGCGGAACGG  GCGGACATAT
51  TTTCCCGCGC  CTGGCGGTGG  CGGATTCATT  GCGCGCGCGC  GGCCATCATG
101 TGATTGGCTG  GGGCAGCAAG  GATTCGATGG  AAGAGCGTAT  CGTGC CGCAA
151 TACGGCATAC  GCTTGGAAAC  GCTGCGCATT  AAAGCGCTGC  GCGGCACCGG
201 CATCAAACGC  AAAC TGATGC  TGCCGGTTAC  TTTGTATCAA  ACCGTC CGCG
251 AAGCGCAGCG  GATTATCCGC  AAACACCGTG  TCGAGT GCGT  CATCGGCTTC
301 GGCGGCTTCG  TTACCTTCCC  CGGCGGTTTG  GCGGGGAAGC  TATTAT GCGT
351 GCCGATTGTG  ATTCACGAGC  AAAACGCCGT  GGCAGGTTTG  TCCAACCGCG
401 ACCTGT GCGC  CTGGGCGAAG  CGGGTGTTGT  ACGCTTTTCC  GAAAGCGCTTC
451 AGCCACGAAG  CGGGCTTGGT  CGGCAACCCC  GTCCGCGCCG  ATATTGCAA
501 CCTGCCCGTG  CCTGCCGAAC  GCTTCCAAGG  GCGTGAAGGC  CGTCTGAAAA
551 TTTTGGTGGT  CGGCGGCAGT  TTGGGCGCGG  ACGTTT TGAA  CAAAACCGTA
601 CCGCATGCAT  TGGCTTTGCT  TGCCGACAAT  GCGCGTCCGC  ATATGTACCA
651 CCAATCGGGA  CGGGGCAAGC  TGGGCATCTT  GCAGGCGGnnn  nnnnnnnnnnn
701 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
751 nnnGCGGGAT  TGGGTGCGTT  GTTAGTGCCG  TATCTCAGC  CGGTTGACGA
801 TCACCAAACC  GCCAACGCGC  GTTTTATGGT  GCAGGCGGAG  GCGGGATTGC
851 TGTTGCCGCA  AACCAGTTG  ACGGCGGAAA  AACTGCGCGA  GATTCTCGGC
901 GGCTTAAAC  GCGAAAAATG  CCTCAAATGG  GCAGAAAACG  CCCGTACGTT
951 GGCATGCGC  CACAGTGCGG  ACGACGTGGC  GGAAGCCGCG  ATTGCGTGTG
1001 CGGCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 280; ORF 087>:

```
m087.pep
1  MGGKTFMLXX  GGTGGHIFPA  LAVADSLRAR  GHVVIWLGSK  DSMEERIVPQ
51  YGRLETLAI  KGV RNGIKR  KLMLPVTLYQ  TVREAQRIIR  KHRVECVIGF
101 GGFVTFPGGL  AAKLLXVPIV  IHEQNAVAGL  SNRHLSRWAK  RVLYAFPKAF
151  SHEGGLVGNP  VRADISNLPV  PAERFQGREG  RLKILVVGGS  LGADVLNKTV
201  PHALALLPDN  ARP MYHQS  RGKLGILQAX  XXXXXXXXXX  XXXXXXXXXX
251  XAGLGALLVP  YPHAVDDHOT  ANARFMVQAE  AGLLLPQTQL  TAEKLAETLG
301  GLNREKCLKW  AENARTLALP  HSADDVAEAA  IACAA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 087 shows 83.9% identity over a 355 aa overlap with a predicted ORF (ORF 087.ng) from *N. gonorrhoeae*:

m087/q087

	10	20	30	40	50	60
m087.pep	MGGKT	FMLXXGGTGGHIFPALAVADSLRAGHHV	IWLGSKDSMEERIV	PQYGIRLETLAI		
g087	MGGKT	FMLMAGGTGGHIFPALAVADSLRVRGHHV	IWLGSKDSMEERIV	PQYGIRLETLAI		
	10	20	30	40	50	60
	70	80	90	100	110	120
m087.pep	KGVRGNGIKRKLMLPVTLYQTVREAQRI	IRKHRVECVIGFGGFVTFPGGLAAKLLXVP	IV			
g087	KGIRGNGIKRKLMLPFTLYKTVREAQRI	IRKHRVECVIGFGGFVTFPGGLAAKLLGVP	IV			
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQ	REG				
g087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQ	REG				
	130	140	150	160	170	180

279

	190	200	210	220	229
m087.pep	RLKILVVGSSLGADVLNKTVP	PHALALLPDNARPHMYHQSGR	GKLGILQA-----		
g087	RLKILVVGSSLGADVLNKTVP	QALALLPEEVRPQMYHQSGR	NKLGNLQADYDALGVKAEC		
	190	200	210	220	230 240
m087.pep	-----			AGLGALLVPYPH	AVDDHQTANARFMVQAE
g087	VEFITDMVSAYRDADLVICR	AGALTIAELTAAGLGALLVP	YPH	AVDDHQTANARFMVQAE	
	250	260	270	280	290 300
m087.pep	AGLLLPQTQLTAEKLAEL	GLGNREKCLKWAENARTL	ALPHSADDDVAEAAIACAAX		
g087	AGLLLPQTQLTAEKLAEL	GLGNREKCLKWAENARTL	ALPHSADDDVAEAAIACAAX		
	310	320	330	340	350

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 281>:

a087.seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GCGGGAACGG GCGGACATAT
51  TTTCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCGC GGCCATCATG
101 TAATTTGGCT GGGCAGCAAG GATTCGATGG AAGAGCGCAT CGTGCCGCAA
151 TACGACATCC TGCTCGAAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TGCCGTTTAC TTTGTATCAA ACTGTCCGCG
251 AAGCGCAGCA GATTATCCGC AAACACCGTG TCGAGTGCGT CATCGGCTTC
301 GCGGGCTTCG TTACCTTTCC CGGCGGTTTG GCGGCGAAGT TATTAGGCGT
351 GCGGATTGTG ATTCACGAGC AAAACGCCGT GCGAGGTTTG TCCAACCGCC
401 ACCTGTCGCG CTGGGCGAAG CGGGTGTTGT ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCGC ATATTAGCAA
501 CCTGCCCGTG CTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCAGT TTGGGCGCGG ACGTTTTGAA CAAACCGTA
601 CCGCAGGCAT TGCTTTGCT GCCCGACAAT GCGCGTCCGC AGATGTACCA
651 CCAATCGGGA CGGGCAAGC TGGGCAGCTT GCAGGCGGAT TACGACGCGC
701 TGGGCGTGCA AGCGGAATGC GTGGAATTTA TTACCGATAT GGTGTCGCGC
751 TACCGCGATG CCGATTTGGT GATTTGCCGT GCCGCGCGC TGACGATTGC
801 CGAGTTGACG GCGGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG
901 GCGGGATTGC TGTGCGCGCA AACCCAGTTG ACGGCGGAAA AACTCGCCGA
951 GATTCTCGGC GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG
1001 CCCGTACGTT GGCAGTCCG CACAGTGCGG ACGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CCGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 282; ORF 087.a>:

a087.pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRAR GHVHVLGSK DSMEERIVPQ
51  YDILLETLAI KVRGNGIKR KLMLPFTLYQ TVREAQIIIR KHRVECVIGF
101 GGFVTFPGGL AAKLLGVPIV IHEQNAVAGL SNRHLSRWAK RVLYAFPKEF
151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKTVP
201 PQALALLPDN ARPQMYHQSG RGKLGSLQAD YDALGVQAE VEFITDMVSA
251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
301 AGLLLPQTQL TAEKLAELG GLNREKCLKW AENARTLALP HSADDDVAEAA
351 IACAA*

```

m087/a087 85.4% identity over a 355 aa overlap

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVHVLGSKDSMEERIVPQY	GIRLETLAI				
a087	MGGKTFMLMAGGTGGHIFPALAVADSLRARGHHVHVLGSKDSMEERIVPQY	DILLETLAI				
	10	20	30	40	50	60

280

	70	80	90	100	110	120
m087.pep	KGVRGNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVP					
a087	KGVRGNGIKRKLMLPFTLYQTVREAQQIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQ					
a087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m087.pep	RLKILVVGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQAXXXXXXXXXXX					
a087	RLKILVVGSLGADVLNKTVPQALALLPDNARPMYHQSGRGKLGSLQADYDALGVQAEC					
	190	200	210	220	230	240
	250	260	270	280	290	300
m087.pep	XX-----XXXXXXXXXAGLGALLVPYPHAVDDHQTANARFMVQAE					
a087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE					
	250	260	270	280	290	300
	290	300	310	320	330	
m087.pep	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
a087	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283>:

```

g088.seq
1  ATGTTTTTAT GGCTCGCACA TTTCAGCAAC TGGTAAACCG GTCTGAATAT
51  TTTTCAATAC ACCACATTCC GCGCCGTTAT GCGGCGTTG ACCGCCTTGG
101 CGTTTTCCCT GATGTTCCGC CCGTGGACGA TACGCAGGCT GACCGCGCTC
151 AAATGCGGGC AGGCAGTGCG TACCGACGGC CCGCAAACCC ACCTCGTCAA
201 AAACGGCACC CCGACGATGG GCGGTTGCTG GATTCTGACC GCCATTACCG
251 TGTCCACCCCT GTTGTGGGGC AACTGGGCGA ACCCGTATAT CTGGATTCTC
301 TTGGGCGTAC TGCTTGCCAC CGGTGCGCTC GGTTTTTACG ACGACTGGCG
351 CAAAGTCGTT TATAAGACC CCAACGGCGT GTCCGCCAAA TTCAAATGG
401 TGTGGCAGTC AAGCGTTGCC GTTatcgCG GTttggcaTT GTTTTACctt
451 gCcgCcaATT CCGCCAACAA TATTTTGATT GTCCCGtttT TCAAACAAAT
501 CGCCCTGCCG CTGGGCGTGG TCGGCTTttt gGtgttgTCT TACCTGACCA
551 TCGTCCGGCAC ATCCAACGCC GTCAACCTCA CcgaCGGCTT GGACGGCCTT
601 GCCGCcttcc cgttcgtcct cgttgccgcC GGGCTCGCCA ttttcgccTA
651 CGTCAGCGGA CACTACCAAT TTCCCAATA CCTCCAGCTT CCCTATGTCG
701 CCGGCGCGAA CGAAGTCGCT ATATTCTGCA CCGCCATGTG CCGCGCGTGC
751 CTCGGATTTT TGTGGTTCAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
801 TGTCGGCGCG CTGGCATTGG GTGCCGCGCT CGGTaccGtt gCCGTcaTcg
851 tCCGCCAAGA ATTTGTcttc gtcattatGG GCGGTCTGTT cgtcgtagaa
901 gccgtgTCCG TTATGCTTCa tgtcggCTGG TACAAGAAAA Ccaaaaaacg
951 CATCTTcCTg acgGcaccga ttcacacca ttaCCaactt cgatgCTGga
1001 aagaaacgca agtcgctcgt CGTTtCTGGA TTAtTAccat cgtcggtggt
1101 tTgatagggt tGagtacctT caAAattcgc ggaactatg ccgTCCGAAC
1101 ACCTTTTcAGA CGGCATTGA ACGCGCAATA A

```

This corresponds to the amino acid sequence <SEQ ID 284; ORF 088.ng>:

```

g088.pep
1  MFLWLAHFSN WLTGLNIFQY TTFRAVMAAL TALAFSLMFG PWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTMGGSILIT AITVSTLLWG NWANPYIWIL
101 LGVLLATGAL GFYDDWRKV YKDPNGVSAK FKMVWQSSVA VIAGLALFYL
151 AANSANNILI VPFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTDGLDGL

```



201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC  
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE  
301 AVSVMLHVWG YKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV  
351 LIGLSTLKIR GNYAVRTPFR RHLNAQ\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 285>:

```
m088.seq
1  ATGTTTTTAT  GGCTCGCACA  TTTCAGCAnC  TGGTTAACCG  GTCTGAATnn
51  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
101 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
151 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
201 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
251 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
301 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
351 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
401 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
451 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
501 nnnnnnnnnnn  nnnGGCGTGG  TCGGCTTTTT  GGTGTTGTCT  TACCTGACCA
551 TCGTCGGCAC  ATCCAATGCC  GTCAACCTCA  CCGACGGCTT  GGACGGCCTT
601 GCGACCTTCC  CCGTCGTCTC  CGTGCGCGCC  GGCCTCGCCA  TCTTCGCCTA
651 TGCCAGCGGC  CACTCACAA  TTGCCAATA  CCTGCAATTA  CCTTACGTTG
701 CCGGCGCAAA  CGAAGTGGT  ATTTTCTGTA  CCGCATATG  CGGCGCGTGC
751 CTCGGTTTCT  TGTGGTTTAA  CGCCTATCCC  GCGCAAGTCT  TTTATGGGCGA
801 TGTCCGTGCA  TTGGCATTGG  GTGCCCGGCT  CGGTACCGTC  GCGGTTATCG
851 TCCGCCAAGA  GTTTGTCTC  GTCAATTATG  GCGGATTATT  TGTCTGATAG
901 GCCGTATCCG  TTATGCTTCA  GGTGGGTGG  TATAAGAAAA  CCAAAAAACG
951 CATCTTCTTG  ATGGCGGCC  TCCATACCA  CTACGAACAA  AAAGGCTGGA
1001 AAGAAACCCA  AGTCGTCGT  CGCTTTTGTA  TTATTACCAT  CGTCTTGGTG
1051 TTGATCGGTT  TGAGTACCCT  CAAAATCCG  TGAACCTATG  CCGTCTGAAC
1101 ATCTTTTACA  CGGCATTTGA  CCGGCAATA  A
```

1 MFLWLAHFSN WLTGLNIFOY TTFRAVMAAL TALAFSLMEG PWTIRRLTAL  
51 KCGQAVRTDG PQTHLVKNGT PTMGSSLILT AITVSTLLWG NWANPYIWIL  
101 LGVLLATGAL GFYDDWRKVY YKDPNGVSAK FKMVQSSVA VIAGLALFYL  
151 AANSANNILI VPFFKQIALP LGVVGFVLVS YLTIVGTSNA VNLTDGLDGL  
201 AAFPFLVAA GLAIFAYVS HYQFSQYLQL PYVAGANEVA IFCTAMCGAC  
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE  
301 AVSVMHLHWG YKTKKRIFL TAPIHHYQL RCWKETQVVV RFWIITIVVV  
351 LIGLSTLKIR GNYAVRTPFR RHLNAQ\*

This corresponds to the amino acid sequence <SEQ ID 286; ORF 088>:

```
m088.pep
1  MFLWLAHFSX WLTGLNXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
51  XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
101 XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
151 XXXXXXXXXXXX XXXXXXXXXXXX XGVVGFVLVS YLTVGTSNA VNLTDGLDGL
201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEV IFCTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
301 AVSVMLOVGW YKTKKRIFL MAPIHHHYEQ KGWKETOQVV RFWIIITVLV
351 LIGLSTLKIR XTYAVXTSFR RHLNAQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 088 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 088.ng) from *N. gonorrhoeae*:

m088/q088

m088.pep  
GVVGFVLVSyltIvGTSNAVNLTdGLDGLA  
g088  
IAGLALFYLAANSANNILIVPFfKQIALPLGVVGFLVLSYltIvGTSNAVNLTdGLDGLA

10      20      30  
150    160    170    180    190    200

```

                                40      50      60      70      80      90
m088.pep  TFPVVLVAAGLAI FAYASGHSQFAQYLQLPYVAGANEVVI FCTAMCGACLGFLWFNAYPA
           :|| ||||| ||||| :|| ||| :||| ||||| ||||| :||| ||||| |||||
g088      AFFPVLVAAGLAI FAYVSGHYQFSQYLQLPYVAGANEVAI FCTAMCGACLGFLWFNAYPA
           210      220      230      240      250      260

                                100     110     120     130     140     150
m088.pep  QVFMGVDGALALGAALGTVAIVIRQEFVLVIMGGLFVVVEAVSVMLQVGWYKTKKRIFLM
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| :||| ||||| |||||
g088      QVFMGVDGALALGAALGTVAIVIRQEFVLVIMGGLFVVVEAVSVMLHVGWYKTKKRIFLT
           270     280     290     300     310     320

                                160     170     180     190     200
m088.pep  APIHHHYEQKGWKETQVVVRFWIIITIVLVLIGLSTLKIRXTYAVXTSFRRHNAQX
           ||||| :| :| ||||| ||||| ||||| ||||| ||||| :||| ||||| |||||
g088      APIHHHYQLRCWKETQVVVRFWIIITIVVVLIGLSTLKIRGNYAVRTPFRRHNAQX
           330     340     350     360     370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 287>:

```
a088.seq
1 ATGTTTTTAT GGCTCGCACA TTTTCAGAAC TGGTTAACCG GTCTGAATAT
51 TTTTCAATAC ACCACATTCC GCGCCGTCAT GGCGCCGTG ACCCGCTTGG
101 CGTTTTTCCCT GATGTTTCGGC CCGTGGACGA TACGCAAGGT GACCGCGCTG
151 AAATGCGGGC AGGCAGTGCG TACCGACGGT CCGCAAACCC ACCTCGTCAA
201 AAACGGCAGC CCGACAGATGG GCGGTTTCGT GATTCTGACC GCCATTACCG
251 TGTCCACCCT GTTGTTGGGGC AACTGGGCAA ACCCGTATAT CTGGATTCTC
301 TTGGGCGTAT TGCTCGCCAC GGGGCGCACT GGGTTTTACG AGCACTGGCG
351 CAAAGTCGTC TATAAAGACC CCAACGGCGT GTCCGCCAAA TTCAAATGG
401 TGTGGCAGTC AAGCGTTGCC ATTATCGCGG GTTTTGGCAT GTTTTACCTT
451 GCCGCCAATT CCGCCAACAA TATTTTGATT GTCCCGTTCT TCAAAACAA
501 CGCCCTGCGC CTGGGCGTGG TCGGCTTTTT GGTGTTGTCT TACCTGACCA
551 TCGTCGGCAC ATCCAATGCC GTCAACCTCA CCGACGGCTT GGACGGCCTT
601 GCGACCTTCC CCGTCGTCTT CGTTGCGGCC GGCTTCGCCA TCTTCGCCTA
651 TGCCAGCGGC CACTACAATT TTGCCAATA CTTGCAATTA CCTTACGTTG
701 CGGGCGCAAA CGAAGTGGTG ATTTTCTGTG CCGCCATGTG CGCCGCGTGC
751 CTCGGTTTCT TGTGGTTTAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
801 TGTGCGTGCA TTGGCATTGG GTGCGCGCTT CGGTACCGTC GCGCTCATCG
851 TCCGCGAAGA GTTTGTCTCT GTCATTATGG CGGATTATT TGTCTAGAA
901 CGCGTATCCG TTATGCTTCA GGTGCGGCTG TATAAGAAAA CCAAAAACG
951 CATCTTCTGT ATGGCGCCCA TCCATACCA CTACGAACAA AAAGGCTGGA
1001 AAGAAACCCA AGTCGTGCTC CGCTTTTGGA TTATTACCAT CGTCTTGGTG
1051 TTGATCGGTT TGAGTACCCT CAAATCCG TGAACCTATG CCGTCTGAAC
1101 ACCTTTTCAGA CGGCATTTGA ACGGCAATA A
```

This corresponds to the amino acid sequence <SEQ ID 288; ORF 088.a>:

```

a088.pep
1  MFLWLAHFSN WLTGLNIFYQ TTFRAVMAAL TALAFSLMEG PWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTMGGSILIT AITVSTLLWG NWANPYIWL
101 LGVLLLATAG GFYDWRKVV YKDPNGVSAR FKMVQSSVA ILAGLAFYL
151 AANSANNILI VPFFKQIALP LGYVGFVLVS YLTIVGTSNA VNLTGDLGL
201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEVV IFTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGYE AVIVRQEFVL VMGGGLFVVE
301 AVSVMLQVGR YKTKKKRIFL MAPIHHHYEQ KGWKETQVVV RFWIITIVLV
351 LIGLSTLKIR *TYAV*TPFR RHLNAQ*

```

**m088/a088** 99.5% identity over a 205 aa overlap

```

                150      160      170      180      190      200
m088.pep  XXXXXXXXXXXXXXXXXXXXXXXXXXXXGVVGFVLVLSYLTIVGTSNAVNLT DGLDGLA
                |||
a088      IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFVLVLSYLTIVGTSNAVNLT DGLDGLA

```

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	150	160	170	180	190	200
m088.pep	210	220	230	240	250	260
	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGFLWFNAYPA					
a088	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGFLWFNAYPA					
	210	220	230	240	250	260
m088.pep	270	280	290	300	310	320
	QVFMGDVGALALGAALGTVAIVIRQEFVLVIMGGFLVVEAVSVMLQVGWYKTKKRIFLM					
a088	QVFMGDVGALALGAALGTVAIVIRQEFVLVIMGGFLVVEAVSVMLQVGWYKTKKRIFLM					
	270	280	290	300	310	320
m088.pep	330	340	350	360	370	
	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
a088	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 289>:

```

g089.seq
1  ATGCCGCCCA AAATCACGAA GAGCGGGTTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATG AATACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACACGGT GCGGCAAGCC TTGGAAGGTT
151 TTGACGTGTT CCAGCAATGC TTCGCGCGGC AAACCGACGG CCTCGCACAA
201 AGCCACGGCA GCCATAACGT TGGCGGCGTT GTGCAAACCT TGCAGCGGGA
251 TGTCTTGCGT AGAAATCAAA TCTTCATTGC CTTGTTTTAA ACAGCCCGTC
301 CCGCGTTCCA ACCAAAAATC GGCTTCGTGT TCCAAGGAAA ACCGTTTCAC
351 TTCACGCCCT GCCCGTTTCA TGGCGCGGCA GAACACGTCG TCCGCATTCA
401 AAACCTGCAC TCCATCGCCA CGGAAAATCT CGGCTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 290; ORF 089.ng>:

```

g089.pep
1  MPPKITKSGF CKPAIAAAVA PTFVLLSSM NTTPFFSPIF STRCGKPWKV
51  LTCSSNASRG KPTASHKATA AITLAALCKP CSGMSCVEIK SSLPCFKQPV
101 PRSNQKSASC SKENRFTSRP ARFMARQNTS SAFKTCTPSP RKISALVCA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 291>:

```

m089.seq
1  ATGCCGCCCA AAATCACKAw GAGCGGATT TGC AAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA AACACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAAGCC TTGGAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG CCTCACACAA
201 AGCCACKGCA GCCATGACGT TAGCGGCGTT GTGCAKACCT TGCAACGGwA
251 TGTCTTGCGT GACAATCAAA TCTTCATTGC CTTGTTTCAG GCGGCCTGTC
301 TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA ACCATTTTAC
351 CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGGCTTGGT ATGCGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 292; ORF 089>:

```

m089.pep
1  MPPKITXSGF CKPAIAAAVA PTFVLLSSI NTTPFFSPIF STRCGRPWKV
51  LTCSSNASRD KPMASHKATA AMTLAALCXP CNGMSCVTIK SSLPCFRRPV
101 SRSNQKSASC SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 089 shows 88.6% identity over a 149 aa overlap with a predicted ORF (ORF 089.ng) from *N. gonorrhoeae*:

m089/g089

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	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPTFVPLLSSINTTPFFSPIFSTRCGRPWKVLTCSSNASRD					
	:       :       :       :       :					
g089	MPPKITXSGFCKPAIAAAVAPTFVPLLSSMNTTPFFSPIFSTRCGKPWKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRSNQKSASCSNENHFTSRP					
	:       :       :       :       :       :					
g089	KPTASHKATAAITLAALCKPCSGMSCVBIKSSLPCFKQPVPRSNQKSASCSKENRFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	:       :       :       :					
g089	ARFMARQNTSSAFKTCTPSPRKISALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 293>:

a089.seq

1	ATGCCGCTTA	AAATCACGAA	GAGCGGATTT	TGCAAACCGG	CAATCGCGGC
51	GGCGGTCGCA	CCGACGTTCT	TGCCTTTGCT	GTCGTCGATG	AACACCACGC
101	CATTTTCTC	GCCGATTTT	TCCACGCGGT	GCGGCAGGCC	TTGAAAGGTT
151	TTGACGTGTT	CGAGCAATGC	TTCGCGCGGC	AAACCGACGG	CTTCGCACAA
201	GGCAACGGCA	GCCATCACGT	TAGTGCGGTT	GTGCAAGCCT	TGCAGCGGAA
251	TATCTTGCGT	GGCAATCAAA	TCTTCATTGC	CTTGTTTCAG	GCGACCTGTC
301	TCACGTTCCA	ACCAAAAATC	GGCTTCGTAT	TCCAACGAAA	ACCATTTCAC
351	CTCGCGCCCG	GCGCGCTTCA	TCGCACGACA	GAACGCATCG	TCCGCATTCA
401	AAACCTGCAC	ACCGTCGCCA	CGGAAAATCT	TGGCTTTGGT	ATGCGCGTAG

This corresponds to the amino acid sequence <SEQ ID 294; ORF 089.a>:

a089.pep

1	MPPKITKSGF	CKPAIAAAVA	PTFVPLLSSM	NTTPFFSPIF	STRCGRP*KV
51	LTCSSNASRG	KPTASHKATA	AITLVALCKP	CSGISCSVAIK	SSLPCFRRPV
101	SRSNQKSASY	SNENHFTSRP	ARFIARQNAS	SAFKTCTPSP	RKILALVCA*

m089/a089 91.9% identity over a 149 aa overlap

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPTFVPLLSSINTTPFFSPIFSTRCGRPWKVLTCSSNASRD					
	:       :       :       :       :					
a089	MPPKITXSGFCKPAIAAAVAPTFVPLLSSMNTTPFFSPIFSTRCGRPXKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRSNQKSASCSNENHFTSRP					
	:       :       :       :       :       :					
a089	KPTASHKATAAITLVALCKPCSGISCSVAIKSSLPCFRRPVSRSNQKSASYSNENHFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	:       :       :       :					
a089	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 295>:

g090.seq

1	ATGCGCGTAG	TCGAGCAAAT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGAAA
---	------------	------------	------------	------------	------------

```

51  TGTTCATCAC CGTCGCCGCA GTCGGGCGCA GGCTTTCGGT GTTTTCAGT
101 TGGAAAGCTGG AAAGCTCcca CACCCACACG TCCGCCTTTT TGCCTTCgcg
151 ctgCAATtct gcctccaaga cgggcgtacc gatATTGCCC GCAATGAcgg
201 tatccagccc gcacttgatg CAGAGatagc ggaccaggct ggttaccgTG
251 GTTttgccgt tgctgCcggt aatcgCaatc accttgtcgC CGCGGCGGtt
301 cAcaaTGTcc gcccaGCAATt ggATGTCGCC TAgCACGCGC .ccgcccTTT
351 TGcttga

```

This corresponds to the amino acid sequence <SEQ ID 296; ORF 090.ng>:

```

g090.pep
1  MRVVEQIVVA VEMVFGNVHH RRRSRAQAFG VFQLEAGKLP HPHVRLFAFA
51  LQFCLQDGRT DIARNDGIQP ALDAEIADQA GYRGFAVAAG NRNHLVAAAV
101 HNVQQQLDVA XHAXRRFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 297>:

```

m090.seq
1  ATGCGCATAG TCGAGCAAGT CGTCGTAGCG GTCGAGATGG TCTTCGAAA
51  TGTTCAGCAC CGTCGCCGCA GTCGACGCA GGCTTTCGGT GTTTTCAGT
101 TGGAAAGCTGG AAAGCTCCAA CACCCACACG TCCGCCTTTT TGCCTTCGCG
151 CTGCCATTCC GCCTCCAAA CCGGCGTGCC GATATTGCC GCGATAACGG
201 TATCCAGCCC GCACTTGATA CAGAGATAGC CGACCAGGCT CGTTACCGTG
251 GTTTTGCCGT TGCTGCCGGT AATCGCAATT ACCTTGTCGT CCCGGCGGTT
301 CACAATGTCC GCCAGCAATT CGATGTCGCC CAACACGCGT .CCGCCGTTT
351 TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 298; ORF 090>:

```

m090.pep
1  MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
51  LPFRLQNRRA DIARNDGIQP ALDTEIADQA RYRGFAVAAG NRNYLVVPAV
101 HNVQQQFDVA QHAXRRFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 090 shows 83.9% identity over a 118 aa overlap with a predicted ORF (ORF 090.ng) from *N. gonorrhoeae*:

```

m090/g090

      10      20      30      40      50      60
m090.pep  MRIVEQVVVA VEMVFGNVQHRRRSRTQAFGVFQLEAGKLQHPHVRLFAFALPFRLQNRRA
||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
g090      MRVVEQIVVA VEMVFGNVHHRRRSRAQAFGVFQLEAGKLPHPHVRLFAFALQFCLQDGRT
      10      20      30      40      50      60

      70      80      90     100     110     119
m090.pep  DIARNDGIQPALDTEIADQARYRGFAVAAGNRNYLVVPAVHNVQQQFDVAQHAXRRFAX
||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
g090      DIARNDGIQPALDAEIADQAGYRGFAVAAGNRNHLVAAAVHNVQQQLDVAXHAXRRFAX
      70      80      90     100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 299>:

```

a090.seq
1  ATGCGCGTAG TCGAGCAAGT CGTCGTAGCG GTCGAGATGG TCTTCGAAA
51  TGTTCAGCAC TGTGCCGCA GTCGGGCGCA GGCTTTCGGT GTTTTCAGT
101 TGGAAACTGG AAAGCTCCAA CACCCACACG TCCGCCTTTT TGCCTTCGCG
151 CTGCAATTCC GCCTCCAAA CCGGCGCGCC GATATTGCC GCGATAACGG
201 TATCCAGCCC ACACTTGATG CAGAGATAGC CGACCAGGCT CGTTACCGTG
251 GTTTTGCCGT TGCTGCCGGT AATCGCAATC ACCTTGTCGC CGCGGCGGTT
301 CACAATGTCC GCCAGCAATT CGATGTCGCC CAACACGCGT C.CGCCGTTT
351 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 300; ORF 090.a>:

**a090.pep**

```

1 MRVVEQVVVA VEMVFGNVQH CRRSRAQAFG VFQLETGKLQ HPHVRLFAFA
51 LQFRLQNRRA DIARDNGIQP TLDAEIADQA RYRGFAVAAG NRNHLVAAAV
101 HNVRRQQFDVA QHAXRRFA*

```

**m09/a090** 91.5% identity over a 117 aa overlap

	10	20	30	40	50	60
m090.pep	MRIVEQVVVA	VEMVFGNVQH	RRRSRTQAF	GVFQLEAGKLQ	HPHVRLFAF	ALPFRLQNRRA
a090	MRVVEQVVVA	VEMVFGNVQH	CRRSRAQAF	GVFQLETGKLQ	HPHVRLFAF	ALQFRLQNRRA
	10	20	30	40	50	60

  

	70	80	90	100	110	119
m090.pep	DIARDNGIQPALDTEIADQ	ARYRGFAVAAGNRN	NYLVVPAVHNVR	QQFDVAQHAXRR	FFAX	
a090	DIARDNGIQPTLDAEIADQ	ARYRGFAVAAGNRN	NHLVAAAVHNVR	QQFDVAQHAXRR	FFAX	
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae*

g090-1.seq This sequence contains multiple stop codons (not shown)

This corresponds to the amino acid sequence < ORF 090-1.ng>:

g090-1.pep (not shown)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2>:

**m090-1.seq**

```

1 ATGACGGCGT TTGCATTCA GACGGCATCA CAAAGCCTTA AACGCTTCGA
51 TAAACACTTC CGAACGGTGC GCGTAGCCTT TGAACATATC AAAGCTCGCG
101 CAGGCGGGGC TGAGCAACAC AATATCGCCT GCTTCGGCTT GGGCATATGC
151 CGTCTGAACG GCTTCTCCCA AAGTGGCGCA GTCGGTCATA TTCAAGCCGC
201 AGCCGTCCAA ATCGCGGCGG ATTTGCGGCG CATCGACACC AATCAAGAAC
251 ACGCCTTTTG CCTTGCCTAC CAGTGCATCG CGCAGGGGCG TGAAGTCCTG
301 CCCTTTACCC ATGCCGCCCA AAATCACGAA GAGCGGATTT TGCAAACCGG
351 CAATCGCGGC GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA
401 AACACCACGC CGTTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC
451 TTGGAAGGTT TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG
501 CCTCACACAA AGCCACGGCA GCCATGACGT TAGCGCGGTT GTGCAGACCT
551 TGCAACGGAA TGTCTTGCGT GACAATCAA TCTTCATTGC CTTGTTTCAG
601 GCGGCCCTGT TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA
651 ACCATTTTAC CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG
701 TCCGCATTCA AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGGCTTTGGT
751 ATGCGCATAG TCGAGCAAGT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA
801 TGTTACGACG CGTCGCCGCA GTCGGACGCA GGCTTTCGGT GTTTTCCAGT
851 TTGGAAGCTG AAAGCTCCAA CACCCACACG TCCGCTTTT TGCCTTCGCG
901 CTGCCATTCC GCCTCCAAAA CCGCGGTGCC GATATTGCCG GCGATAACGG
951 TATCCAGCCC GCACTTGATA CAGAGATAGC CGACCAGGCT CGTTACCGTG
1001 GTTTTGCCGT TGCTGCCGGT AATCGCAATT ACCTTGTCGT CCCGGCGGTT
1051 CACAATGTCC GCCAGCAATT CGATGTCGCC CAACACGCGT CCGCCGTTTT
1101 GCTTGAACGC CTCATATACC GGCTGCCGCT CGCTGATGCC GGGACTGAGA
1151 GCCAGAATAT CGAAACCGTT GTCCAGCGCA TCTTTCAGAC GGCCCGTGTA
1201 AAACACCAAC CCGTCAAACA TCTTACCGAT TTGCGACACG CGTTCCGGCT
1251 TCAGTCCGCG ATCATACGCA GCAACCTCCG CGCCGTTTTT GCGCAGGTAG
1301 GCAATCATGG AAATACCCGT ACCGCCGAGT CCGGCGACGA GGATTTTTTT
1351 GTTTTGAAAA GTCATTTTGG TTTGTCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3; ORF 090-1>:

**m090-1.pep**

```

1 MTAFAFQTAS QSLKRFDKHF RTVRVAFEH I KARAGGAEQH NIACFGLGIC
51 RLNGFSQSGA VGHQAQAAVQ IAADLRRI DT NOEHAFCLAY QCIAQGREVL
101 PFTHAAQNHE ERIQTGNRG GSRADIRAF VVDKHHAVFL ADFFHAVRQA
151 LEGFDVFEQC FARQTDGLTQ SHGSHDVSGV VQTLQRNVLR DNQIFIALEQ
201 AACLAFAQE I SFVFQKPFY LAPGTLHRAA ERIVRIQNLH AVATENLGFG
251 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
301 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNHLVVPVAV
351 HNVRRQQFDVA QHASAVLLER LNIRLPLADA GTESQNIETV VQRIQFQARV
401 KHQPVKHLTD LRHAFRLQLR IIRSNLRAVF AQVGNHGNTR TAESGDEDDF
451 VLKSHFGLS*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 303>:

```
g091.seq
1  ATGGAAATAC CCGTGCCGCC AAGTCCGGCG ACGAGGATTT TTTTGTGTTGA
51  AAGTCATTTT GGTTTGTGCC TAAACAAAT CATATTGGGC AGGAGACGTC
101 CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCCG ATTAATAACC
151 CGCCTTCAGG CGTTGGTCAT TGTCGCAGCT GTTTTGGTCT CCGTTTGGAC
201 AAGCCTTGCC AAGCCATTGT TGAGCGAGCG CAAGGTCTTG GCGCACGCCG
251 CGTCCATCGT AATACATCAA GCCCAAATTG TATTGGGCTT GGGCATCCCC
301 TTGTTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 304; ORF 091.ng>:

```
g091.pep
1  MEIPVPPSPA TRIFLFESHF GFVLKQIILG RRRPPLPKPL SDGIASRLIT
51  RLQALVIVAA VLVSVLTSLA KPLLSEKVL  AHAASIVIHQ AQIVLGLGIP
101 LF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 305>:

```
m091.seq
1  ATGGAAATAC CCGTACCGCC GAGTCCGGCG ACGAGGATTT TTTTGTGTTGA
51  AAAGTCATTT TGGTTGTGCC TAAACAAAT CATATTGAGC AGGAGATGTC
101 CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151 CGCCTTCAGG CGTTGGTCAT TGTCGCAGCC GTCTTGGTCT CCGTTTGGAC
201 AAGCCTTGCC AAACATTCT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251 CGTCTTTCGG CATAATCAC GCCCAAATTG TTTTGGGCTT GGGCTACCCC
301 CTGCGC...
```

This corresponds to the amino acid sequence <SEQ ID 306; ORF 091>:

```
m091.pep
1  MEIPVPPSPA TRIFLFEKSF WFVLKQIILS RRCPLPKPL SDGIASCSIT
51  RLQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLGLGYP
101 LR.
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 091 shows 84.2% identity over a 101 aa overlap with a predicted ORF (ORF 091.ng) from *N. gonorrhoeae*:

m091/g091

	10	20	30	40	50	60
m091.pep	MEIPVPPSPATRIFLFEKSFWFVLKQIILSRRCPLPKPLSDGIASCSITRLQALVIVAA					
	:         :					
g091	MEIPVPPSPATRIFLFESHFGFVLKQIILGRRRPLPKPLSDGIASRLITRLQALVIVAA					
	10	20	30	40	50	60
	70	80	90	100		
m091.pep	VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAQIVLGLGYPLR					
	:  :      :   :					
g091	VLVSVLTSLAKPLLSEKVLHAHAASIVIHAQIVLGLGIPLFX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 307>:

```
a091.seq
1  ATGGAAATAC CCGTGCCGCC AAGTCCGGCG ACGAGGATTT TTTTGTGTTG
51  GAAATCATTT TGGTTGTGCC TAAACAAAT CATATTGAGC AGGGGATGTC
101 TGATCCTGCT CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151 CGCTTTCAGG CGTTGGTCAT TGTCGCAGCT GTCTTGGTAT CCGTTTGGAC
201 AAGCCTTGCC AAGCCATTCT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251 CGTCTTTCGG CATAATCAC GCCCAAATTG TTTTGGGC
```

This corresponds to the amino acid sequence <SEQ ID 308; ORF 091.a>:

a091.pep

```

1  MEIPVPPSPA TRIFLFWKSF WFLVKQIILS RGCLILLKPL SDGIASCSIT
51  RFQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLG

```

m091/a091 93.8% identity over a 96 aa overlap

```

              10      20      30      40      50      60
m091.pep      MEIPVPPSPATRIFLFEKSFWFVLKQIILSRRCPLPKPLSDGIASCSITRLQALVIVAA
               |||||
a091           MEIPVPPSPATRIFLFEKSFWFVLKQIILSRGCLILLKPLSDGIASCSITRFQALVIVAA
              10      20      30      40      50      60

              70      80      90      100
m091.pep      VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAQIVLGLGYPLR
               |||||
a091           VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAQIVLG
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 309>:

g092.seq

```

1  ATGTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGTGC GC
51  AACCGGTCAG ACCTTTAAAA TAACGCCTTT ACGCACTAAA AACCAACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTAA GCAACATCCA TTTTGTCCGT
151 ATCGGCGGCG TCGGCATGAG CCGTATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGAGCAGCCT GGGCATTCAA GTTATCCCG GCCATACCGC AGAACACGTT
301 AACGGTgcgg ATGTCGTCGT TGCCTCTACC GCCGTCAAGA AAGAAaatcc
351 CGAAGTtgtc gcTGC GTTGG AGCGGCAAAT TCCGTTATT CCGCGCGCCT
401 TGATGCTGCG AGAGCTGATG CGCTTCCGTG ACGgcatcgc cattgccggT
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTC GACCCCACTT TCGTTATCGG CGGCAAACTC AACGCCGCAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAATCCGATG CCTCTTTCCT ACATCTGACC CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTGTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGG CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GGC GCGCAA TGAAATTAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGc gtggcGTgg
1001 aagtcGgCGC ATcggttgAA GCGAtcCAA AaggCTTGCT CGGCTTTGAA
1051 GCGTCGGCC GCGCTTCCA AAAATAcggc gacatCAagt tgccaaacgg
1101 cggGaccgCT TTgttGGTGG ACGATTAcgg ACACCACCCC GTCGAAATGG
1151 CGGcaaccct tgccgcTGCA CGCGGCGCGT ATCCGAAAAA acgtTTGGTG
1201 CtgcCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAA GTACTCAATA CCGTTGatgC GCTGGTACTG ACCGAAGTTT
1301 AtgccgcccG CGAAGAGCCG GTTGCCGCCG CCGactcCCG CGCCTTGGCG
1351 CGTGCTATCC GCGTATTGGG CAAACTTGAG CCGATTACT GCGAAAatgt
1401 cgcgcACCTG CCGCAAATGC TGATGAATGT TTTACAGGAT Ggcgatgttg
1451 tgttgAATAT GggTgcggga agcatcaacc gcgttccttc cgcgctgttg
1501 gaattgtcga AACAGatttg A

```

This corresponds to the amino acid sequence <SEQ ID 310; ORF 092.ng>:

g092.pep

```

1  MFFISIRYIF VRKLWCANGQ TFKITPLRTK NQPERNIMMK NRVSNIHVFG
51  IGGVGMGSGIA EVLHNLGFKV SGSDQARNAA TEHLSSLGIQ VYPGHTAEHV
101 NGADV VVAST AVKKNPEVV AALERQIPVI PRALMLAELM RFRDGI AIAAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK

```



```

251 AFLCVDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP VAAADSRALA
451 RAIRVLGKLE PIYCENVADL PQMLMNVLQD GDVVLNMGAG SINRVPSALL
501 ELSKQI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 311>:

```

m092.seq
1 ATGTTT TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AAACGGTCAG CCCTTTAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTTA CCAACATCCA TTTTGTCCGT
151 ATCGGCGGCG TCGGCATGAG CGGCATCGCC GAAGTCTTGC ACAATTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGGGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC CGAACACGTT
301 AACGGTGCAG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACCT AACGCCGAG
551 GCACTAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGCGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 CGGGACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGGCGACCCT TGCCGCCGCA CGCGGCGCGT ATCTGAAAAA ACGTTTGTA
1201 CTCGCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAA GTCCTCAATA CCGTTGACGC GCTGGTCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCCGC CCGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTTGCAGGAC GCGGACATCG
1451 TGTTGAATAT GGGCGCGGGA AGCATCAACC GCGTCCCGC CGCGCTGCTG
1501 GCATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 312; ORF 092>:

```

m092.pep
1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFVG
51 IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKNPEVV AALEQQIPVI PRALMLAELM RFRDGIAG
151 THGKTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYLEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMGAG SINRVPAALL
501 ALSKQI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 092 shows 96.6% identity over a 506 aa overlap with a predicted ORF (ORF 092.ng) from *N. gonorrhoeae*:

m092/g092

```

10      20      30      40      50      60
m092.pep  MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVMSGIA

```

g092	MFFISIRYIFVRKLWCANGQTFKITPLRTKNQPERNIMMKNRVSNIHVFVIGGVGMSGIA	10	20	30	40	50	60
m092.pep	EVLHNLGFKVSGSDQARNAATEHLGSLGIQVYPGHTAEHVNAGDVVVTSTAVKKENPEVV	70	80	90	100	110	120
g092	EVLHNLGFKVSGSDQARNAATEHLSSLGIQVYPGHTAEHVNAGDVVVASTAVKKENPEVV	70	80	90	100	110	120
m092.pep	AALEQQIPVIPRALMLAELMRFRDGIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL	130	140	150	160	170	180
g092	AALERQIPVIPRALMLAELMRFRDGIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL	130	140	150	160	170	180
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID	190	200	210	220	230	240
g092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID	190	200	210	220	230	240
m092.pep	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV	250	260	270	280	290	300
g092	FIHRMPFYGKAFLCVDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV	250	260	270	280	290	300
m092.pep	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEVGAESVEAIQKGLLGFEVGRRFQKYG	310	320	330	340	350	360
g092	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEVGAESVEAIQKGLLGFEVGRRFQKYG	310	320	330	340	350	360
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLAFOPHRYTRTRDLFEDFTK	370	380	390	400	410	420
g092	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYPEKRLVLAFOPHRYTRTRDLFEDFTK	370	380	390	400	410	420
m092.pep	VLNTVDALVLTEVYAAGEEPIAAADSRLARAIRVLGKLEPIYCENVADLPEMLLNVLQD	430	440	450	460	470	480
g092	VLNTVDALVLTEVYAAGEEPVAAADSRLARAIRVLGKLEPIYCENVADLPQMLMNVLQD	430	440	450	460	470	480
m092.pep	GDIVLNMGAGSINRVPAALLALSQIX	490	500				
g092	GDVVLNMGAGSINRVPSALLELSQIX	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 313>:

**a092.seq**

```
1   ATGTTTAAAAA   TTTCAATCCG   CTATATATTT   GTCAGAAAAC   TATGGCGCGC
51  AAACGGTCAG   CCTTTAAAA   TAACGCCTTT   ACGCATCGAA   AATCCACCGG
101 AACGCAACAT   TATGATGAAA   AATCGAGTGA   CCAACATCCA   TTTTGTCTGGT
151 ATCCGCGGCG   TCGGCATGAG   CGGTATCGCC   GAAGTCTTGC   ACAATTTGGG
201 TTTTAAAGTT   TCCGTTTCGG   ATCAGGCGCG   AAATGCCGCT   ACGGAGCATT
251 TGGGCAGCCT   GGGCATTCAA   GTTTATCCCG   GCCATACCCG   AGCAACAGTT
```

```

301 AACGGTGC GG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACTC AACGCGCGAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGT GTTGAGAAGC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCGCAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CCGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGTGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 TGGAACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGCGCAGCCT TTCCGCGCGCA CGCGCGCGCT ATCCGGAAAA ACGTTTGTA
1201 CTCGCTTCC AGCCGCACCG CTATACCGCG ACGCGCGATT TGTTGAAGA
1251 CTTTACCAA GTCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CTGATTCGCC CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTTGCAGGAC GGCACATCG
1451 TGTGAATAT GGGTGCGGGA AGCATCAACC GCGTCCCCGC CGCGCTGCTG
1501 GAATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 314; ORF 092.a>:

**a092.pep**

```

1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFGV
51 IGGVGMGSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKNPEVV AALEQQIPVI PRALMLAELM RFRDGIAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 VGVRFRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLSAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMAG SINRVPAALL
501 ELSKQI*

```

**m092/a092** 99.4% identity over a 506 aa overlap

	10	20	30	40	50	60
m092.pep	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMGSGIA					
a092	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMGSGIA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m092.pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKNPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKNPEVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m092.pep	AALEQQIPVI PRALMLAELMRFRDGIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
a092	AALEQQIPVI PRALMLAELMRFRDGIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					

292

	190	200	210	220	230	240
m092.pep	250	260	270	280	290	300
a092	250	260	270	280	290	300
m092.pep	310	320	330	340	350	360
a092	310	320	330	340	350	360
m092.pep	370	380	390	400	410	420
a092	370	380	390	400	410	420
m092.pep	430	440	450	460	470	480
a092	430	440	450	460	470	480
m092.pep	490	500				
a092	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 315>:

g093.seq

```

1  aTGCAGAAAtt ttgGCAAAGT ggccgtATTG ATGGGtggtT TTTCCAGCGA
51  ACGAGAAatc tcgcTGGACA GCgGTACCGC CATTTTGAAC GCCTTAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGACC CTAAGGAAAC GCCGTTATCC
151 GAACTGAAGG AGCGGGGCTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAACCTG TTGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCCTCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTACCCGTC CCGAGTTCGC
351 CGTACTGTAC GATGATACCG ATTTCGATGC CGTCGAAGAA AAATTGGGTC
401 TGCCGATGTT TGTGAAGCCG GCGGCCGAAG GCAGCAGCgt cggcgtggta
451 aaAGTCAAAG AAAaaggccg TCTGAAAAGC GTTtacgaag aatTGAAaCA
501 CTTcagggg cgaAAtcatt gccgAacgTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCGG TCCTGAACGG CAAAGGGCTG CCCGGCATAC ACATCATCCC
601 CGCAACCGAG TTTTACGAct acgaagccaa GtacaacCGA GACGAcacca
651 tttatCAATG TCCTTCGGAA GATTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTCGCGG CGCACAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 316; ORF 093.ng>:

g093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKERGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLY DDTDFDAVEE KLGLPMFVKP AAEGLSSVGVV
151 KVKEKGR LKS VYEELKHLQG RNHCRTFYRR RRIFLPRPER QRAARHTHP
201 RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS RRTGNRCGR LR
251 ARRFPRQYRR QTLVSGNQHP ARYDRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 317>:

m093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CTAAAGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCfAA GACGGGGCGG TTCAGGGTGC ATTGGAAGTGTG TGGGGCATTTC
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTTCGATGC CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CCTTCAGGG. CGAAATCATT GCCGAACGTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATAAC ACATCATTCC
601 CGCAACCGAG TTTTACGACT ACGAAGCCAA GTACAACCGC GACGACACCA
651 TTTATCAATG TCCTTCGGAA GATTTCGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTCGCGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACGAGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 318; ORF 093>:

m093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGX DGA VQGALEL LGIPYTGSGV AASAI GMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAE GSSVGVV
151 KVKGKGR LKS VYEELKHLQX RNHCRTFYRR RRI FLPRPER QRAARH THS
201 RNRVLR LRSQ VQPRRHLSM SFRFRDRSRR KPDARTGGS RAGNR CGRLR
251 ARRFQRYRR QTL SVGNQHP ARYDEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 093 shows 96.7% identity over a 276 aa overlap with a predicted ORF (ORF 093.ng) from *N. gonorrhoeae*:

m093/g093

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKAQGFQTA					
g093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKERGFQTA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m093.pep	FNILHGTYGX DGA VQGALELL LGIPYTGSGV AASAI GMDKY RCKLIWQAL GLPVPEFAVLH					
g093	FNILHGTYGED GAVQGALELL LGIPYTGSGV AASAI GMDKY RCKLIWQAL GLPVPEFAVLV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m093.pep	DDTDFDAVEE KLGLPMFVKP AAE GSSVGVV KVKGKGR LKS VYEELKHLQX RNHCRTFYRR					
g093	DDTDFDAVEE KLGLPMFVKP AAE GSSVGVV KVKGKGR LKS VYEELKHLQX RNHCRTFYRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m093.pep	RRI FLPRPERQRAARH THSRNRVLR LRSQVQPRRHLSM SFRFRDRSRR KPDARTGGS R					
g093	RRI FLPRPERQRAARH THSRNRVLR LRSQVQPRRHLSM SFRFRDRSRR KPDARTGGS R					
	190	200	210	220	230	240
	250	260	270			
m093.pep	RAGNR CGRLR ARRFQRYRR QTL SVGNQHP ARYDEPX					
g093	RTGNRCGRLR ARRFQRYRR QTL SVGNQHP ARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 319>:

## a093.seq

```

1  ATGCAGAAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CCAAGGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAAGT TTGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGCGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCTGCAC GACGACACTG ATTTTCGATG CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTACGAAG AATTGAAACA
501 CTTTCAGGG. CGAAATCATT GCCGAACGGT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCTG TGTGAAACCG CAAAGGCCTG CCCGGCATA ACATCATCCC
601 CGCGACCGAG TTTTATGACT ACGAAGCCAA GTACAACCGC AACGACACCA
651 TTTATCAATG TCCTTCGGAA GATCTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGAAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 320; ORF 093.a>:

## a093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGE DGA VQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAE GSSVGVV
151 KVKGKGR LKS VYEELKHFQX RNHCRTVYRR RRIFLPCVER QRP ARH THHP
201 RDRVL* LRSQ VQPQRHLSM SFG RSDRSRR KPDARTGGS RAGNRCGR LR
251 ARRF PQRYRR QTL SVGNQHP ARYDRP*

```

m093/a093 95.7% identity over a 276 aa overlap

m093.pep	10	20	30	40	50	60
a093	10	20	30	40	50	60
m093.pep	70	80	90	100	110	120
a093	70	80	90	100	110	120
m093.pep	130	140	150	160	170	180
a093	130	140	150	160	170	180
m093.pep	190	200	210	220	230	240
a093	190	200	210	220	230	240
m093.pep	250	260	270			
a093	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 321>:

g094.seq

1	ATGTATTTCG	CTTTGCCCAA	GCGGGCGTTG	GTGCCTGCGG	CGTTGAGTTT
51	GCCGCCGATA	ACGAAAGTCG	GGTCGAGTCC	TGCCCGCGCG	AGGATGGAGG
101	CGGTCAGGCT	GGTGGTCTGT	GTTTTCGCGT	CCGTAccggc	aatggcgatg
151	cCGTCACGGA	AGCGCATCAG	CTCTGCCAGC	ATCAAGGCGC	GCGGAATAAC
201	GGGAATTTCG	CGCTCCAACG	CAGcgacaAC	TTCGGgattT	TCTTCTTGA
251	CGGCGGTAGA	GGCAACGACG	ACATccgcAC	CGTTAACGTG	TTCTGCGGTA
301	TGGCCGGGAT	AA			

This corresponds to the amino acid sequence <SEQ ID 322; ORF 094.ng>:

g094.pep  
1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM  
51 PSRKRISSAS IKARGITGIC RSNAATTSGF SFLTAVEATT TSAPLTCSAV  
101 WPG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 323>:

```
m094.seq
1  ATGTATTTCG  CTTTGCCCAA  GCGGGCGTTA  GTGCTGCGG  CGTTGAGTTT
51  GCCCGCCGAT  ACGAAAGTCG  GGTCAAGTCC  TGCCGCGCCG  AGGATAGGAG
101 CGGTACGGCT  GGTGGTCGTG  GTTTTGCCCT  GCGTGCCCGC  AATGGCGATG
151 CCGTCACGGA  AGCGCATCAA  CTCGCCAAC  ATCAGGGCGC  GCGGAATAAC
201 GGGAAATTGC  TGCTCCAACG  CAGCGACAAC  TTCGGGATTT  TCTTTTTTGA
251 CGCGCGTAGA  GGTAACGACG  ACATCCGCAG  CGTTAACGTG  TTCGGCGGTA
301 TGGCCGGGAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 324; ORF 094>:

```
m094.pep
1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKRINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101 WPG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 094 shows 95.1% identity over a 103 aa overlap with a predicted ORF (ORF 094.ng) from *N. gonorrhoeae*:

m094/q094

```

      10      20      30      40      50      60
m094.pep  MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRINSAN
          |||||
g094      MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRISAS
          |||||

      70      80      90     100
m094.pep  IRARGITGICCSNAATTSGFSFLTAVEVTTTTSAPLTCSAVWPGX
          :|||
g094      IKARGITGICRSNAATTSGFSFLTAVEATTTSAPLTCSAVWPGX
          |||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 325>:

```

a094.seq
1  ATGTATTTCG  CTTTGCCCAA  GCGGGCGCTG  GTGCTGCGG  CGTTGAGTTT
51  GCGCCGCGAT  ACGAAAGTCG  GGTCAAGTCC  TGCCGCGCCG  AGGATGAGAG
101 CGGTCAGGCT  GGTGTCGTG  GTTTTGCCGT  GCGTGCCCGC  AATGGCCGATG
151 CCGTCACGGA  AGCGCATCAA  CTCGCCAAC  ATCAGGGCGC  GCGGAATAAC
201 GGGAAATTGC  TGCTCCAACG  CAGCGACAAC  TTCGGGATT  TCTTTTTTGA
251 CGGCGGTAGA  GGTAACGACG  ACATCCGCAC  CGTTAACGTG  TTCTGCGGTA
301 TGGCCGGGAT  AA

```

This corresponds to the amino acid sequence <SEO ID 326; ORF 094.a>:

## a094.pep

```

1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101 WPG*

```

m094/a094 100.0% identity over a 103 aa overlap

```

              10      20      30      40      50      60
m094.pep  MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKINSAN
          |||
a094      MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKINSAN
              10      20      30      40      50      60

              70      80      90      100
m094.pep  IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
          |||
a094      IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 327>:

```

g095.seq
1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
51  TTTGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAATC GCGCGGACGT GTTCGCTGTC
151 AACACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGGGTCA GTGTAGGAAA
301 GAGGCATCGG ATCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351 CGGGCGTTGG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 328; ORF 095.ng&gt;:

```

g095.pep
1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCCKR
101 EASDRRLRQR CIRLCPGRW CLRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 329>:

```

m095.seq
1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
51  TTTGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351 CGGGCGTTAG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 330; ORF 095&gt;:

```

m095.pep
1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCCKR
101 DASDRRLRQR CIRLCPGRX CLRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 095 shows 97.6% identity over a 124 aa overlap with a predicted ORF (ORF 095.ng) from *N. gonorrhoeae*:

m095/g095

```

              10      20      30      40      50      60
m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
          |||

```



297

```

g095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
g095      HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKEASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
g095      CLRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 331>:

```

a095.seq
1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTGTC GCGCCGACGT
51  TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CACACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGCTTC TCAACACTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTGCC TTTGCCCAAG
351 CGGGCGTTGG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 332; ORF 095.a>:

```

a095.pep
1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQLLNTVPVG IHMFVDIGN DGHNRCQCRK
101 DASDRRLRQR CIRLCPSGRW CLRR*

```

m095/a095 96.0% identity in 124 aa overlap

```

           10      20      30      40      50      60
m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           |||||
a095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
a095      HTVDEIDKRLMQLLNTVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
a095      CLRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 333>:

```

g096.seq
1  ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGTGCGC CGCGAACCGC CAGTTCGCGC ATCAGGCTTT CTCGGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGataaat ggtgTCGTCT CGGttgtact

```

```

201  tggcttcgta gTCGTAAAC TCGGTGCGG GGATGATGTG TATGCCGGGC
251  AGCCCTTTGC CGTTCAGGAC GGGGCAGGAA TATTCGCCGC CGCCGATAAA
301  AcgtTcggca atgaTTtcgc ccctgAAGGT GttTCAattc ttcgtaAACG
351  CTTTTCAGAc ggccttTTTC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 334; ORF 096.ng>:

**g096.pep**

```

1  MAGHTGQGVDFQQIEFAVGI FEEIDAHAAF RTDCLCAANR QFAHQAFFGF
51  GQIFRRTLIN GVVSVVLGFV VVKLGCGDDV YAGQPFQAVQD GAGIFAAADK
101 TFGNDFAPEG VSILRKRFSD GLFL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 335>:

**m096.seq**

```

1  ATGGCTCGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGCGCGC CGCGAACC GCAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGATAAAT GGTGTCGTCG CGGTTGTA
201 TGGCTTCGTA GTCGTAAAC TCGGTGCGG GAATGATGTG TATGCCGGGC
251 AGCCCTTTGC CGTTCAGGAC GGGGCAGGAA TATTCGCCGC CGCCGATAAA
301 ACGTTCGGCA ATGATTTCGC CC.TGAAGGT GTTCAATTC TTCGTAAACG
351 CTTTTCAGAC GGCCTTTTCC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 336; ORF 096>:

**m096.pep**

```

1  MARHTGQGVDFQQIEFAVGI FEEIDAHAAF RTDCLRAANR QFAHQAFFGF
51  GQIFRRTLIN GVVAVVLGFV VVKLGCGNDV YAGQPFQAVQD GAGIFAAADK
101 TFGNDFAXEG VSILRKRFSD GLFL*

```

**m096/g096** 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGI	FEEIDAHAAFRTDCLRAANR	QFAHQAFFGFGQIFRRTLIN			
g096	MAGHTGQGVDFQQIEFAVGI	FEEIDAHAAFRTDCLCAANR	QFAHQAFFGFGQIFRRTLIN			
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDV	YAGQPFQAVQDGAGIFAAADK	TFGNDFAXEGVSILRKRFSD			
g096	GVVSVVLGFVVVKLGCGDDV	YAGQPFQAVQDGAGIFAAADK	TFGNDFAPEGVSILRKRFSD			
	70	80	90	100	110	120
m096.pep	GLFLX					
g096	GLFLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 337>:

**a096.seq**

```

1  ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGCGCGC CGCGAACC GCAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151 GGTCAATCT TCCGAAGGAC ATTGATAAAT GGTGTCGTTG CGGTTGTA
201 TGGCTTCGTA GTCATAAAC TCGGTGCGG GGATGATGTG TATGCCGGGC
251 AGGCCTTTGC CGTTCAACAC AGGGCAGGAA TATTCGCCGC CGCCGATAAA
301 CCGTTCGGCA ATGATTTCGC CCT.GAAAGT GTTCAATTC TTCGTAAACG
351 CTTTTCAGAC GGCCTTTTCC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 338; ORF 096.ng>:

**a096.pep**

```

1  MAGHTGQGVDFQQIEFAVGI FEEIDAHAAF RTDCLRAANR QFAHQAFFGF

```

51 GQIFRRTLIN GVVAVVLGFV VIKLGRGDDV YAGQAFVQH RAGIFAAADK  
 101 PFGNDFAXES VSILRKRFSD GLFL\*

m096/a096 92.7% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGIFEEIDAHAAFR	TDCLRAANRQFAHQAFFGFGQIFRRTLIN				
a096	MAGHTGQGVDFQQIEFAVGIFEEIDAHAAFR	TDCLRAANRQFAHQAFFGFGQIFRRTLIN				
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDVYAGQPF	FAVDGAGIFAAADKTFGNDFA	EGVSILRKRFSD			
a096	GVVAVVLGFVVIKLGRGDDVYAGQAF	VQHRAGIFAAADKPF	GNDFAXESVSILRKRFSD			
	70	80	90	100	110	120
m096.pep	GLFLX					
a096	GLFLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 339>:

g097.seq

```

1  ATGGATATTT CAAACAAAC ATTGCTGGAT AGGGTTTTTA ACCTGAAGGC
51  AACGGTACG ACGGTACGTA CCGAGTTGAT GGCGGGTTTG ACGACCTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAATC CCCTGATTTT GGGCGAGACC
151 GGAATGGATA TGGGGCGGT ATTCGTCGCT ACCTGTATCG CATCCGCCAT
201 CGGCTGTTTT GTCATGGGTT TTATCGGCAA CTATCCGATT GCGCTTGCCC
251 CGGGGATGGG GCTGAATGCC TATTTCACTT TTGCCGTCGT TAAGGGTATG
301 GCGGTGCCTT GGCAGGTGGC GTTGGGTGCG GTGTTCACTT CCGGTCTGAT
351 TTTTCATCTG TTCAGCTTTT TTAAAGTCAG GGAATGCTG GTCAACGCAC
401 TGCCTATGGG TTTGAAATG TCGATTGCCG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTGTCCA ATCCGGCAAC
501 CTTGTCGGC TTGGGCGATA TTCATCAGCC CAGCGCACTG TTGGCATTGT
551 TCGGTTTTGT CATGGTGGTC GTATTGGGGT ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATTCTGAC GATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAACGAGTTT CACGGCGTGG TCGGCGAAGT ACCGGGCATT GCGCCGACCT
701 TTATGCAGAT GGATTTTAAA GGTCTGTTA CCGTCAGCAT GGTGACGCTG
751 ATTTTCGTCT TCTTCTGGT CGATTGTTC GACAGTACCG GAACGCTGGT
801 CGGCGTATCC CACCGTGCCG GACTGCTGGT GGACGGTAAG CTGCCCCGCC
851 TGAAACGCGC ACTGCTTGCA GACTCTACCG CCATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTTCAACCAC GCCTTATGTG GAAAGCGCGG CGGGCGTATC
951 GGCAGGCGGA CGGACCGGCC TGACGGCGGT TACCGTCGGC GTATTGATGC
1001 TGGCGTGTCT GATGTTCTCC CCATTGGCGA AAAGTGTTC GGTATTTGCC
1051 ACCGCGCCCC CACTGCTTTA TGTGCGCACG CAGATGCTCC GCAGTGCGAG
1101 GGACATTGAT TGGGACGATA TGAAGTGAAG CGCGCCCGCG TTCCTGACCA
1151 TTGTCTTCAT GCCGTTTACC TATTCGATTG CAGACGGCAT CGCCTTCGGC
1201 TTCATCAGCT ATGCCGTTG CAAACTTTTG TGTGCGCGGA CTGGGGACGT
1251 GCCGCTATG GTATGGGTTG TTGCCGTATT GTGGGCATTG AAATTCTGGT
1301 ATTTGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 340; ORF 097.ng>:

g097.pep

```

1  MDISKQTLDD RVFNLKANGT TVRTELMAGL TTFLTMCYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFIGNYPI ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFVMV VLGYFRVQGA
201 IIITILTITV IASLMGLNEF HGVVGEVPGI APTFMQMDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPVFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG

```

401 FISYAVVKLL CRRTGDVPPM VWVAVLWAL KFWYLG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 341>:

m097.seq

```

1 ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51 AAACGGTACK ACGGTGCGTA CCGAGTTGAT GGCGGGTTTG ACAACTTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCyGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGGCGGT ATTCGTCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGGATGGG GCTGAATGCC TATTTACCTT TTGCCGTCGT TAAGGGTATG
301 GGC GTGCCTT GGCAGGTTGC GTTGGGTGCG GTGTTTCATCT CCGGTCTGAT
351 TTTTATCCTG TTCAGCTTTT TTAAGTTCAG GAAATGCTG GTCAAACGCAC
401 TGCCTATGGG TTTGAAAATG TCGATTGCTG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTCGGT TTGGGCGATA TTCATCAGCC GTCCGCGTTG TTGGCATTGT
551 TCGGTTTTGC TATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATCTTGAC CATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAATGAATTT CACGCGATCA TCGGCGAAGT ACCGAGCATT GCGCCGACTT
701 TTATGCAGAT GGATTTTGAA GGCCTGTTTA CCGTCAGCAT GGTCAGTGTG
751 ATTTTCGTCT TCTTCTTGGT CGATCTATTT GACAGTACCG GAACGCTGGT
801 CGGCATATCC CACCGTGCCG GGCTGCTGGT GGACGGTAAG CTGCCCGGCC
851 TGAACGCGC ACTGCTTGCA GACTCTACCG CCATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTTCCACCAC GCCTTATGTG GAAAGCGCGG CGGGCGTATC
951 GGCAGGCGGA CGGACCGGCC TGACGCGGCT TACCGTCGGC GTATTGATGC
1001 TCGCCTGCCT GATGTTTTCA CCTTTGGCGA AAAGTGTTCC CGCTTTTGCC
1051 ACCGCGCCCG CCCTGCTTTA TGTCGGCACG CAGATGCTCC GCAGTGCAG
1101 GGATATTGAT TGGGACGATA TGACGGAAGC CGCACCTGCG TTCCTGACCA
1151 TTGTTTTTCAT GCCGTTTACT TATTCGATTG CAGACGGCAT CGCTTTCCGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCGCCGCA CCAAAGACGT
1251 TCCGCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCTGGT
1301 ATTTGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 342; ORF 097>:

m097.pep

```

1 MDTSKQTLDD GIFKLKANGT TVRTELMAGL TTFLTCYIV IVNPXILGET
51 GMDMGAVFVA TCIASAIGCF VMGFVGNYP IALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFE GLFTVSMVSV
251 IFVFLVDLF DSTGTLVGIS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAFTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDMTEAAPA FLTIVFMFFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVP PM VWIIVAVLWAL KFWYLG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 097 shows 96.3% identity over a 436 aa overlap with a predicted ORF (ORF 097.ng) from *N. gonorrhoeae*:

m097/g097

	10	20	30	40	50	60
m097.pep	MDTSKQTLDDGIFKLKANGTTVRTELMAGLTTFLTCYIVIVNPXILGETGMDMGAVFVA					
	:					
g097	MDISKQTLDDRNFNLKANGTTVRTELMAGLTTFLTCYIVIVNPXILGETGMDMGAVFVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m097.pep	TCIASAIGCFVMGFVGNYP IALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	:					
g097	TCIASAIGCFVMGFIGNYP IALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	70	80	90	100	110	120
	130	140	150	160	170	180

m097.pep	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL
g097	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL
	130 140 150 160 170 180
m097.pep	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGIIGEVPSIAPTTFMQMDFE
g097	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGVVGEVPGIAPTTFMQMDFK
	190 200 210 220 230 240
m097.pep	GLFTVSMVSVIFVFFLVDFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIIVAGAA
g097	GLFTVSMVSVIFVFFLVDFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIIVAGAA
	250 260 270 280 290 300
m097.pep	LGTSSSTPPYVESAAGVSAGGRGLTAVTVGVMLACLMPSPAKSVPAFATAPALLYVGT
g097	LGTSSSTPPYVESAAGVSAGGRGLTAVTVGVMLACLMPSPAKSVPAFATAPALLYVGT
	310 320 330 340 350 360
m097.pep	QMLRSARDIDWDDMTAAAPFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM
g097	QMLRSARDIDWDDMTAAAPFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTGDVPPM
	370 380 390 400 410 420
m097.pep	VWIVAVLWALKFWYLGX
g097	VWVAVLWALKFWYLGX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 343>

a097.seq

```

1  ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51  AACGGTACG ACGGTGCGTA CCGAGTTGAT GCGGGGTTTG ACAACTTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCTGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGGCGGT ATTCGTCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGATGGG GCTGAATGCC TATTACACCT TTGCCGTCGT TAAGGGTATG
301 GCGGTGCCTT GGCAGGTTGC GTTGGGTGCG GTGTTCATCT CCGGTCTGAT
351 TTTCATCCTG TTCAGCTTTT TTAAAGTCAG GGAAATGCTG GTCAACGCAC
401 TGCCTATGGG TTTGAAAATG TCGATTGCTG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTTCGC TTGGGCGATA TTCATCAGCC GTCCGCGTTG TTGGCACTGT
551 TCGGTTTTGC CATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATTTTGAC GATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAACGAATTT CACGGCATCA TCGGCGAAGT GCCGAGCATT GCGCCGACTT
701 TTATGCAGAT GGATTTTAAA GGGTTGTTTA CCGTCAGCAT GGTGAGCTGT
751 ATTTTCGTCT TTTTCTAGT CGATCTGTTT GACAGTACCG GAACACTGGT
801 CGGTGTATCG CATCGTGCCG GACTGCTGGT GGACGGTAAG CTGCCCGGCC
851 TGAACGCGC ACTGCTTGCA GACTCTACCG CTATTGTGGC AGGTGCGGCT
901 TTGGTACTT CTTCAACCAC GCCTTATGTG GAAAGTGCGG CGGCGGTATC
951 GGCAGGCGGG CGGACAGGTC TGACGGCGGT TACCGTCGGC GTATTGTATG
1001 TCGCCTGCCT GATGTTTTCA CCTTTGGCGA AAAGTGTTCC CGCTTTTGCC
1051 ACCGCGCCCG CCCTGCTTTA TGTCGGCAGC CAGATGCTCC GCAGTGCGAG
1101 GGACATCGAT TGGGACGATA TGACGGAAGC CGCACCCGCA TTCCTGACCA
1151 TTGTCTTCAT CCGGTTTACC TATTCGATTG CAGACGGCAT CGCTTTCGGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCGCGGCA CCAAAGACGT
1251 TCCGCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCTGGT

```

1301 ATTTGGGCTG A

This corresponds to the amino acid sequence &lt;SEQ ID 344; ORF 097.a&gt;:

a097.pep

```
1  MDTSKQTLLD GIFKLGKANGT TVRTELMAGL TTFLTMCYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP I ALAPGMGLNA YTFFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVPPM VWIVAVLWAL KFWYLG*
```

m097/a097 99.3% identity in 436 aa overlap

m097.pep	10	20	30	40	50	60
	MDTSKQTLLDGIFKLGKANGTTVRTELMAGLTTFLTMCYIVIVNPNILGETGMDMGAVFVA					
a097	MDTSKQTLLDGIFKLGKANGTTVRTELMAGLTTFLTMCYIVIVNPLILGETGMDMGAVFVA					
	10	20	30	40	50	60
m097.pep	70	80	90	100	110	120
	TCIASAIGCFVMGFVGNYPALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
a097	TCIASAIGCFVMGFVGNYPALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	70	80	90	100	110	120
m097.pep	130	140	150	160	170	180
	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
a097	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
	130	140	150	160	170	180
m097.pep	190	200	210	220	230	240
	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGIIGEVPSIAPTFMQMDFE					
a097	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGIIGEVPSIAPTFMQMDFK					
	190	200	210	220	230	240
m097.pep	250	260	270	280	290	300
	GLFTVSMVSVIFVFFLVDLFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA					
a097	GLFTVSMVSVIFVFFLVDLFDSTGTLVGVS HRAGLLVDGKLPRLKRALLADSTAIVAGAA					
	250	260	270	280	290	300
m097.pep	310	320	330	340	350	360
	LGTSSTTPYVESAAGVSAGGRTGLTAVTVGVMLACLMFSPLAKSVPAFATAPALLYVGT					
a097	LGTSSTTPYVESAAGVSAGGRTGLTAVTVGVMLACLMFSPLAKSVPAFATAPALLYVGT					
	310	320	330	340	350	360
m097.pep	370	380	390	400	410	420
	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM					
a097	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM					
	370	380	390	400	410	420
m097.pep	430					
	VWIVAVLWALKFWYLGX					
a097	VWIVAVLWALKFWYLGX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 345>:

```
g098.seq
  1  ATGACCGCCG  ACGGTCTCTT  CGTCGCTTTC  AACTTCAATA  CGTTTGCCGT
 51  TGTGCGAATA  TTGATACCAG  TACAGCAGGA  TGCTGCCAG  GCTGGCGATC
101  AGTTTGTCCG  CGATGTCGCG  CGCTTCGCTG  TCGGGATGGC  TTTCGCGTTC
151  GGGATGAACG  CAGCCGAGCA  TGGACACGCC  GGTACGCATC  ACGTCCATCG
201  GATGGGTATG  TGCAGGCAGG  CTTTCCAAAA  CTTTAATCAC  ACGGATAGGC
251  AGGCCGCGCA  TGGATTGAG  CTTGGTTTTA  TAAGCGGCCA  GCTCGAATTT
301  GTTGGGCAGA  TGGCCGTGAA  TCAGCAAGTG  TCGACTTCT  TCAAACTCGC
351  ATTTTGTGTC  CAAATTAGAA  TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 346; ORF 098.ng>:

```
g098.pep
  1  MTADGLFVAF  NFNTFAVVRI  LIPVQDAAQ  AGDQFVGDDVA  RFAVGMAFAF
 51  GMNAAEHGHA  GTHVHRMGM  CRQAFQNFH  TDRQAAHGFE  LGFISGQLEF
101  VGQMAVNQQV  CDFKLAFLC  QIRMS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 347>:

```
m098.seq
  1  ATGACCGCCG  ATGGTCTCTT  CGTCGCTTTC  AACCTCAATG  CGTTTGCCGT
 51  TGTGCGAATA  TTGATACCAG  TACAAGAGGA  TGCTGCCAG  GCTGGCGATC
101  AGTTTGTCCG  CGATGTCGCG  CGCTTCACTT  TCCGGATGGC  TTTCACGTTC
151  AGGATGAACG  CAGCCCAGCA  TGGATACGCC  GGTACGCATT  ACGTCCATCG
201  GATGGGTATG  TGCAGGCAGG  CTTTCCAAAA  CTTTAATCAC  ACGGATAGGC
251  AGGCCGCGCA  TGGATTGAG  CTTGGTTTTA  TAAGCGGCCA  GCTCGAATTT
301  GTTGGGCAGA  TGGCCGTGAA  TCAGCAGGTG  GCGACTTCT  TCAAACTCGC
351  ATTTTGTGTC  CAAATCAGAA  TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 348; ORF 098>:

```
m098.pep
  1  MTADGLFVAF  NLNAFAVVRI  LIPVQEDAAE  AGDQFVGDDVA  RFTFRMAFTF
 51  RMNAAQHGYA  GTHVHRMGM  CRQAFQNFH  TDRQAAHGFE  LGFISGQLEF
101  VGQMAVNQQV  GDFKLAFLC  QIRMS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 098 shows 89.6% identity over a 125 aa overlap with a predicted ORF (ORF 098.ng) from *N. gonorrhoeae*:

```
m098/g098

      10      20      30      40      50      60
m098.pep  MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA
          |||:|||||:|||||:|||||:|||||: |||: |||: |||:
g098      MTADGLFVAFNFNTFAVVRI LIPVQDAAQAGDQFVGDDVARFAVGMAFAFGMNAAEHGHA
          10      20      30      40      50      60

      70      80      90     100     110     120
m098.pep  GTHVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQVGDFFKLAFLC
          |||:|||||:|||||:|||||:|||||: |||: |||: |||:
g098      GTHVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQVCDFFKLAFLC
          70      80      90     100     110     120

m098.pep  QIRMSX
          |||||
g098      QIRMSX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 349>:

```
a098.seq
  1  ATGACCGCCG  ATGGTCTCTT  CGTCGCTTTC  AACCTCAATG  CGTTTGCCGT
 51  TGTGCGAATA  TTGATACCAG  TACAAGAGGA  TGCTGCCAG  GCTGGCGATC
```

304

```

101 AGTTTGTCGG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTGAG CTTGGTTT TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GCGACTTCT TCAAACTCGC
351 ATTTTGTGC CAAATCAGAA TGTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 350; ORF 098.a>:

a098.pep

```

1 MTADGLFVAF NLNAFAVVRI LIPVQEDAAE AGDQFVGDDA RFTFRMAFTF
51 RMNAAQHGYA GTHYVHRMGM CRQAFQNFH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*

```

m098/a098 100.0% identity in 125 aa overlap

	10	20	30	40	50	60
m098.pep	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARETFRMAFTFRMNAAQHGYA					
a098	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARETFRMAFTFRMNAAQHGYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m098.pep	GTHYVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQV GDFFKLAFLC					
a098	GTHYVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQV GDFFKLAFLC					
	70	80	90	100	110	120
m098.pep	QIRMSX					
a098	QIRMSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 351>:

g099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTGGA
51 GCTGACGGGC AAACGCGCAGG CGGGCATTAC TGCCACAGAC ATCGTGTGG
101 CACTGACCGA ATTCTTGCGT AAAGAGCGCG TGGTCGGGGC GTTTGTGCGAA
151 TTTTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGAGT TCGGCGCGAC TGCCGCCATG TTCGCCATCG
251 ACGCGCAAAC TATTGATTAT TTGAACTGA CCGGACGTGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTAT GGGCAGGTGG
351 CTTGAAAACC GCCGTTTATC CGCGCGTTTT GAAATTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCCACC
451 GCCGATTGG CCGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCGTGTA
551 CCAATACTTC CAACCCGCGC AACGTTGTCG CCGCCGCACT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GAAACGCAA CTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGGAATCTA TTTGAAAGAA GCAGGCTTGT
701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAgcgG CGCGCTCgaC CCGAAAATCC AACAAGAAAT
801 CATCGACCGC GAttgtacg cCACCGCCGT ATTGTCAGGC AACCGCAACT
851 TCGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCCT
901 CCTTTGGTCG TTGCCTACGC ATTGGCAGGT AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCCG CGAAATCCGC CTGAAAGATA
1001 TCTGGCCGAC AGACGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAACAAT TCCGCGACAT TTATATCCCG ATGTCGACAC CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCGCG TGTACGACTG GCGACCGATG TCCACCTACA
1151 TCCGCGGTCC GCCCTATTGG GAAGGCGCAC TGGCAGGGGA ACGTACATTA
1201 AGAGGTATGC GTCCGCGGCG GATTTTGCCC GACAACATCA CCACCGACCA
1251 CATCTCgcca tCCAATGCGA TTTTGGCCGG cagTGCcgca ggtgaATATT

```



```

1301 TGGCGAAAAT GGGTTTGCCT GAAGAagaCT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTtcgt
1451 tggcacgcgT tgaacCAGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTT ATCATCATTG CCGGTGCGGA
1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC GCGAAGGGC GTGCGGCTGG
1601 CGGGTGTGGA AGCCATCGCC GCCGAAGGTT TCGAGCGCAT CCACCGCACC
1651 AACCTCATCG GCATGGGCGT CTTGCCGCTG CAATTCAAAC CCGGCACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGGC CTGACCCTCG TGATTCACCG TAAAAACGGA
1801 GAAACCGTCG AAGTTCGGT TACCTGCCGC CCCGATACCG CAGAAGAAGC
1851 ATTGGTATAT GAAGCCGGCG GCGTATTGCA ACGGTTTGCA CAGGACTTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 352; ORF 099.ng>:

g099.pep

```

1 MLGRASMMRL PDIVGVELTG KRQAGITATD IVLALTEFLR KERVVGAFVE
51 FFEGEGARSLS IGDRAATISNM TPEFGATAAM FAIDAQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWAGGLKT AVYPRVLKFD LSSVTRNMAG PSNP HARFAT
151 ADLAAKGLAK PYEPPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRR PWVKSSFAPG SKVAGIYLKE AGLLPEMEKL GFGIVAFACF
251 TCNGMSGALD PKIQEIIDR DLYATAVLGS NRNFDGRIHP YAKQAF LASF
301 PLVVAYALAG SIRFDIENDV LGVADGREIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDIYIP MSDTGTAQKA PSPLYDWRPM STYIRPPPYW EGALAGERTL
401 RGMRPAILP DNITTDHISP SNAILAGSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMRKQPL I IAGADYQG GSSRDWAAGK VRLAGVEAIA AEGFERIHRF
551 NLIGMGVLP L QFKPGTNRHT LQLDGTETYD VVGERTPRCG LTLVIHRKNG
601 ETVEVPVTCR PDTAEEALVY EAGGVLQRFA QDFLEGNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 353>:

m099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51 GCTGAACGGC AAACGGCAGG CGGCATTAC GGCGACGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACCGG TGCTCGGGGC GTTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAACC GCCGTTTATC CTCGCGTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCAAGTAACC CGCATGCCCG TTTTGCAGCC
451 GCCGATTGG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCGGA
501 CGGCCAAATG CCCGACGGCT CGGTCATCAT CGCCGCGATT ACCAGTTGCA
551 CCAACACTTC CAACCCGCGC AACGTTGTTG CCGCCGCGCT CTTGGCACGC
601 AATGCCAACC GTCTCGGCTT GAAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCGGGCCTGT
701 TGCCCCGAAAT GGAAGAACTC GGCTTCGGTA TCGTCGCCTT CGCCTGCACC
751 ACCTGCAACG GCATGAGTGG CGGCTGGAT CCGAAATCC AGAAAGAAAT
801 CATCGACCGC GATTGTACG CCACCGCCGT ATTATCAGGC AACCGCAACT
851 TCGACGGCCG TATCCACCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCCT
901 CCGTTGGTCG TTGCCTACGC GCTGGCAGGC AGTATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCAA GGAAATCCGC CTGAAAGACA
1001 TTTGGCCTGC CGATGAAGAA ATCGATGCCG TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAGT TCCGCGATGT GTATGTACCG ATGTTGACA CCGCGACAGC
1101 GCAAAAAGCA CCCAGTCCGC TGTACGATTG GCGTCCGATG TCCACCTACA
1151 TCCGCCGTCC GCCTTACTGG GAAGGCGCGC TGGCAGGGGA ACGCACATTA
1201 AGAGGTATGC GTCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CCTCTCGCCG TCCAATGCGA TTTTGGCCGT CAGTGCCGCA GGCAGATATT
1301 TGGCGAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCT ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAAAA ACGAAGACGG CAGCGTGC GC CAAGGCTCGT
1451 TCGCCCCGCT CGAACCCGAA GCGGAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGTGCGGA

```

```

1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTAGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACCTTATCG GCATGGGCGT GTTGCCGCTG CAGTTCAAAC CCGACACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTGGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTCG TGATTCACCG TAAAAACGGC
1801 GAAACCGTTG AAGTTCCCGT TACCTGCTGC CTCGATACTG CAGAAGAAGT
1851 ATTGGTATAT GAAGCCGGCG GCGTGTGCA ACGGTTTGA CAGGATTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 354; ORF 099>:

```

m099.pep
  1  MLGRASMMRL PDIVGVELNG KRQAGITATD IVLALTEFLR KERVVGAFVE
 51  FFGEGARSLs IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101  VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151  ADLAAKGLAK PYEEPSDGOM PDGSVIAAI TSCTNTSNPR NVVAAALLAR
201  NANRLGLKRW PVWKSSFAPG SKVAEIIYLK EAGLLPEMEKL GFGIVAFAC
251  TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFLAS
301  PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPADEE IDAVVAEYVK
351  PQQFRDVYVP MFDTGTAQKA PSPLYDWRPM STYIRPPYEW EGALAGERTL
401  RGMRLAILLP DNITTDHLSP SNAILAVSAA GEYLAKMGLP EEDFNSYATH
451  RGDHLTAQRA TFANPKLFNE MVKNEDGSVR QGSFARVEPE GETMRMWEAI
501  ETYMNRRKQPL IIAAGADYQG GSSRDWAAKG VRLAGVEAIV AEGFERIHRT
551  NLIGMGVLP LQFKPDNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601  ETVEVPVTC LDTAEVLVY EAGGVLRFA QDFLEGNA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 099 shows 96.2% identity over a 639 aa overlap with a predicted ORF (ORF 099.ng) from *N. gonorrhoeae*:

m099/g099

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFEGEGARSLs					
g099	MLGRASMMRLPDIVGVELTGKRQAGITATDIVLALTEFLRKERVVGAFVEFFEGEGARSLs					
	10	20	30	40	50	60
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDYKLKTGRDDAQVKLVETYAKTAGLWADALKT					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDYKLKTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNP HARFATADLAAKGLAKPYEEPSDGQMPDGSVIAAI					
g099	AVYPRVLKFDLSSVTRNMAGPSNP HARFATADLAAKGLAKPYEEPSDGQMPDGA V IAAI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAEIIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m099.pep	GFGIVAFAC TTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFLAS					
g099	GFGIVAFAC TTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFLAS					
	250	260	270	280	290	300
	310	320	330	340	350	360

m099.pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIIWPADEEIDAVVAEYVVKPQQFRDVIYP					
g099	PLVVAYALAGSIRFDIENDVLGVADGREIRLKDIIWPTDEEIDAIVA EYVVKPQQFRDIYIP	310	320	330	340	350
		370	380	390	400	410
m099.pep	MFDTGTAQKAPSPLYDWRPMSTYIRRPYPYEWEGALAGERTLRGMRPLAILPDNITTDHLS					
g099	MSDTGTAQKAPSPLYDWRPMSTYIRRPYPYEWEGALAGERTLRGMRPPAILPDNITTDHISP	370	380	390	400	410
		430	440	450	460	470
m099.pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR					
g099	SNAILAGSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR	430	440	450	460	470
		490	500	510	520	530
m099.pep	QGSFARVEPEGETMRMWEAIIETYMNRKQPLIIAGADYQGSSRDWAAKGVRLAGVEAIV					
g099	QGSLARVEPEGQTMRMWEAIIETYMNRKQPLIIAGADYQGSSRDWAAKGVRLAGVEAIA	490	500	510	520	530
		550	560	570	580	590
m099.pep	AEGFERIHRTNLIGMGVLPLOQFKPDNRHTLQLDGTETDYDVVGERTPRCDLTLVIHRKNG					
g099	AEGFERIHRTNLIGMGVLPLOQFKPGTNRHTLQLDGTETDYDVVGERTPRCGLTLVIHRKNG	550	560	570	580	590
		610	620	630	640	
m099.pep	ETVEVPVTCCLDTAE EVLVYEAGGVLRQFAQDFLEGNAAX					
g099	ETVEVPVTCRPDTAE EALVYEAGGVLRQFAQDFLEGNAAX	610	620	630	640	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 355>:

a099.seq

1	ATGCTGGGAC	GCGCGTCCAT	GATGCGCCTG	CCCGATATTG	TCGGCGTTGA
51	GCTGAACGGC	AAACGGGAAG	CGGGCATTAC	GGCGACGGAT	ATTGTGTTGG
101	CAC TGACCGA	GTTTCTGC GC	AAAGAACGGC	TGGTCTGGGGC	GTTTGTTCGAA
151	TTCTTCGGCG	AGGGCGCGAG	AAGCCTGTCT	ATCGGCGACC	GGTGCACATT
201	TTCCAACATG	ACGCCGGAGT	TCGGCGCGAC	TGCCGCGATG	TTCGCTATTG
251	ATGAGCAAAAC	CATTGATTAT	TTGAAACTGA	CCGGACGCGA	CGACGCGCAG
301	GTGAAATTGG	TGGA AACCTA	CGCCAAAACC	GCAGGCTTGT	GGGCAGATGC
351	CTTGAAAAACC	CGCGTTTATC	CGCGCGTTTT	GAAATTTGAT	TTGAGCAGCG
401	TAAACGCGCAA	TATGGCAGGC	CCGAGCAACC	GCACACGCGC	TTTTGCGACC
451	GCCGATTTGG	CCGGCAAAGG	CTTGGCTAAA	CCTTACGAAG	AGCCTTCAGA
501	CGCGCAAATG	CCTGACGGTG	CAGTGATTAT	TGCCGCGGAT	ACTTCTCTGA
551	CCAATACTTC	CAATCCGCGC	AACGTTGTGC	CGCCGCGCGT	GTTGGCAGCG
601	AATGCCAACCC	GCCTCGGCTT	GCAACGCAAA	CCTTGGGTGA	AATCTTCGTT
651	TGCCCCGGGT	TCAAAAGTAG	CCGAAATCTA	TTTGAAGAGAA	GCAGATCTGC
701	TGCCCCGAAAT	GGAAAAAATC	GGCTTCGGTA	TCGTTGCGCTT	CGCATGTACC
751	ACCTGTAAACG	GCATAGACGG	CGCGCTGGAT	CCGAAAATCC	AGAAAGAAAT
801	CATCGAACCGC	GATTTGTACG	CCACCGCGGT	ATTGTCAAGC	AACCGCAACT
851	TTGACGGCCG	TATCCATCCG	TATGCGAAAC	AGGCTTTCCT	CGCTTCGCCT
901	CCGTTTGGTGC	TTGCCTACGC	GCTGGCAGCG	AGCATCCGTT	TCGATATTGA
951	AAACGACGTA	CTCGGCGTTG	CAGACGGCAA	AGAAATCCGC	CTGAAAGACA
1001	TTTGGCCTAC	CGATGAAGAA	ATCGATGCCA	TCGTTGGCGA	ATATGTGAAA
1051	CCGCAGCAAT	TTCGCGACGT	TTATATCCCG	ATGTTTCGACA	CCGGCACAGC
1101	GCAAAAAGCA	CCAAGCCCCG	TGTACGACTG	GCGTCCAATG	TCTACCTATA
1151	TCCGCGCCGC	ACCTTACTGG	GAAAGCGCAC	TGGCAGGGGA	ACCGACATTA
1201	AGCGGTATGCG	TTCCGCTGGC	GATTTTGGCC	GACAACATCA	CCACCGACCC

```
1251 TCTCTCGCCA TCCAATGCGA TTTTGGCAAG CAGTGCCGCA GGCGAATATT
1301 TGGCAAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGTGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTTCCG
1451 TGGCACGCGT TGAACCCGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGCGCGGA
1551 CTACGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTGGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACTTGATCG GTATGGGCGT GTTGCCGCTG CAGTTCAAAC CGGGTACCAA
1701 CCGCCACACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTTG TGATTCACCG TAAAAACGGC
1801 GAGACCGTCG AAGTCCCAT TACCTGCCGC CTCGATACCG CAGAAGAAGT
1851 GTTGGTATAT GAAGCCGGTG GCGTATTGCA ACGGTTTGCA CAGGATTTTT
1901 TGAAGGGAA CCGCGCTTAG
```

This corresponds to the amino acid sequence <SEQ ID 356; ORF 099.a>:

a099.pep

```
1 MLGRASMMRL PDIVGVELNG KRKAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLS IGDRTISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAGKGLAK PYEPPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLQRK PWKSSSFAPG SKVAEIYLKE ADLLPEMEKL GFGIVAFACF
251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFILASP
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDVYIP MFDGTGAQKA PSPLYDWRPM STYIRPPYW EGALAGERTL
401 SGMRLPLAILP DNITDHLSP SNAILASSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNKQPL IIIAGADYQG GSSRDWAAKG VRLAGVEAIV AEGFERIHRF
551 NLIGMGVPL QFKPGTNRHT LQLDGTETD VVGERTPRCD LTLVIHRKNG
601 ETVEVPITCR LDTAEVLVY EAGGVLRFA QDFLEGNA*
```

m099/a099 97.5% identity in 639 aa overlap

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
a099	MLGRASMMRLPDIVGVELNGKRKAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDYLLKLTGRDDAQVKLVETYAKTAGLWADALKT					
a099	IGDRATISNMTPEFGATAAMFAIDEQTIDYLLKLTGRDDAQVKLVETYAKTAGLWADALKT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEPPSDGQMPDGSVIAAI					
a099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAGKGLAKPYEPPSDGQMPDGAIVIAAI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSSFAPGSKVAEIYLKEAGLLPEMEKL					
a099	TSCTNTSNPRNVVAAALLARNANRLGLQRPWKSSSFAPGSKVAEIYLKEADLLPEMEKL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m099.pep	GFGIVAFACFCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFILASP					
a099	GFGIVAFACFCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFILASP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m099.pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVYVP					

a099	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIIWPTDEEIDAIVA EYVKPQQFRDVYIP	310	320	330	340	350	360
m099.pep	MFDGTGTAQKAPSPLYDWRPMSITYIRRPYPYEGALAGERTLRGMRPLAILPDNITTDHLS	370	380	390	400	410	420
a099	MFDGTGTAQKAPSPLYDWRPMSITYIRRPYPYEGALAGERTLSGMRPLAILPDNITTDHLS	370	380	390	400	410	420
m099.pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR	430	440	450	460	470	480
a099	SNAILASSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR	430	440	450	460	470	480
m099.pep	QGSFARVEPEGETMRMWEAIEITYMNRKQPLIIAGADYQGSSRDWAAGVRLAGVEAIV	490	500	510	520	530	540
a099	QGSRLARVEPEGQTRMWEAIEITYMNRKQPLIIAGADYQGSSRDWAAGVRLAGVEAIV	490	500	510	520	530	540
m099.pep	AEGFERIHRNTNLIGMGVLPQFKPDTNRHTLQLDGTETDYDVVGERTPRCDLTLVIHRKNG	550	560	570	580	590	600
a099	AEGFERIHRNTNLIGMGVLPQFKPGTNRHTLQLDGTETDYDVVGERTPRCDLTLVIHRKNG	550	560	570	580	590	600
m099.pep	ETVEVPVTCCLDTAAEEVLVYEAGGVLQRFAQDFLEGNAAX	610	620	630	640		
a099	ETVEVPITCRLDTAAEEVLVYEAGGVLQRFAQDFLEGNAAX	610	620	630	640		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 357>:

```

g102.seq
1      AtgtCCGCCA  AAactccgtc  gctcttcggc  ggcgcgatga  Ttatcgccgg
51     gaagggttatc  ggcgcAGgta  tgttcccaa  cccacgcgc  aacttggggg
101    acggggttaat  aggcctcgctg  attgtgtctg  tgtacacctg  gtttccattc
151    tcctcccgcg  cctctcatgat  tttggaagtc  aacaccata  acCCcggagg
201    ggcaAGtttt  gacaccATTg  tCAaagacct  gctcgGACg  ggctggaaca
251    tcatcaacg  catcgcgctc  gctttggTc  tactaggctc  gacctaacga
301    tacattttag  tcggcgggtga  cctGACGcC  AAAGGCatcg  GCAGCGcAGT
351    AGGCGGCAAA  ATTTCgctca  CCGTCGGACA  actcgtcttc  tTCGGCATCC
401    TCGCCTTTTG  CGTATGGGCA  TCCGCACGCT  TGGTFCAGCC  CTTTACCGCG
451    GTCCTCATCG  GCGGCATGGT  ATTAACCTTT  ATTTGGGCAA  CCGGCGCCTT
501    GGTTCGCCAT  GCCAAACCGT  CCGTCCTCTT  CGACACCcAA  GCCCCCGCTG
551    GCACCGGCTA  CTGGATTATC  GCGCGCACCG  CCCTGCCCGT  CTGCCTCGCT
601    TCCTTCGGCT  TCCACGGCAA  CGTTCCAGC  CTGCTCAAAT  ACTTTAAAGG
651    GCACGcgCc  aaagtGgCA  aATCcatctg  gGcaggtaca  ttgtTTGCCT
701    tggtaattta  cgtctCTGg  caaacgcgca  TCaaagcaca  ctGCGcgcc
751    aacgagttcg  cCCcCgtgat  tgcgcgcgag  aggcaactCT  CCGTCTGgac
801    tgaaaccctT  tccaaattcg  cccaaaccgg  cगतattgat  aAaatattgt
851    cctattttc  ctcataggca  atcgcacctc  cctttttagg  cgTAAcctta
901    ggctgtttg  acaaacctcg  cgacatcttc  aaatggaag  acagtatgtc
951    cgggcggggc  accaaaaccg  tcgcgctgaa  cttctctgg  CCCCTgattt
1001   cctggtgct  cctccccacc  ggaattctta  cgcgccattg  tgcgtctcga
1051   ctggcgggcaa  ccgctctggga  ccctGcGcat  atccccgcca  tgcgtcgcta
1101   cgtttccccc  caaaaaattG  gcGcggcgaa  gactataAa  gtttaCGCG
1151   gcttctggct  gatgttagtc  ttccctttgc  gtatcgccaa  catcgcgcga
1201   CAGGTATTGA  GccaAatGgA  ACTcgtCccc  GTATTTAAAG  GATAA

```

This corresponds to the amino acid sequence <SEQ ID 358; ORF 102.ng>:

g102.pep

```

1  MSAKTPSLFG GAMIAGKVI GAGMFPNPTA NLGDGLIGSL IVLLYTWFPF
51  SSGALMILEV NTHNPRGASF DTMVKDLLGR GWNIIINGIAV ALVLYGSTYA
101 YILVGGDLTA KGIGSAVGGK ISLTVGQLVF FGILAFVCWA SARLVDRFTG
151 VLIGGMVLTF IWATGGLVAD AKPSVLFDQ APVGTGYWIY AATALPVCLA
201 SFGFHGNVSS LLKYFKGDAP KVAKSIWAGT LVALVIYVLW QTAIQSNLPR
251 NEFAPVIAAE RQLSVLNETL SKFAQTGDM D KILSLFPYMA IATSEFLGVTL
301 GLFDNIADIF KWNDSMSGRG TKTVALNFLP PLISWLLLP GFFTAIGASG
351 LAATVWDQGI IPAMLLYVSP QKIGAGKTYK VYGGWLMLV FLFGIANIAA
401 QVLSQMEVLP VFKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 359>:

```

m102.seq
1  ATGCCCAACA AAACCCCTTC ACTGTTCCGC GCGCGCATGA TTATCGCCGG
51  CACGGTCATC GCGCGAGGCA TGCTCGCCAA CCCGACCGCC ACATCCGGCG
101 TATGGTTTAC CGCTCGCTG GCGGTGTTC TGTACACCTG GTTTCTATG
151 CTTTCCAGCG GCCTGATGAT TTTGGAAGTC AACACCCATT ATCCGCACGG
201 CGCAAGTTTC GACACGATGG TCAAAGACCT GCTCGGACGC GGCTGGAACA
251 TCATCAACGG CATCGCCGTC GCCTTCGTTT TATACCTGCT TACTTACGCT
301 TATATCTTCG TCGGCGGCGA CCGTACCGCC AAAGGCTTAG GCAGCGCGGC
351 AGCGGCGGAC GTTCTACTCA CCGTCGGACA ACTCGTCTTC TTCGGCATCC
401 TCGCCTTTTG CGTATGGGCA TCCGCAGCCT TGGTCGACCG CTTACCGGCG
451 GTCCTTATCG GCGGCATGGT ATTGACCTTT ATTTGGGCGG CCGGCGGGCT
501 GATTGCGCAT GCCAAGCCGT CCGTCTCTT CGATACCCAA GCCCCGCGCG
551 GCACAAACTA CTGGATTAC GCCGCCACCG CCCTGCCCGT TCGCCTCGCT
601 TCCTTCGGCT TCCACGGCAA CGTCTCCAGC CTGCTCAAA ACTTTAAAGG
651 CGACGCGCCC AAAGTGGCTA AATCCATCTG GACGGGCACA CTGATTGCGC
701 TGGTAATTTA CGTCTCTGG CAAACCGCCA TCCAAGGCAA CCTGCCGCGC
751 AACGAGTTCG CCCCCGTCAT CGCGCCGAA GGGCAAGTCT CCGTCTCAT
801 CGAAACCTCG TCCAAATTCG CCCAAACCGG CAATATGGAC AAAATATTGT
851 CCCTGTTTTT CTATATGGCG ATCGCCACCT CGTTTTTAGG CGTAACGCTC
901 GGACTCTTCG ACTACATCGC CGACATCTT AAATGGAACG ACAGCATCTC
951 CGGCGCGACC AAAACCGCGC CGCTGACCTT CCGCGCGCCC CTGATTTCCT
1001 GCGTGTCTTT CCCCACGGC TTCGTTACCG CCATCGGCTA CGTCGGCTG
1051 GCGGCAACCG TCTGGACAGG CATCATCCCC GCCATGCTGC TCTACCGTTC
1101 GCGCAAAAAA TTCGCGCAG GCAAAACCTA TAAAGTTTAC GCGCGCTTGT
1151 GGCTGATGGT TTGGGTCTTC CTTTCGGCA TCGTCAACAT CGCCGCACAG
1201 GTATTGAGCC AAATGGAAC CTGCCCGTA TTTAAAGGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 360; ORF 102>:

```

m102.pep.
1  MPNKTPSLFG GAMIAGTVI GAGMLANPTA TSGVWFTGSL AVLLYTWFSM
51  LSSGLMILEV NTHYPHGASF DTMVKDLLGR GWNIIINGIAV AFVLYLLTYA
101 YIFVGGDLTA KGLGSAAGGD VSLTVGQLVF FGILAFVCWA SARLVDRFTG
151 VLIGGMVLTF IWAAGGLIAD AKPSVLFDQ APAGTNYWIY AATALPVCLA
201 SFGFHGNVSS LLKYFKGDAP KVAKSIWGT LIALVIYVLW QTAIQGNLPR
251 NEFAPVIAAE GQVSVLIETL SKFAQTGNMD KILSLFSYMA IATSEFLGVTL
301 GLFDYIADIF KWNDSISGRT KTAALTFLEP LISCLLEPTG FVTAIGYVGL
351 AATVWTGIIP AMLLYRSRKK FGAGKTYKVY GGLWLMVWVF LFGIVNIAAQ
401 VLSQMEVLPV FKG*

```

m102/g102 86.0% identity in 415 aa overlap

	10	20	30	40	50	60
m102.pep	MPNKTPSLFGGAMIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
g102	MSAKTPSLFGGAMIAGKVIAGMFPNPTANLGDGLIGSLIVLLYTWFPFSSGALMILEV					
	10	20	30	40	50	60
m102.pep	NTHYPHGASFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAIFVGGDLTAKGLGSAAGGD					
g102	NTHNPRGASFDTMVKDLLGRGWNIIINGIAVALVLYGSTYAYILVGGDLTAKGIGSAVGGK					
	70	80	90	100	110	120
m102.pep	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDQ					
g102	ISLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIATGGLVADAKPSVLFDQ					
	130	140	150	160	170	180
m102.pep	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWGTIALLVIYVLW					
g102	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWGTIALLVIYVLW					

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 361>:

a102.seq

1	ATGCCACCA	AAACCCCTTC	ACTGTTTCGGC	GGCGCGATGA	TTATCGCCGG
51	CACGNTCATC	GGCGCAGGTA	TGCTCGCCAA	CCCGACCGCC	ACATCGGGCG
101	TATGTTTAC	CGGCTCGCTG	GCCCTGTTGC	TGTACACCTG	GTTTTCATGT
151	CTCTCCAGCG	GCCTGATGAT	TTTGGAAAGTC	AACACCCACT	ACCCCAACGG
201	CGCGANCTTC	GACACCATGG	TTAAAGACCT	GCTCGGACGG	AGCTGGAACA
251	TCATCAACGG	CATCGCCGTC	GCCTTCGTTT	TATACCTGCT	TACTTACGCT
301	TATATCTTCG	TCGGCGCGCA	CCTGACCGCC	AAAGGCTTAG	GCAGCGCGTC
351	AGGCGGCAAT	GTTTCACTCA	CCGTCCGACA	ACTCGTCTTC	TTCCGGCAGG
401	TCGCGCTTTG	CGTATGGGCA	TCCGCAACGT	TGGTCCGACG	ATTACACGAG
451	GTCTCATCG	GCGGCATGGT	ATTAACCTTT	ATTTGGGCAA	CCGGCGGCCT
501	GATTGCGCAT	GCCAAACTGC	CCGTCTCTTT	CGACACCCAA	GCCCTTACCG
551	GCACCAACTA	TCGGATTTAT	GTGCCCACCG	CCCTGCCCGT	CTGCCTTGCG
601	TCATTTCGTT	CCTGAGGCAA	CGTCTCCAGC	CTGCTCAACT	AATTTAAAGG
651	CGACGCGCCC	AAAGTGGCTA	AATCCATCTG	GACGGGCACA	CTGATTGCGC
701	TGGTAATTTA	CGTCTCTGG	CAAACGCGCA	TCCAANGCAA	CCTGCCGCGC
751	AACGAGTTCG	CCCCCGTGAT	TGCCGCGCGA	GGGCAAGTCT	CCGTCTNGAT
801	TGAACCCCTG	TCCAAATTCT	CCCAACCCGG	CAATATGGAC	AAAATATTGT
851	CCCTGTTTTC	CTATATGGCG	ATCGCCACCT	CGTTTTTAGG	CGTAACGCTC
901	GGACTCTTCG	ACTACATCGC	CGACATCTTC	AAATGGAACG	ACAGCGTGTC
951	CGGCCGCGCC	AAAACCGCGC	CGCTGACCTT	CCTGCCGCGT	NTAATTTCTT
1001	GCCTGCTCTT	CCCCACCGGC	TTTGTTACCG	CCATCGGNTA	CGTCGGCGCTG
1051	CGCGCAACCG	CTTGGACAGG	CATCATCCCC	GCCATCTGTC	TNTACCGTTC
1101	GCGCAAAAAA	TTGGGCGCAG	GCAAAACCTA	TAAAGTTTAC	GGCGGCTTGT
1151	GGCTGATGGT	TTGGGTCTTC	CTTTTCGGCA	TCNTCAACAT	CGCCGCACAN
1201	GTATTGAGCC	AAATGGAAGT	CGTCCCCGTA	TTTAAAGGAT	AA
1202					

This corresponds to the amino acid sequence <SEQ ID 362; ORF 102.a>:

**a102.ppt**

1	MPTKTPSLFG	GAMIIAGTXI	GAGMLANPTA	TSGVWFTGSL	AVLLYTWFMS
51	LSSGLMILEV	NTHYPHGAXF	DTMVKDLLGR	SWNIINGIAV	AFVLYLLTYA
101	YIFVGGDLTA	KGLGSAAGGN	VSLTVGQLVF	FGILAFVCWA	SARLVDRFST
151	VLIGMGVLT	IWATGGLIAD	AKLPVLFDTQ	APTGTNYWIY	VATALPVCLA
201	SFGFHGNVSS	LLKYFKGDAP	KVAKSIWTFQ	LIALVIYVLW	QTAIQXNLPR
251	NEFAPVIAAE	GOVSXKIETL	SKFAQTGNMD	KILSLFSYMA	IATSFLGVTL
301	GLFDYIADIF	KWNDSSVSGRT	KTAALTFLPP	XISCLLFPTG	FVTAIGYVGL
351	AATVWGTIIP	AMLLYRSRKK	FGAGKTYKVY	GGLWLMVWVF	LFGIXNIAAX
401	VLSSOMELPV	FKG*			

m102 / a102 95.9% identity in 413 aa overlap

m102.pep	10	20	30	40	50	60
	MPNKTPSLFGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
a102	MPTKTPSLFGGAMIIAGTXIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
	10	20	30	40	50	60
m102.pep	70	80	90	100	110	120
	NTHYPHGASEFTMVKDLLGRGWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
a102	NTHYPHGAXEFTMVKDLLGRSWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGN					
	70	80	90	100	110	120
m102.pep	130	140	150	160	170	180
	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFFIWAAGGLIADAKPSVLFDTQ					
a102	VSLTVGQLVFFGILAFVCWASARLVDRFTSVLIGGMVLTFFIWTGGLIADAKLPVLFDTQ					
	130	140	150	160	170	180
m102.pep	190	200	210	220	230	240
	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTIALVIYVLW					
a102	APTGTNYWIYVATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTIALVIYVLW					
	190	200	210	220	230	240
m102.pep	250	260	270	280	290	300
	QTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
a102	QTAIQXNLPRNEFAPVIAAEGQVSVXIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
	250	260	270	280	290	300
m102.pep	310	320	330	340	350	360
	GLFDYIADIFKWNDSISGRTKTAALTFPLPPLISCLLFPTGFVTAIGYVGLAATVWTGIIP					
a102	GLFDYIADIFKWNDSVSGRTKTAALTFLPPIXISCLLFPTGFVTAIGYVGLAATVWTGIIP					
	310	320	330	340	350	360
m102.pep	370	380	390	400	410	
	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIVNIAAQVLSQMELVPVFKGX					
a102	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIXNIAAXVLSQMELVPVFKGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 363>:

g105.seq

```

1  Atgtccgcag aaaCATACac acAAAatcggc tGGgtaggct taggGcaaat
51  gGgtctgcct atgGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCcgC CAAAGGAGCA
151 AAAGTTTACG GCagcACCGC CGAACTCGTC CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAACAAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAACA CGCTTCCAAA GacctTAACC TCGcggtcAA AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```



This corresponds to the amino acid sequence <SEQ ID 364; ORF 105.ng>:

g105.pcp

1	MSAETTYTQIG	VWGLGQMGLP	MVTRLDDGGI	EVGVYNRSPD	KTAPISAKGA
51	KVYGSTAE LV	RACPVIFLMV	SDYAAVCDIL	NGVRDGLAGK	IVNMSTISP
101	TENLAVKALV	EAAAGQFAEA	PVSGSVGPAT	NGTLLILFGP	SEAVLNLPLQK
151	IFSLVGKKT F	HFGDVGKGS G	AKLVNLSLGG	IFGEAYSEAM	LMARQFGIDT
201	DTIVEATIGGS	AMDSMPFQTK	KLWANREFP	PAFALKHASK	DLNLVAKELE
251	QAGNTLPAVE	TVAASYRKAV	EAGYGEQDVS	GVYLKLAEH	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 365>:

m105.seq

1	ATGTCGCGCAA	ACGAATACGC	ACAAATCGGC	TGgaTAGGCT	TAGGGCAAAT
51	GGGTCTGCCT	ATGGTAACGC	GGCTCTTGGA	CGGCGGCATC	GAAGTCGCGC
101	TATACAACCG	CTCGCCCGAC	AAAAC TGCCC	CCATCTCCGC	CAAAGGCGCA
151	AAAGTTTACG	GCAACACCGC	CGAACTCGTC	CGCGACTATC	CCGTCAATTT
201	CTGATGGTT	TCGCAGTATG	CCGCGCTGTG	CGACATCTCG	AACCGAGTCC
251	GCGACGGATT	GGCCGCGCAm	ATCATCGTCA	ACATGAGCAC	CATCTCCCCG
301	ACCGAAaGC	TCGCCGTCaA	AGCACTTGTC	GAAGCGCAGm	GaCAGTTTGC
351	CGAAGCACCC	GTTTCGCGAT	CGGTCTGGGC	CGCCACCAAC	GGCACGCTGC
401	TGATTCTGTT	CGGCGGCAGC	GAaCCgtTTT	AAACCCGCTG	CAAAAAATAT
451	TTTCCCTCTG	CGGCAAAAAA	ACCTTCCATT	TCGGCGATGT	CGGCAAAAGT
501	TCGGGCGCGA	AACTCGTCTT	GAACTCGCTC	TTGGGCAATT	TCGGCGAaCG
551	TAcAGCGAAa	GmTgCTGATG	GCGCGGCAGT	TCGGCATCGA	TACCGACACC
601	ATCGTCGAAG	CCATCGGSGA	CTCGGCAATG	GACTCGCCCA	TGTTCCAAAC
651	CAAAAAATCC	CTGTGGGCAA	ACCGCGAATT	CCCGmCCGmC	TTGCGCCTCA
701	AACACGCCTC	CAAAGACCTC	AACCTCGCCG	TCAAAGAGCT	TGAACAGGCA
751	GGCAACACCC	TGCCCGCCGT	CGAAACCGTT	GCTGCCAGCT	ACCGCAAAAG
801	AGTCGAAGCC	GGTACGGGA	CACAGGACGT	TTCCGGCGTT	TACCTGAAC
851	TGGCAGAACA	CTGA			

This corresponds to the amino acid sequence <SEQ ID 366; ORF 105>:

m105.pcp

1	MSANEYAQIG	WIGLGQMGLP	MVTRLDDGGI	EVGVYNRSPD	KTAPISAKGA
51	KVYGNTAELV	RDYPVIFLMV	<u>SDYAAVCDIL</u>	NGVRDGLAGX	IIVNMSTISP
101	TEKLAVKALV	EAQRQFAEAP	VSSGSGPATN	GTLLILFGGS	EPFXTRCKKY
151	FPSSAKKPSI	SAMSQKVRAR	NSNXTSRWFN	SANVRQXXLM	ARQFGIDTDT
201	IVEAIGDSAM	DSPMFQTKKS	LWANREFPPX	FALKHASKDL	NLAVKELEQA
251	GNTLPAVETV	AASYRKAVEA	GYGTQDVSGV	YLKLAEH	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 105 shows 79.9% identity over a 289 aa overlap with a predicted ORF (ORF 105.ng) from *N. gonorrhoeae*:

m105/g105

		10	20	30	40	50	60
g105.pep		MSAETYTQIGWVGLGQMGLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGSTAE					L
		: :    :					:
m105		MSANEYAQIGWIGLGQMGLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAE					L
		10	20	30	40	50	60
		70	80	90	100	110	120
g105.pep		RACPFVIFLMVSDYAAVCDILNGVRDGLAGKIIVN					MS
							:
m105		RDYPVIFLMVSDYAAVCDILNGVRDGLAGXIIVN					MS
		70	80	90	100	110	
		130	140	150	160	170	180
g105.pep		PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLV					GK
							:
m105		PVSGSVGPATNGTLLILFGGSEPFXT					RCKKYPSSAKKP-SISAMSAKVRARNSSX
		120	130	140	150	160	170

314

	190	200	210	220	230	240
g105.pep	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK					
m105	AFSANVQRXXLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPXXFALKHASK					
	180	190	200	210	220	230
	250	260	270	280	289	
g105.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEH					
m105	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGTQDVSGVYLKLAEH					
	240	250	260	270	280	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 367>:

a105.seq

```

1  ATGTCCGCAA  ACGAATACAC  ACAAATCGGC  TGGATAGGCT  TAGGGCAAAT
51  GGGTCTGCCT  ATGGTAACGC  GGCTCTTGGA  CGGCGGCATC  GAAGTCGGCG
101 TATACAACCG  CTCGCCCGAC  AAAACTGCCC  CCATCTCCGC  CAAAGGCGCA
151 AAAGTTTACG  GCAACACCGC  CGAACTCGTC  CGCGACTATC  CCGTCATTTT
201 CCTGATGGTT  TCCGACTATG  CCGCCGTGTG  CGACATCCTG  AACGGAGTCC
251 GCGACGGATT  GGCCGGCAAA  ATCATCGTCA  ACATGAGCAC  CATCTCCCGG
301 ACCGAAAACC  TCGCCGTCAA  AGCACTTGTC  GAAGCCGCAG  GCGGACAGTT
351 TGCCGAAGCA  CCCGTTTCCG  GATCGGTCGG  GCCCGCCACC  AACGGCACGC
401 TGCTGATTCT  GTTCGGCGGC  AGCGAAGCCG  TTTTAAACCC  GCTGCAAAAA
451 ATATTTTCCC  TCGTCGGCAA  AAAAACCTTC  CATTTCGGCG  ATGTCGGCAA
501 AGGTTGGGGC  GCGAACTCG  TCTTGAATC  GCTCTTGGGC  ATTTTCGGCG
551 AAGCGTACAG  CGAAGCGATG  CTGATGGCGC  GGCAGTTCGG  CATCGATACC
601 GACACCATCG  TCGAAGCCAT  CGGCGGCTCG  GCAATGGACT  CGCCCATGTT
651 CCAAACCAA  AAATCCCTGT  GGGCAAACCG  CGAATCCCA  CCCGCCTTCG
701 CCCTCAAACA  CGCCTCCAAA  GACCTCAACC  TCGCCGTCAA  AGAGCTTGAA
751 CAGGCAGGCA  ACACCCTGCC  CGCCGTCGAA  ACCGTTGCTG  CCAGCTACCG
801 CAAAGCAGTC  GAAGCCGGCT  ACGGCGAACA  GGACGTTTCC  GGCCTTACC
851 TGAAATTGGC  AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 368; ORF 105.a>:

a105.pep

```

1  MSANEYTQIG  WIGLGQMGLP  MVTRLLDGGI  EVGVYNRSPD  KTAPISAKGA
51  KVGNTAELV  RDYPVIFLMV  SDYAAVCDIL  NGVRDGLAGK  IIVNMSTISP
101 TENLAVKALV  EAAGGQFAEA  PVSGSVGPAT  NGTLLILFGG  SEAVLNPLQK
151 IFSLVGKKT  FFGDVKGKSG  AKLVLNSLLG  IFGEAYSEAM  LMARQFGIDT
201 DTIVEAIGGS  AMDSPMFQTK  KSLWANREFP  PAFALKHASK  DLNLAVKELE
251 QAGNTLPAVE  TVAASYRKAV  EAGYGEQDVS  GVYLKLAEH*

```

m105/a105 96.5% identity in 289 aa overlap

	10	20	30	40	50	60
m105.pep	MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
a105	MSANEYTQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m105.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAG-QFAEA					
a105	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
	120	130	140	150	160	170
m105.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVKGSGAKLVLNSLLG					
a105	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVKGSGAKLVLNSLLG					
	130	140	150	160	170	180
	180	190	200	210	220	230

```

m105.pep    IFGDV-QRXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK
             |||:: :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
             190      200      210      220      230      240

m105.pep    240      250      260      270      280
             DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
             250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 369>:

```

g105-1.seq
1  ATGTCCGCAG AAACATACAC ACAAATCGGC TGGGTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGAGCA
151 AAAGTTTACG GCAGCACC GCAGACTCGT CGCGCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAA ATCATCGTCA ACATGAGCAC CATCTCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAACAAA AAATCACTAT GGGCAAACCG TGAGTTCCCG CCTGCCTTTG
701 CACTCAAAAC CGCTTCCAAA GACCTTAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GGCCTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 370; ORF 105-1.ng>:

```

g105-1.pep
1  MSAETYTIQIG WVGLGQMLP MVTRLLDGGI EVGVYNRSPD KTAPISARGA
51  KVYGSTAEVLV RACPVIPLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGQGFQFAE PVSQSVGPAT NGTLILFLFG SEAVLNPLQK
151 IFSLVGKKTFF HFGDVGKGS AKLVLSNLIG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 371>:

```

m105-1.seq
1  ATGTCCGCAA ACGAATACGC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACCGC CGAAGTCTGC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAA ATCATCGTCA ACATGAGCAC CATCTCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCCGCCACC AACGGCACGC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
501 AGGTTCGGGC GCGAAACTCG TCTTGAATC GCTCTGGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGAGACTCG GCAATGGACT CGCCCATGTT
651 CCAAACAAA AAATCCCTGT GGGCAAACCG CGAATCCCG CCCGCTTTCG
701 CCCTCAAAAC CGCTTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTCC GGCCTTACC
851 TGAAACTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 372; ORF 105-1>:

```

m105-1.pep
1  MSANEYAQIG WIGLGQMLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
51  KVGNTAEVLV RDPVIFPLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP

```

316

101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK  
 151 IFSLVGKKTFF HFGDVGKGS AKLVNLSLLG IFGEAYSEX LMARQFGIDT  
 201 DTIVEAIGDS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE  
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH\*

m105-1/g105-1 96.9% identity in 289 aa overlap

	10	20	30	40	50	60
m105-1.pep	MSANEYAQIGWIGLQMG	MPMVT	RLLDGGIEVGVY	NRSPDKTAPISAKGAKVY	GN	TAE
g105-1	MSAETYTQIGWVGLGQMG	MPMVT	RLLDGGIEVGVY	NRSPDKTAPISAKGAKVY	GS	TAE
	10	20	30	40	50	60
	70	80	90	100	110	120
m105-1.pep	RDYPVIFILMVSDYAAVCDIL	NGVRDGLAGKII	VNMSTISPTENLAVKALVEA	AGGQFAEA		
g105-1	RACPVIFILMVSDYAAVCDIL	NGVRDGLAGKII	VNMSTISPTENLAVKALVEA	AGGQFAEA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m105-1.pep	PVSGSVGPATNGTLLILFGG	SEAVLNPLQKIFSLVGKKT	FHFGDVGKGSGAKLV	NLSLLG		
g105-1	PVSGSVGPATNGTLLILFGG	SEAVLNPLQKIFSLVGKKT	FHFGDVGKGSGAKLV	NLSLLG		
	130	140	150	160	170	180
	190	200	210	220	230	240
m105-1.pep	IFGEAYSEXLMARQFGIDT	DTIVEAIGDSAMDSPMFQTK	KSLWANREFPPAFALKHASK			
g105-1	IFGEAYSEAMLARQFGIDT	DTIVEAIGGSAMDSPMFQTK	KSLWANREFPPAFALKHASK			
	190	200	210	220	230	240
	250	260	270	280	290	
m105-1.pep	DLNLAVKELEQAGNTLPAVET	VAAASYRKAVEAGYGEQDVS	GVYLKLAEHX			
g105-1	DLNLAVKELEQAGNTLPAVET	VAAASYRKAVEAGYGEQDVS	GVYLKLAEHX			
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 373>:

a105-1.seq  
 1 ATGTCCGCCAA ACGAATACAC ACAAATCGGC TGGATAGGCT TAGGGCAAAT  
 51 GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG  
 101 TATACAACCG CTCGCCCGAC AAAACTCGCC CCATCTCCGC CAAAGCGCA  
 151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT  
 201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCTG AACGGAGTCC  
 251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCG  
 301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT  
 351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCCGCCACC AACGGCACGC  
 401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAA  
 451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGCG ATGTCGGCAA  
 501 AGGTTCCGGG GCGAACTCG TCTTGAATC GCTCTTGGG ATTTCGGCG  
 551 AAGCGTACAG CGAAGCGATG CTGATGGCG GGCAGTTCCG CATCGATACC  
 601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCCATGTT  
 651 CCAAACCAAA AAATCCCTGT GGGCAAACCG CGAATCCCCA CCCGCTTCG  
 701 CCCTCAACA CGCCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA  
 751 CAGGCAGGCA ACACCTGCC CGCCGTGCAA ACCGTTGCTG CCAGCTACCG  
 801 CAAAGCAGTC GAAGCCGCT ACGGCGAACA GGACGTTCC GCGCTTACC  
 851 TGAAATTGGC AGAACACTGA

This corresponds to the amino acid sequence <SEQ ID 374; ORF 105-1.a>:

a105-1.pep  
 1 MSANEYTQIG WIGLQMG LPMVT RLLDGGI EVGVYNRSPD KTAPISAKGA  
 51 KVGNTAE LV RDYPVIFILMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP  
 101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK  
 151 IFSLVGKKTFF HFGDVGKGS AKLVNLSLLG IFGEAYSEAM LMARQFGIDT  
 201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE  
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH\*

a105-1/m105-1 99.0% identity in 289 aa overlap

	10	20	30	40	50	60
a105-1.pep	MSANEYTQIGWIGLQMG	LPMVT	RLLDGGIEVGVY	NRSPDKTAPISAKGAKVY	GN	TAE

```

m105-1      MSANEYAQIGWIGLGMGLPMVTRLDDGGIEVGVNRSRSPDKTAPISAKGAKVYGNTAELV
              10      20      30      40      50      60
a105-1.pep  RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
              70      80      90      100     110     120
m105-1      RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
              70      80      90      100     110     120
a105-1.pep  PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVNLSLLG
              130     140     150     160     170     180
m105-1      PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVNLSLLG
              130     140     150     160     170     180
a105-1.pep  IFGEAYSEAMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
              190     200     210     220     230     240
m105-1      IFGEAYSEXMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
              190     200     210     220     230     240
a105-1.pep  DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAHX
              250     260     270     280     290
m105-1      DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAHX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 375>:

```

g107.seq
1   ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCTGCTGTTG CCGATGCCAA
51  ACCGTCCGTC CTCTTCGACA CCAAGCCCC CGTCGGCACC GGCTACTGGA
101 TTTACGCCGC CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCCTGCT CAAATACTTT AAAGGCGACG cgcCcaaagt
201 GgCGAaATCc atctggGcag gtacattggT TGCCttggta atttacgtcc
251 TCTggcaaac cgccatCcaa agcaaccTGC cgcgcaacga gttcgcCCCC
301 gtgattgccg ccgagaggca actCTCCGTC CTgaatgaaa cccTGtccaa
351 attcgcccaa accggcgata tggataAaat attgtcccta tttccctaca
401 tggcaatcgc cacctccttt ttaggcgTAA Ccttaggcct gtttgacaac
451 atcgccggac atcttcaaat ggaacgacag tatgtccggg cggcaccaaa
501 accgtcgcg c tga

```

This corresponds to the amino acid sequence <SEQ ID 376; ORF 107.ng>:

```

g107.pep
1   MVLTFIWATG GLVADAKPSV LFDTQAPVGT GYWIYAATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWAGTLVALV IYVLWQTAIQ SNLPRNEFAP
101 VIAAERQLSV LNETLSKFAQ TGDMDKILSL FPYMAIATSF LGVTGLGLFDN
151 IAGHLQMERQ YVRAAPKPSR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 377>:

```

m107.seq
1   ATGGTATTGA CCTTTATTTG GGCGGCCGCG GGGCTGATTG CCGATGCCAA
51  GCCGTCCGTC CTCTTCGATA CCAAGCCCC CGCCGGCACA AACTACTGGA
101 TTTACGCCGg CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCGCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTCATCGCCG CCGAAGGGCA AGTCTCCGTC CTCATCGAAA CCTGTCCAA
351 ATTTCGCCAA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCCATC TTCAAATGGA ACGACAGCAT CTCCGGgCCG CACCAAAACC
501 GCCGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 378; ORF 107>:

```

m107.pep..
1   MVLTFIWAAG GLIADAKPSV LFDTQAPAGT NYWIYAXTAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP

```

101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY  
151 IAHQMERQH LRAAPKPPR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 107 shows 89.4% identity over a 170 aa overlap with a predicted ORF (ORF 107.ng) from *N. gonorrhoeae*:

m107/g107

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	:     :     :     :     :					
g107	MVLTFIWAATGGLVADAKPSVLFDTQAPVGTGYWIIYAATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWGTGLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	:     :     :     :     :					
g107	KGDAPKVAKSIWGTGLVALVIYVLWQTAIQSNLPRNEFAPVIAERQLSVLNETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIA-HQMERQHLRAAPKPPR					
	:     :     :     :     :					
g107	TGDMDKILSLFPYMAIATSFLGVTGLGLFDNIAGHLQMERQYVRAAPKPSR					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 379>:

a107.seq

```

1  ATGGTATTAA CCTTATTG GGC AACCGGC GGCCTGATTG CCGATGCCAA
51  ACTGCCCCGTC CTCTCGACA CCCAAGCCCC TACCGGCACC AACTACTGGA
101 TTTATGTCGC CACCGCCCTG CCCGTCTGCC TTGCGTCATT CGGTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTGATTGCCG CCGAAGGGCA AGTCTCCGTC CTGATTGAAA CCCTGTCCAA
351 ATTCGCCCCA ACCGGCAATA TGGACAAAT ATTGTCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCGACA TCTTCAAATG GAACGACAGC GTGTCCGGCC GCACCAAAC
501 CGCCGCGCTG ACCTTCCTGC CGCCTCTAAT TTCCTGCCTG CTCTCCCCA
551 CCGGCTTTGT TACCGCCATC GGCTACGTCG GCCTGGCGGC AACCGTCTGG
601 ACAGGCATCA TCCCCGCCAT GCTGCTCTAC CGTTCGCGCA AAAAATTCGG
651 CGCAGGCAAA ACCTATAAAG TTTACGGCGG CTTGTGGCTG ATGTTTGGG
701 TCTTCCTTTT CGGCATCGTC AACATCGCCG CACAGGTATT GAGCCAAATG
751 GAACTCGTCC CCGTATTAA AGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 380; ORF 107.a>:

a107.pep

```

1  MVLTFIWATG GLIADAKLPV LFDQAPTGT NYWIYVATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP
101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
151 IADIFKWNDS VSGRTKTAAL TFLPPLISCL LFPTGFVTAI GYVGLAATVW
201 TGIIPAMLLY RSRKKFGAGK TYKVYGLWL MVVFLFGIV NIAAQVLSQM
251 ELVPVFKG*

```

m107/a107 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	:     :     :     :     :					
a107	MVLTFIWAATGGLIADAKLPVLFDTQAPTGTNYWIYVATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60

```

              70      80      90      100      110      120
m107.pep      KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ
              |||||
a107           KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ
              70      80      90      100      110      120

              130      140      150      160      170
m107.pep      TGNMDKILSLFSYMAIATSFLGVTLGLFDYIAHLQMERQHLRAAPKPPRX
              |||||
a107           TGNMDKILSLFSYMAIATSFLGVTLGLFDYIADIFKWNDSVSGRTKTAALTFLPPLISCL
              130      140      150      160      170      180

a107           LFPTGFVTAIGYVGLAATVWTGIIPAMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIV
              190      200      210      220      230      240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 381>:

```

g108.seq
1   ATGttgccgg gCTTCAACCG GATATTCAaa cggTTTGCTC CAACACTCGG
51  AAcggCGCAT AAAACGCCGc ccTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATCCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTGCGCGCG GCAATCTTAC TCGGCGGGTG
201 CGCCGCCGGC GGCAACACAT TCGGCAGCTT AGACGGCGGC ACGGGTATGG
251 GTGGCAGCAT CGTCAAAATG ACGGTAGAAA gccAATGCCG TCGGGAATTG
301 GACAGGCGCA GCGAATGGCG TTGACCGCG CTGGCGATGA GTCCGAAAAA
351 ACAGGCGGAA TGGGAAAACA AGATTTCGGG CTGCGCTACC GAAGAAGCAC
401 CTAACCAAGT GACCGGCAAC GATGTGATGC AGATGCTGaa ccagtccacG
451 CGCaatcagg cacTtgccgc CCtgaccgTC AAAacgggTT CgcgctgcTT
501 CAAacgcctg tACCGCTAa

```

This corresponds to the amino acid sequence <SEQ ID 382; ORF 108.ng>:

```

g108.pep
1   MLPGFNRIFK RFAPTLGTAH KTPPFALSRT GRLIRSYRHK RRGFNRKGIE
51  MNKTLSILPA AILLGGCAAG GNTFGSLDGG TGMGGSIVKM TVESQCRAEL
101 DRRSEWRLTA LAMSAEKQAE WENKICGCAT EBAPNQLTGN DVMQMLNQST
151 RNQALAAALTV KTVSACFKRL YR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 383>:

```

m108.seq
1   ATGTTGCCGG GCTTCAACCG GATATTCAAA CGGTTTGTTT CAACACTCGG
51  AACGGCGCAT AAAACGCCGC CCTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATTCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTGCGCGTG GCAATCTTAC TCGGCGGGTG
201 CGCCGCCGGA GGCGGTAAAC CATTCGGCAG CTTAGACGGT GGCACAGGCA
251 TGGCGGCAG CATCGTCAA ATGGCGGTTG GGAGCCAATG CCGTGCGGAA
301 TTGGACAAAC GCAGCGAATG GCGTTTGACC GCGCTGGCGA TGAGTGCCGA
351 AAAACAGGCG GAGTGGGAAA ACAAGATTG CGCTTGCGTC GCCCAAGAAG
401 CACCCGAACG GATGACCGGC AACGATGTGA TGCAGATGCT GGCTCCGTCC
451 ACGCGCAATC AGGCATTGCG CGCCCTGACC GCCAAACGG TTTCCGCCTG
501 CTTCAAACAC CTGTACCGCT AA

```

This corresponds to the amino acid sequence <SEQ ID 384; ORF 108>:

```

m108.pep
1   MLPGFNRIFK RFVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNRKGIE
51  MNKTLSILPV AILLGGCAAG GGNTFGSLDG GTMGGSIVK MAVGSQCRAE
101 LDKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPERMTG NDVMQMLAPS
151 TRNQALAAALT AKTVSACFKH LYR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 108 shows 89.6% identity over a 173 aa overlap with a predicted ORF (ORF 108.ng) from *N. gonorrhoeae*:

m108/g108



**a108.seq**

This corresponds to the amino acid sequence <SEQ ID 386; ORF 108.a>:

**a108.ppt**

1 MLPGFNRIKF RFVPTLGTAH KTPPFALSRT GLRIRFYRHK RRGFNKRKIE  
51 MNKTLTSLPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE  
101 LNKRESWRLT ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS  
151 TRNOALAALT AKTVSACFKH LYS\*

m108/a108 96.5% identity in 173 aa overlap

	10	20	30	40	50	60
m108.pep	MLPGFNRI	FKRFVPTL	GTAKHTPP	FALSRTGR	LIRFYRHK	RGRGFNRK
a108	MLPGFNRI	FKRFVPTL	GTAKHTPP	FALSRTGR	LIRFYRHK	RGRGFNRK
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCA	AGGGNTFG	SLDGGTGM	GGSIVKMA	VGSSQCRA	ELDKRSEW
a108	AILLGGCA	AGGGNTFG	SLDGGTGM	GGSIVKMA	VGSSQCRA	ELDKRSEW
	70	80	90	100	110	120
	130	140	150	160	170	
m108.pep	EWENKICAC	VAQEAPER	MTGNDVMQ	MLAPSTRN	QALAAALT	AKTVSACF
a108	EWENKICAC	VAQEAPER	MTGNDVMQ	MLAPSTRN	QALAAALT	AKTVSACF
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 387>:



1	ATGTATTATC	GCCGGGTGTG	GGGGCTATCC	GATGGACTTG	GCGATTTGCC
51	AGCCGGTATT	GATCGTAGGC	GTATGCTTAC	CGCTTTTGGG	AGCCGGCATG
101	GAAATGACGC	GCAAAGGCAA	AACCACCCAA	TCCGCCGCCA	TCGTGGTGTT
151	CTCTTCCGTC	TGGTCAATCC	GGTTTTCCGC	TGGGCGTTGA	CGATGCTGTT
201	GGATAATTTG	GGCTTAATCG	GCTGCAAAGA	ACGCAGCGCG	CAATTAGGTT
251	TTGTCGGACG	AGTATTGATA	CCCGCAGTAG	GTTTCTTAAT	CTTGTTGTGTG
301	GCGATGGGTG	CGGTGGGGAT	GCTGCCCGGT	ATCCCTCCGT	TTTGGAGCA
351	GGTCAATCT	TTGGGCTAG			

g109.pep

1 MYYYRVVGLS DGLGDLAAGI DRRRMLTAFG SGHGNDARQ RQ NHPIRRHRGV  
51 LFRLLVNPVFG WALTMLLDNL GLIGCKERSA QLGFVGRVLI PAVGFLILCV  
101 AMGAVGMLPG IPPFELOEKS LG

m109.seq

1	ATGTATTATC	GCCGGGTTAT	GGGGCTATCC	GATGGACTTG	GCGATTTTGGC
51	AGCCGGTATT	GAGCGTAGCC	TTGGTCGTAG	GCGTATACTT	ACCGCTTTTG
101	GAAGCGGGCA	TGGAATGAC	GCGCAAGGC	AAAACCACC	AATCCGCCGC
151	CATCGTGGTG	TTCTCTCCG	CCTTGTCAT	CCGTTTTTCG	GCTGGGCGTT
201	GACGATGCTG	TTGGATAATT	TGGGCTTAAT	CGGCTGCAA	GAGCGCAGTG
251	CGCAATTAGG	TTTCGCCGGA	CGCGTGTGA	TACCCGCAGT	AGGTTTCTTG
301	ATTTTGTGTG	TGCGGTAGGG	TGCGTGGGG	ATGCTGCCCG	GTATCCCGCC
351	GTTTTTGGAA	CAGTCAAAT	CTTTGGGCTA	G	

m109.pep

1 MYYYRVVGLS DGLGDLAAGI ERSLGRRRIL TAFSGSHGND AQRQNHPIRR  
51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFAG RVLIPAVGFL  
101 ILCVAMGAVG MLPGIIPFLE HFKSLG\*

Homology with a predicted ORF from *N. gonorrhoeae*

m109/q109

```

      10          20          30          40          50          60
m109.pep  MYRRVRVGLSDGLGDLAAGIERSLGRRRIILTAFGSGHGNDAGRQNHPIRRHRGVLFRLVN
           |||||:|||||||:|||:|||||||
g109      MYRRRVVGLSDGLGDLAAGIDR---RRMLTAFSGSHGNDAGRQNHPIRRHRGVLFRLVN
           10          20          30          40          50

      70          80          90         100         110         120
m109.pep  PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLI PAVGFLILCVAMGAVGM LPGIPPFLE
           |||||:|||||||
g109      PVFGWALTMLLDNLGLIGCKERSAQLGFVGRVLI PAVGFLILCVAMGAVGM LPGIPPFLE
           60          70          80          90         100         110

m109.pep  HFKSLGX
           :|||||
g109      QFKSLGX
           120

```

a109.seq

1 ATGTATTATC GCCGGGTGT GGGGCTATCC GATGGACTTG GCGATTTGGC  
51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG  
101 GAAGCGGGCA TGGAATGAC GCGCAAGGC AAAACCACCC AATCCGCCGC  
151 CACCGTGGTG TTCTCTCCG CTTGGTCAAT CCGGTTTTCG GCTGGGCGTT

201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAAA GAGCGCAGCG  
251 CGCAATTAGG TTTCACCGGA CGCGTATTGA TACCCGTAGT AGGTTTCTTG  
301 ATCTTGTGTG TGGCGATGGG TGCGGTCGGG ATGCTGCCCG GTATCCCGCC  
351 GTTTTTGGAG CACTTCAAAT CTTTGGGCTA G

This corresponds to the amino acid sequence <SEQ ID 392; ORF 109>:

**a109.pep**

1 MYYYRVVGLS DGLGLAAGI ERSLGRRRIL TAFSGSHGND AQRQNHPIRR  
51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFTG RVLIIPVVGFL  
101 ILCVAMGAVG MLPGIPPFLE HFKSLG\*

m109/a109 97.6% identity in 126 aa overlap

		10	20	30	40	50	60
m109.pep		MYRRVVMGLSDGLGDLAAGIERSLGRRRILTAFGSGHGND	AQRQNHPIRRHRGVLFRLVN				
a109		MYRRVVGLSDGLGDLAAGIERSLGRRRILTAFGSGHGND	AQRQNHPIRRHRGVLFRLVN				
		10	20	30	40	50	60
		70	80	90	100	110	120
m109.pep		PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLIPAVGF	LILCVAMGAVGMLPGIPPFLE				
a109		PVFGWALTMLLDNLGLIGCKERSAQLGFTGRVLIPVVG	LILCVAMGAVGMLPGIPPFLE				
		70	80	90	100	110	120
m109.pep	HF	KSLGX					
a109	HF	KSLGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 393>:

q111.seq

1	ATGCCGTC	TAACACGCCT	GCCGAACCTT	ATCCGCGCCT	TGATATTTCG
51	CCTGGGTTC	ATCTTCTG	ACGCTTGTT	GAacaaacC	GCGCaaaccg
101	TTACCTGTCA	AGGGCAAACG	ATGGGTACGA	CCTATACCTG	CAAAATACCTT
151	TCAAATAATC	GGGACAAACT	CCCTCCCTC	GCCAAAAATAC	AAAAGCGCAT
201	TGATGATGCG	CTTAAAGAAG	TCAACCGGCA	GATGtccaCC	TACCAGACCG
251	ATTCGAAAT	CAGCGCGGTT	atagacagan	atgctggaga	gctcttcgcg
301	tnctatcgag	nttctataat	tgattccgcc	gaagactgtc	tgccataatac
351	gcctatctca	tcqqcgctct	qa		

This corresponds to the amino acid sequence <SEQ ID 394; ORF 111.ng>:

g111.pap

```

1  MPSETRLPNL  IRALIFALGF  IFLNACSEQT  AQTVTLQGET  MGTTYTVKYL
51  SNNRDKLPSP  AKIQKRIDDA  LKEVNRQMST  YQTDSEISRF  IQTAGELFAH
101 ASITDSAEDC  LPNTPISSAL  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 395>:

m111.seq

1	ATGCCGCTCTG	AAACACGCCT	GCCGAAC TTT	ATCCGCGTCT	TGATATTTGC
51	CCTGGGTTTC	ATCTTCTCTGA	ACGCTGTTC	GGAACAAACC	GCGCCAACCG
101	TTACCCCTGCA	AGGC GAAACG	ATGGGCACGA	CCTATaYcGT	CAAATACCTT
151	TCAAATAATC	GGGACAAACT	CCCCTACCT	GCCGAAATAC	AwAAACGCAT
201	CGATAGACGG	CTTAAAGAAk	TCAACCGGYA	GATGTCCACC	TATCAGCCCG
251	ACTCCGAAAT	CAGCCGGTTC	AACCAACGa	CAGCCGGCAA	GCCCCCTCGC
301	ATTTCAAGCG	ACTTCGCACA	CGTTACTGCC	GAAGCCGTCC	GCCTGAACCG
351	CCTGACACAC	GGCGGCTGG	ACGTAACCGT	CGGCCCTTG	GTCAACCTTT
401	GGGGATTTCG	CCCCGACAA	TCCGTTACCC	GTGAACCGTC	GCCGGAACAA
451	ATCAAAACAG	CGGCATCTTA	TACGGGCATA	GACAAATACTA	TTTTGAAACA
501	AGGCCAAGAT	TACGTTCTCT	TGACGCAAAAC	CACCCCCAAG	GCCTATTTTG
551	ATTTATCTTC	GATTGCCAAA	GGCTTCGGCG	TTGATAAAGT	TGCGGGCGAA

323

```

601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTTCTCTG ATTGTCAGGG
1001 ATAAAGGCGG cTACCGCACC GCCATGTCTT CCGAATTGTA AAAAGTGCtTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 396; ORF 111>:

```

m111.pep
1  MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLQGET MGTITYXVKYL
51  SNNRDKLPSP AEIXKRIDDA LKEXNRXMST YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTGVL VNLWGFPGDK SVTREPSP EQ
151 IKQAASYTGI DKIIKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPWR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPISHNLA SISVVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

ORF 111 shows 88.7% identity over a 97 aa overlap with a predicted ORF (ORF 111.ng) from *N. gonorrhoeae*:

m111.pep/g111.pep

	10	20	30	40	50	60
m111.pep	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTITYXVKYLSNNRDKLPSP					
	: : :     :     :     :     :     :     :     :     :					
g111	MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLQGETMGTITYXVKYLSNNRDKLPSP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m111.pep	AEIXKRIDDALKEXNRXMSTYQPDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
	:                         : :					
g111	AKIQKRIDDALKEVNRQMSTYQTDSEISRFIQTXAGELFAXHAXSITDSAEDCLPNTPI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m111.pep	GALDVTGVLVNLWGFPGDKSVTREPSPQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
g111	SALX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 397>:

a111.seq

```

1  ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTTGC
51  CCTGAGTTTT ATCTTCTCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAAATATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG
351 CCTGACACAC GGCGCGCTGG ACGTAACCGT CGGCCCTTGG GTCAACCTTT
401 GGGGATTCGG CCCGACAAA TCCGTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCAAG GCCTATTGCG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCTTGGCGC ATCGGTATCG
701 AACAGCCCAA CATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA

```

324

801 TAAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC  
 851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG  
 901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC  
 951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTCCTG ATTGTAGGG  
 1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGA AAAAGTGCTC  
 1051 CGCTAA

This corresponds to the amino acid sequence <SEQ ID 398; ORF 111.a>:

a111.pep

1 MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLQGET MGTTYTVKYL  
 51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMS YQPDSEISRF NQHTAGKPLR  
 101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ  
 151 IKQAASYTGI DKIIKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE  
 201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIVPL  
 251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS SISVVADSAM  
 301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL  
 351 R\*

m111/a111 97.7% identity in 351 aa overlap

m111.pep	10	20	30	40	50	60
	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSP					
a111	10	20	30	40	50	60
	MPSETRLPNFIRTLIFALSFIPLNACSEQTAQTVTLQGETMGTTYTVKYLSNNRDKLPSP					
m111.pep	70	80	90	100	110	120
	AEIXKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISDFAHVTAEAVRLNRLTH					
a111	70	80	90	100	110	120
	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISDFAHVTAEAVHLNRLTH					
m111.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
a111	130	140	150	160	170	180
	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
m111.pep	190	200	210	220	230	240
	AYLDLSSIAKGFVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRWIGIEQPNIVQ					
a111	190	200	210	220	230	240
	AYLDLSSIAKGFVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRWIGIEQPNIVQ					
m111.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVADSAM					
a111	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVVADSAM					
m111.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
a111	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 399>:

g111-1.seq

1 ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTGTC  
 51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTT GGAACAAACC GCGCAAACCG  
 101 TTACCCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT  
 151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAAATAC AAAAGCGCAT  
 201 TGATGATGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TACCAGACCG

325

```

251 ATTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ATTTGCGACA CGTTACCGCC GAAGCCGTCC GCCTGAACCG
351 CCGTACTCAC GCGGCACTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGGTTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAACAA
501 AGGCAAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAA GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCggcGAGTT
651 GCACGGCAAA GGCAAAAATG CGCACGGCGA ACCGTGGCGC ATCGGTATAG
701 AGCAACCCAA TATcatccaa ggcggcaata cgcAGattat cgtcccgctg
751 aaCaaccgtt cgcttgccac ttccggcgAT taccgtaTTT tccacgtcgA
801 TAAAACGGC Aaacgccttt cccacATCAT CAATCCCAAC AACAAACGAC
851 CCATCAGcCA CAacctcgcc tcCATCagCg TGGTCTCAGA CAGTGCATG
901 ACGGCGGACG GTTTATCCAC AGGATTATTT GTTTTAGCGG AAACCGAAGC
951 CTTAAGGCTG GCAGAACAAG AAAAATCTCG TGTTCCTTA ATTGTCCGGG
1001 ATAAGGACGG CTACCGCACC GCCATGTCTT CCGAATTTCG CAAGCTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 400; ORF 111-1.ng>:

g111-1.pep

```

1 MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLQGET MGTITYVKYL
51 SNNRDKLPSP AKIQKRIDDA LKEVNRQMSY YQTDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGPK SVTREPSPEQ
151 IKQAASYTGI DKIIILQOGKD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNHGEFWR IGIEQPNIIQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPISHNLA SISVVSADSAM
301 TADGLSTGLF VLGETEALRL AEQEKLAFL IVRDKDGYRT AMSSEFAKLL
351 R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 401>:

m111-1.seq

```

1 ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCGTCT TGATATTGCG
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGCGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAAATAAT GGGACAAACT CCCCTCACTT GCCGAAATAC AAAAACGCAT
201 CGATGACGGG CTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGATTTCG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAACAA
501 AGGCAAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAA GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GCGGGAATA CGCAGATTAT CGTCCCCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGCGG AAACCGAAGC
951 CTTAAGCTG GCAGAGCGCG AAAAATCTCG TGTTCCTTA ATTGTAGGG
1001 ATAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTTCG AAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 402; ORF 111-1>:

m111-1.pep

```

1 MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLQGET MGTITYVKYL
51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGPK SVTREPSPEQ
151 IKQAASYTGI DKIIILQOGKD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNHGEFWR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPISHNLA SISVVSADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAFL IVRDKDGYRT AMSSEFEKLL
351 R*

```

m111-1/g111-1 96.6% identity in 351 aa overlap

```

          10      20      30      40      50      60
m111-1.pep MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTITYVKYLSNNRDKLPSP
          |||
g111-1      MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLQGETMGTITYVKYLSNNRDKLPSP

```

326

	10	20	30	40	50	60
m111-1.pep	70	80	90	100	110	120
	AEIQKRIDDALKEVNROMSTYQPDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
g111-1	AKIQKRIDDALKEVNROMSTYQTDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
	70	80	90	100	110	120
m111-1.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFGPDKSVTREPSPEQIKQAASYTGIDKILKQGGDYASLSKTHPK					
g111-1	GALDVTVGPLVNLWGFGPDKSVTREPSPEQIKQAASYTGIDKILKQGGDYASLSKTHPK					
	130	140	150	160	170	180
m111-1.pep	190	200	210	220	230	240
	AYLDLSSIAKFGVDKVGAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQ					
g111-1	AYLDLSSIAKFGVDKVGAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIIQ					
	190	200	210	220	230	240
m111-1.pep	250	260	270	280	290	300
	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPISHNLASISVVADSAM					
g111-1	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPISHNLASISVVSDSAM					
	250	260	270	280	290	300
m111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
g111-1	TADGLSTGLFVLGETEALRLAEQEKLAFLIVRDKDGYRTAMSSEFAKLLRX					
	310	320	330	340	350	

## g111-1/p44550

sp|P44550|YOJL\_HAEIN HYPOTHETICAL LIPOPROTEIN HI0172 PRECURSOR >gi|1074292|pir||C64144  
 hypothetical protein HI0172 - Haemophilus influenzae (strain Rd KW20) >gi|1573128 (U32702)  
 lipoprotein, putative [Haemophilus influenzae Rd] Length = 346  
 Score = 349 bits (885), Expect = 2e-95  
 Identities = 177/328 (53%), Positives = 240/328 (72%), Gaps = 4/328 (1%)

Query: 23 LNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSPAEIXKRIDDALKEVNRXRMSTYQ 82  
 L AC ++T + ++L G+TMGTTY VKYL + S + + I+ LK+ N MSTY+  
 Sbjct: 17 LAACQKET -KVISLSGKTMGTTYHVKYLDGGSITATS-EKTHEEIEAILKDVNAKMSTYK 74

Query: 83 PDSEISRFNQHT-AGKPLRISSDFAHVTAEAVRLNRLTHGALDVTVGPLVNLWGFGPDKS 141  
 DSE+SRFNQ+T P+ IS+DFA V AEA+RLN++T GALDVTVG+VNLWGFGP+K  
 Sbjct: 75 KDSELSRFNQHTQVNTPIEISADFAKVLAEAIRLNKVTEGALDVTVGPPVNLWGFGPEKR 134

Query: 142 VTREPSPEQIKQAASYTGIDKILKQGGDYASLSKTHPKAYLDLSSIAKFGVDKVGAGEL 201  
 ++P+PEQ+ + ++ GIDKI L K+ A+LSK P+ Y+DLSSIAKFGVD+VA +L  
 Sbjct: 135 PEKQPTPEQLAERQAWVGIDKITLDTNKEKATLSKALPQVYVDLSSIAKFGVDQVAEKL 194

Query: 202 EKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQGGNTQIIIVPLNNRSLATSGDY 261  
 E+ QNY+VEIGGE+ KGKN G+PW+I IE+P + ++ LNN +A+SGDY  
 Sbjct: 195 EQLNAQNYMVEIGGEIRAKGNIEGKPPWQIAIEKPTTTGERAVEAVIGLNNMGMASSGDY 254

Query: 262 RIFHVDKNGKRLSHIINPNKRPISHNLASISVVADSAMTADGLSTGLFVLGETEALKLA 321  
 RI+ ++NGKR +H I+P PI H+LASI+V+A ++MTADGLSTGLFVLGE +AL++A  
 Sbjct: 255 RIY-FEENGKRFAHEIDPKTYPIQHHLASITVLAPTSMTADGLSTGLFVLGEDKALEVA 313

Query: 322 EREKLAVFLIVRDKGGYRTAMSSEFEKL 349  
 E+ LAV+LI+R G+ T SS F+KL  
 Sbjct: 314 EKNNLAVYLIIRTDNGFVTKSSSAFKKL 341

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 403>:

## a111-1.seq

```

1  ATGCCGCTCG AAACACGCCCT GCCGAACCTT ATCCGCACCT TGATATTTCG
51  CCTGAGTTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG

```

327

```

351 CCTGACACAC GGGCGGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAATCA TTTGAAACA
501 AGGCAAAAGT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGCGGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGC AAAACG CGCGCGGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GGGCGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATT TCCACGTCGA
801 TAAAAGCGCG AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAA ACTCG TGTTCCTG ATTGTCAGGG
1001 ATAAAGCGCG CTACCGCACC GCCATGTCTT CCGAATTGA AAAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 404; ORF 111-1.a>:

a111-1.pep

```

1 MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLQGET MGTITYTVKYL
51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMS YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWFGGPK SVTREPSPEQ
151 IKQAASYTGI DKILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPISHNLA SISVVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAFLV IVRDKGGYRT AMSSEFEKLL
351 R*

```

a111-1/m111-1 98.9% identity in 351 aa overlap

a111-1.pep	10	20	30	40	50	60
m111-1	10	20	30	40	50	60
a111-1.pep	70	80	90	100	110	120
m111-1	70	80	90	100	110	120
a111-1.pep	130	140	150	160	170	180
m111-1	130	140	150	160	170	180
a111-1.pep	190	200	210	220	230	240
m111-1	190	200	210	220	230	240
a111-1.pep	250	260	270	280	290	300
m111-1	250	260	270	280	290	300
a111-1.pep	310	320	330	340	350	
m111-1	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 405>:

g114.seq

```

1 ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCAGCAGG AATGCAGCAA
51 GACTTTTTTA TGTCCGCCGG GCGGGACGAG TATGGGGCGG TCAATGTCCG

```

```

101 TAACGGTAGG TTTGTTTTGT GTTCCATTA ACTTAACAAT ATCTGTCGAA
151 TACGGTCAAA GCGGCTATTT TACCAGAGCC GCCGAATGTA AAACAGGGTG
201 TCAGGGCATC AGCCCAGAGCT GCCTGAACGA ACGGACGGTT TGCAGAGTAA
251 CGATAAAATG GTCGAGCAGC GAAACATCAA CCAGCGACAT GGCCTGTGCC
301 AGCCGCCTTG TGAACATGAT GTCTTCCTGC GAAGGTCAG GCGAGCCGCC
351 CGGATGGTTG TGCAGCATAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
401 GTTTGACGAT TTCGCGGATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 406; ORF 114.ng>:

```

g114.pep
  1 MASITSPLHG AQQECSTFL CPPGGTSMGR SMSVTVGLFC VSINLTISVE
  51 YGQSGYFTRA AECKTGCGI SPSCLNERTV CEVTIKWSSS ETSTSDMACA
 101 SRLVNMSSC EGSGEPPGWL CAIIRLSAYS SNASLTISRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 407>:

```

m114.seq
  1 ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCACAGAG AATGCAGCAA
  51 GACTTTTTTA TGTCCACCGG GCGGACGAG TATAGGCGG TCAATGTCGG
 101 TAACGGTAGG TTTGTTTTGT GTTCCATTA ACTTAACAAT ATCTGTTGAA
 151 TACGGTTGAA GCGGCTATTT TATCAGAGCC GCCGCATGTA AAACAGAGTG
 201 TCAGGGCATC AACCCAGAGCT GTCTGAACGA ACAGACGCTT TCGCAkGTAA
 251 CGATAAAATG GTCGAGCAGC GACACATCGA CCAGCGACAT TGCCTGTGCC
 301 AGCCGCCTTG TGAACATGAT GTCTTCCTGC GAAGTTCsG GCGAGCCGcC
 351 CGgATGGTTG TGCgCAATAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
 401 GTTTGACGAT TTCGCGGATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 408; ORF 114>:

```

m114.pep
  1 MASITSPLHG AHRECSKFL CPPGGTSIGR SMSVTVGLFC VSINLTISVE
  51 YGXSGYFIRA AACKTECQGI NPSCLEQTL CXVTIKWSSS DTSTSDIACA
 101 SRLVNMSSC EXSGEPPGWL CAIIRLSAYS SNASLTISRM *

```

m114/g114 90.0% identity over a 140 aa overlap

	10	20	30	40	50	60
m114.pep	MASITSPLHGAHRECSKFLCPPGGTSIGRSMVTVGLFCVSINLTISVEYGXSGYFIRA					
g114	MASITSPLHGAQQECSKFLCPPGGTSMGRSMVTVGLFCVSINLTISVEYQSGYFTRA					
	10	20	30	40	50	60
m114.pep	AACKTECQGINPSCLEQTLCXVTIKWSSSDTSTSDIACASRLVNMSSCEXS					
g114	AECKTGCGGISPSCLNERTVCEVTIKWSSSETSTSDMACASRLVNMSSCEGS					
	70	80	90	100	110	120
m114.pep	GEPGWL					
g114	GEPGWL					
	70	80	90	100	110	120
m114.pep	CAIIRLSAYSSNASLTISRMX					
g114	CAIIRLSAYSSNASLTISRMX					
	130	140				
m114.pep	CAIIRLSAYSSNASLTISRMX					
g114	CAIIRLSAYSSNASLTISRMX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 409>:

```

a114.seq
  1 ATGCCGAGG CAAGCATCGC CTCCATCACT TCGCCGCTGC ACGGGGCGCA
  51 ACAGGAATGC AGCAAGACTT TTTTATGTCC GCCGGGCGGG ACGAGTATGG
 101 GGGCGTCAAT GTCGGTAACG GTAGGTTTGT TTTGTGTTTC CATTAACTTA
 151 ACGATATCTG TCGAATACGG TTGAAGCGGC TATTTTATCA GAGCCGCCGC
 201 ATGTAAAACA GGGTGTGAGG GCATCAGCCC GAGCTGCCTG AACGAACGGA
 251 CGGTTTGC GCATTACGATA AAATGGTCGA GCAGCGACAC ATCGACCAGC
 301 GACATTGCCT GTGCCAGCCG CCTTGTGAAC ATGATGTCTT CCTGCGAAGG
 351 TTCGGGCGAG CCGCCCGGAT GGTGTGCGC GATAATCAGG CTGTCGGCAT
 401 ATTCGTCAA TGCCAGTTTG ACAATTTCAC GGATGTAA

```



This corresponds to the amino acid sequence <SEQ ID 410; ORF 114.a>:

a114.pep

```

1  MPEASIASIT SPLHGAQQEC SKTFLCPPGG TSMGRSMSVT VGLFCVSINL
51 TISVEYG*SG YFIRAAACKT GCQGISPSCL NERTVCAVTI KWSSSDTSTS
101 DIACASRLVN MMSSCEGSGE PPGWLCIIIR LSAYSSNASL TISM*
```

m114/a114 92.9% identity in 140 aa overlap

```

              10      20      30      40      50
m114.pep      MASITSPLHGAHRECSKTFLCPPGGTSGRSMSTVGLFCVSINLTISVEYGXSG
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           MPEASIASITSPLHGAQQECSTFLCPPGGTSMGRSMSTVGLFCVSINLTISVEYGXSG
              10      20      30      40      50      60

              60      70      80      90      100     110
m114.pep      YFIRAAACKTECQGINPSCLNEQTLXVTIKWSSSDTSTSDIACASRLVNMMSCEXSSE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           YFIRAAACKTGCQGISPSCLNERTVCAVTIKWSSSDTSTSDIACASRLVNMMSCEGSSE
              70      80      90      100     110     120

              120     130     140
m114.pep      PPGWLCIIIRLSAYSSNASLTISM*
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           PPGWLCIIIRLSAYSSNASLTISM*
              130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 411>:

g117.seq

```

1  atggtcgacg aactcgacCT GCTGCCCAGT GCCGTCGCCG CCACCCGTGCT
51 TGCCGACATC GGACGCTACG TCCCCGATTG GAACCTATTG GTTCCGAGC
101 GCTGCAACAG CACCGTCGCC GAGCTGGTCA AAGGTGtgga CGAAGTGCAG
151 AAACCTACCC ACTTCGCCCG GGTGGACAGC CTCGCCACGC CGGAAGAACG
201 CGCACAGCAA GCGGAAACCA TGCGGAAAT GCTGCTGGCg atggttaccg
251 Acatccgcgt cgtatTAATC AAACCTGGCGA TGCGTaccg caccCTGcta
301 ttTTtaagCA ACGCCCCGA CAGCCCTGAA AAACgcccG TCgcaaAga
351 aacccTCGAC ATCTTCGCCC CGCTCGCCA CCGCTTGGGC GTGTGGCAGC
401 TCAAATGGCA GCTCGAAGAT TTGGGCTTCC GCCATCAAGA ACCCGAAAAA
451 TACCGGAAA TCGCCCTGCT TTTGGACGAA AAACGCACCG AACGCCTCGA
501 ATACATCGAA AACTTCCTCG ATATCCTGCG TACGGAATC AAAAAATACA
551 ATATCCAATT TGAAGTCGCC GGCCGTCCGA AACACATCTA CTCCATTAC
601 AAAAAAATGG TGAAGAAAAA ACTCAGCTTC GACGgctGT TCGACATCCG
651 CGCCGTGCGG ATTCTGGTCG ATACCGTCCC CGaGTGTAC ACCACGCTGG
701 gcaTCGTCCA CAGCCTCTGG CAGCCCATT CCGGCGagtt CGAcgactAC
751 ATCGCCAACC CCAAAGgcaA CGgttATAAA AGtTTGCACA CCGTCATCGT
801 cggcccGGAa gacaaaggtg tggaaGtgCA AATCCGCACC TTCGAtatGC
851 accAATTcAa CgaatTcggT gtcgcccGCC ACTGGCGtta caaagaaggc
901 ggcaaaggcg attccGCCtA cgaacaaAAA ATcgccTggt TCGcgaACT
951 CTTGGACTGG CGCGAAAATA TGGCGGAAAG CGGCAAGGAA GACCTCGCCG
1001 CCGCCTTCAA AACCGAGCTT TTCAACGACA CGATTATGT TTTGACCCCG
1051 CACGGCAAAG TCCTCTCTCT GCCAACGGGC GCAACCCCA TCGACTTCGC
1101 CTACGCCCTG CACAGCAGCA TcggCGACCG CTGCCGGGGC GCGAAAGTCG
1151 AaggGCAGAT TGTGCGCTG TCCACCCCG TCGAAAACGG ACAGCGCGTC
1201 GAAATcatta cCGCcaaAGA AGGGCATCCT TCCGTCAACT GGCTTTACGA
1251 AGGctgGGtc aAATCCGCA AGGCCATCGG caaAATCCGC GCCTAcacCC
1301 GCCAGcaaAa cgCgaCACC GTGCGGAAG AAGGCCGTGT CCAACTCGAC
1351 AAGCAGCTTG CCAAACTCAC GCCCAAACCC AACCTGCAAG AGCTTgccga
1401 aaATCTCGGC tacaaAAAGC cagaagacct ctacacCGCc gtcggacaag
1451 gcgaatttc caaccgccc atCcaaaaag cctgcccgcac GCTgaacgaa
1501 ccgccccCGG TGCCCGTCAG CGCAACCACC ATCGTCAAAC AGTCCAAAT
```

```

1551 CAAAAAAGGT GGCAAACCG GCGTGCTCAT CGACGGCGAA GACGGCTTGA
1601 TGACCACGCT TGCCAAATGC TGCAAACCGG CGCCGCCCGA CGATATTGCC
1651 GGCTTCGTTA CCCGCGAGCG CGGCATTTCG GTCCACCGCA AACCTGCCCC
1701 CTCTTTCCGA CACCTTGCCG AACACGCGCC CGAAAAAGTA CTGGACGCAA
1751 GTTGGGCGGC GTTGCAGGAA GGGCAAGTGT TCGCCGTCGA TATCGAAATC
1801 CGCGCCCAAG ACCGCTCCGG GCTTTTGC GC GACGTATCCG ACGCGCTCGC
1851 CCGCCACAAA CTCAACGTTA CCGCCGTGCA AACCCAGTCC CGCGACTTGG
1901 AAGCCAGCAT GAGGTTCACG CTCGAAGTCA AACAAGtCAA CGacCTCCCC
1951 CGCGTCCTCG CCGGCCTCGG CGATGTCAA GCGGTATTGA GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 412; ORF 117.ng>:

g117.pep

```

1 MVDEL DLLPD AVAATLLADI GRYPDWNLL VSERCNSTVA ELVKGVDEVQ
51 KLTHFARVDS LATPEERAQQ AETMRKMLLA MVTDIRVLI KLAMRTRTLL
101 FLSNAPDSPE KRAVAKETLD IFAPLANRLG VWQLKWQLED LGFRHQEPEK
151 YREIALLLDE KRTERLEYIE NFDLILRTEL KKYNIHFEDA GRPKHIYSIY
201 KKMVKKKLSF DGLFDIRAVR ILVDTVPECY TTLGIVHSLW QPIPGFDDY
251 IANPKNGYK SLHTVIVGPE DKGVEVQIRT FDMHQFNEFG VAAHWRYKEG
301 KGKDSAYEQK IAWLRQLLDW RENMAESGKE DLAAAFKTEL FNDTIYVLTLP
351 HGKVLSLPTG ATPIDFAYAL HSSIGDRCRG AKVEGQIVPL STPLENGQRV
401 EIITAKEGHP SVNWLYEGWV KSGKAIGKIR AYIRQONADT VREEGRVQLD
451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLINE
501 PPPVPVSATT IVKQSKIKKG GKTGVLLIDG DGLMTTLAKC CKPAPPDDIA
551 GFVTRERGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GOVFAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVTAQTQS RDLEASMRFT LEVKQVNDLP
651 RVLAGLGDVK GVLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 413>:

m117.seq (partial)

```

1 ..GTGAACTCA AGAAATACAA TGTCCATTTC GAAGTCGCCG GCCGCCCGAA
51 ACACATCTAC TCCATTTACA AAAAAATGGT GAAGAAAAAA CTCAGCTTCG
101 ACGGCTCTT TGACATCCGC GCCGTGCGAA TTCTGGTTGA TACCGTCCCC
151 GAGTGTACA CCACGCTGGG TATCGTCCAC AGCCTCTGGC AGCCCATTC
201 CGGCGAGTTC GACGACTACA TCGCCAATCC CAAAGGCAAC GGCTATAAAA
251 GTTTGCACAC CGTCATCGTC GGCCCGGAAG ACAAAGGCGT GGAAGTACAA
301 ATCCGCACCT TCGATATGCA CCAATTCAAC GAATTCTGGT TCGCCGCCCA
351 CTGgCGTTAC AAAGAGGGCG GCAAGGGCGA TTCCGCCTAC GAACAGAAAA
401 TCGCCTGGTT GCGCCAACTC TTGGACTGGC GCGAAAACAT GCGCGAAAGC
451 GGCAAGGAAG ACCTCGCCGC CGCCTTCAA ACCGAGCTTT TCAACGACAC
501 GATTTATGTT TTGACCCCGC ACGGCAAAGT CCTCTCCCTG CCCACGGGCG
551 CGACCCCAT CGACTTCGCC TACGCCCTGC ACAGCAGCAT CGGCGACCGT
601 TGCCCGCGTG CGAAAGTCGA AGGGCAGATT GTGCCGCTGT CCACCCCGCT
651 CGAAACCGGA CAGCGCGTCG AAATCATTAC CGCCAAAGAA GGGCATCCTT
701 CCGTCAACTG GCTTTACGAA GGCTGGGTCA AATCCAACAA GGCAATCGGC
751 AAAATCCGCG CCTACATCCG CCAGCAAAAC GCCGACACCG TGCGCGAAGA
801 AGGCCGCGTC CAACTCGACA AACAGCTTGC CAAACTCAGC CCCAAACCCA
851 ACCTGCAAGA GCTTGCCGAA AATCTCGGCT ACAAAAAGCC AGAAGACCTC
901 TACACCGCGC TCGGACAAGG CGAAATTTC AACCGCGCCA TCCAAAAGC
951 CTGCGGCACg CTGAACGAAC CGCCGCCCGT ACCCGTCAGC GAAACCACCA
1001 TCGTCAAACA GTCCAAAATC AAAAAAGGCG GCAAAAACGG CGTGCTCATC
1051 GACGGCGAAG ACGGTCTGAT GACCACGCTT GCCAAATGCT GCAAACCCGC
1101 GCCGCCGAC GATATTATCG GCTTCGTTAC CCGCGAGCGC GgCATTTCAG
1151 TGCACCGCAA AwyyTkCyCG TCTTTCCAAC ACCTCGCCGA ACACGCGCCC
1201 GAwAAAGTGC TGGACGCAAG CTGGGCGGCA TTGCAGGAAG GACAAGTATT
1251 CGCCGTCGAT ATCGAAATCC GCGCCCAAGA CCGCTCCGGG CTTTTCGCGC
1301 ACGTATCCGA CGCGCTCGCC CGCCACAAAC TCAACGTTAC CGCCGTGCAA
1351 ACCCAGTCCC GCGACTTGGG AGCCAGCATG AGGTTACAGC TCGAAGTCAA
1401 ACAAGTCAAC GACCTCCGCG GCGTCCTCGC CAGCCTCGGC GACGTCAAAG
1451 GCGTATTGAG CGTTACCCGG CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 414; ORF 117>:

m117.pep (partial)

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 117 shows 97.6% identity over a 490 aa overlap with a predicted ORF (ORF 117.ng) from *N. gonorrhoeae*:

m117/q117

m117.pep  
VKLKKNVNHFEVAGRPKHIYSIYKKMVKKKL  
:  
g117  
EKYREIALLLDEKRTERLEYIENFLDILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKKL

10      20      30  
150    160    170    180    190    200

40 50 60 70 80 90  
 m117.pep SFDGLFDIRAVRILVDTVP ECTYTLGIVHSLWQPIPG EFDYIANPKGNGYKSLHTVIVG  
 |||||  
 g117 SFDGLFDIRAVRILVDTVP ECTYTLGIVHSLWQPIPG EFDYIANPKGNGYKSLHTVIVG  
 210 220 230 240 250 260

```

      100      110      120      130      140      150
m117.pep  PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGDSAYEQKIAWLRQLLDWRENMAESG
          |||||
g117      PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGDSAYEQKIAWLRQLLDWRENMAESG
          |||||
      270      280      290      300      310      320

```

160 170 180 190 200 210  
 m117.pep KEDLAAAFKTELFNDTIYVLTPHGKVLSPGTGATPIDFAYALHSSIGDRCRGAKVEGQIV  
 |||||  
 g117 KEDLAAAFKTELFNDTIYVLTPHGKVLSPGTGATPIDFAYALHSSIGDRCRGAKVEGQIV  
 330 340 350 360 370 380

220            230            240            250            260            270  
 m117.pep    PLSTPLENGQRV E I I TAKEGHPSVNWLYEGWVKS NKAIGKIRAYIRQQNADTVREEGRVQ  
 |||||  
 g117        PLSTPLENGQRV E I I TAKEGHPSVNWLYEGWVKS GKAIGKIRAYIRQQNADTVREEGRVQ  
 390            400            410            420            430            440

280 290 300 310 320 330  
m117.pep LDKQLAKLTPKPNLQELAENLGYYKKPEDLYTAVGQGEISNRAIQKACGTLNEPPPPVPVSE  
g117 LDKQLAKLTPKPNLQELAENLGYYKKPEDLYTAVGQGEISNRAIQKACGTLNEPPPPVPVSA  
450 460 470 480 490 500

```

          340      350      360      370      380      390
m117.pep  TTIVKQSKI KKGKNGVLIDGEDGLMTTLAKCKPAPDDIIGFVTRERGISVHRKXXS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g117      TTIVKQSKI KKGKGTGVLDGEDGLMTTLAKCKPAPDDIAGFVTRERGISVHRKTCPS
          510      520      530      540      550      560

```

400 410 420 430 440 450  
ml17.pep FQHLAEHAPXKVLDSWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLVNTAVOT

g117	FRHLAEHAPEKVLDSWAALQEGQVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQT
	570 580 590 600 610 620
m117.pep	QSRDLEASMRFTLEV KQVNDLPRVLASLG DVKGVLSVTRLX
	460 470 480 490
g117	QSRDLEASMRFTLEV KQVNDLPRVLASLG DVKGVLSVTRLX
	630 640 650 660

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 415>:

a117.seq

```

1  ATGGTTCATG  AACTCGACCT  GCTCCCGCAT  GCCGTCGCCG  CCACCCTGCT
51  TGCCGACATC  GGACGCTACG  TCCCGGACTG  GAACCTATTG  GTTCCCGAAC
101 GCTGCAACAG  TACCGTCGCC  GAGCTGGTCA  AAGGTGTGGA  CGAAGTGCAG
151 AAACCTACCC  ACTTCGCCCC  GGTGGACAGC  CTCGCCACGC  CGGAAGAACG
201 CGCCCAGCAG  GCAGAACTA  TCGGGAAT  GCTGCTGGCG  ATGGTTACCG
251 ACATCCGCGT  CGTGTTAATC  AAACCTGGCG  TCGGTACGCG  CACCCTGCAA
301 TTTTAAAGCA  ACGCCCCGGA  CAGCCCCGAA  AAACGCGCCG  TCGCCAAAGA
351 AACCCTCGAC  ATCTTCGCCC  CGCTCGCCAA  CCGTTTGGGC  GTGTGGCAGC
401 TCAAAATGGCA  GTCGAAGAT  TTGGGCTTCC  GCCATCAAGA  ACCCGAAAAA
451 TACCGCGAAA  TCGCCCTGCT  TTTGGACGAA  AAACGCACCG  AACGCCTCGA
501 ATACATCGAA  AACTTCCTTA  ATATCCTGCG  TACGGAATC  AAAAAATACA
551 ATATCCACTT  TGAAGTCGCC  GGCCGTCCGA  AACACATCTA  CTCCATTTAC
601 AAAAAAATGG  TGAAGAAAAA  ACTCAGCTTC  GACGGGTGT  TCGACATCCG
651 CGCCGTGCGG  ATTCTGGTTG  ATACCGTCCC  CGAGTGTAC  ACCACACTGG
701 GCATTGTCCA  CAGCCTCTGG  CAGCCCATTC  CCGGCGAGTT  CGACGACTAC
751 ATCGCCAACC  CGAAAGGCAA  CGGCTATAAA  AGTTTGACA  CCGTCATCGT
801 CGGCCCGGAA  GACAAAGGCG  TGGAAGTGCA  AATCCGCACC  TTCGATATGC
851 ACCAATTCAA  CGAATTCGGT  GTCGCCGCGC  ACTGGCGTTA  CAAAGAGGGC
901 GGCAAAGGCG  ATTCCGCCTA  CGAACAAAAA  ATCGCCTGGT  TACGCCAACT
951 TTTGGACTGG  CGCGAAAACA  TGGCGGAAAG  CGGCAAGGAA  GACCTCGCCG
1001 CCGCCTTCAA  AACCGAGCTT  TTCAACGACA  CGATTTATGT  TTTGACCCCG
1051 CACGGCAAAG  TCCTCTCCT  GCCACAGGC  GCGACCCCA  TCGACTTCGC
1101 CTACGCCCTG  CACAGCAGCA  TCGGCGACCG  TTGCCGCGGT  GCGAAAGTCG
1151 AAGGGCAGAT  TGTGCCGCTG  TCCACCCCGC  TCGAAAACGG  ACAGCGTGTG
1201 GAAATCATT  CCGCCAAAGA  AGGGCATCCT  TCCGTCAACT  GGCTTTACGA
1251 AGGCTGGGTC  AAATCCAACA  AGGCAATCGG  CAAAATCCGC  GCCTACATCC
1301 GCCAGCAAAA  CGCCGACACC  GTGCGCGAAG  AAGGCCGCGT  CCAACTCGAC
1351 AAACAGCTTG  CCAAACCTAC  GCCCAAACCC  AACCTGCAAG  AGCTTGCCGA
1401 AAATCTCGGC  TACAAAAGC  CAGAAGACCT  CTACACCGCC  GTCGGACAAG
1451 GCGAAATTC  CAACCGCGCC  ATCCAAAAG  CCTGCGGCAC  GCTGAACGAA
1501 CGCCCGCCG  TACCCGTCAG  CGAAACCACC  ATCGTCAAAC  AGTCCAAAT
1551 CAAAAAGGC  GGCAAAAACG  GCGTGCTCAT  CGACGGCGAA  GACGGTCTGA
1601 TGACCACGCT  TGCCAAATGC  TGCAAACCCG  CGCCGCCCGA  CGACATTGTC
1651 GGCTTCGTTA  CCCGCGATCG  CGGCATTTG  GTACACCGCA  AAACCTGCCC
1701 CTCTTTCCGA  CACCTCGCCG  AACACGCGCC  CGAAAAAGTA  CTGGACGCAA
1751 GTTGGGCGGC  GTTGCAAGAA  GGACAAGTGT  TCGCCGTCGA  TATCGAAATC
1801 CGCGCCCAAG  ACCGCTCCGG  GCTTTTGCGC  GACGTATCCG  ACGCGCTCGC
1851 CCGCCACAAA  CTCAACGTTA  CCGCCGTGCA  AACCCAGTCC  CGCGACTTGG
1901 AAGCCAGCAT  GAGGTTCACG  CTCGAAGTCA  AACAAGTTAC  CGACCTCCCA
1951 CGCGTCCTCG  CCAGCCTCGG  CGACGTCAA  GCGGTATTGA  GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 416; ORF 117.a>:

a117.pep

```

1  MVHELDLLPD  AVAATLLADI  GRYVPDWNLL  VSERCNSTVA  ELVKGVDEVQ
51  KLTHFARVDS  LATPEERAQQ  AETMRKMLLA  MVTDIRVLI  KLAMRTRTLQ
101  FLSNAPDSPE  KRAVAKETLD  IFAPLANRLG  VWQLKWQLED  LGFRHQPEK
151  YREIALLLDE  KRTERLEYIE  NFLNILRTEL  KKYNIHFEVA  GRPKHIYSIY
201  KKMVKKKLSF  DGLFDIRAVR  ILVDTVPECY  TTLGIVHSLW  QPIPGFDDY
251  IANPKNGNYK  SLHTVIVGPE  DKGVEVQIRT  FDMHQFNEFG  VAAHWRYKEG
301  GKGDSEYEQK  IAWLRQLLDW  RENMAESGKE  DLAAAFKTEL  FNDTIYVLTP
351  HGKVLSLPTG  ATPIDFAYAL  HSSIGDRCRG  AKVEGQIVPL  STPLENGQRV

```

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 417>:

g117-1.seq

```

1   ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CCCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGTCTGCGG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTCGTGG CGCAGGAACA TTATCCTGCC
151 GATGCCGCCA GCCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GGCAGAAATG GTCGACGAAC TCGACCTGCT GCCCGATGCC GTCGCCGCCA
251 CCCTGCTTGC CGACATCGGA CGTACGTCC CCGATTGGAA CCTATTGGTT
301 TCCGAGCGCT GCAACAGCAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTTACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC ACAGCAAGCG GAAACCATGC GAAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT ATTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCTGAAAAA CGCGCCGTCG
551 CCAAGAAAC CCTCGACATC TTCGCCCCGC TCGCCAACCG CTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAGAAC
651 CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAC TTCCTCGATA TCCTGCGTAC GGAACCAAAA
751 AAATACAATA TCCACTTGA AGTCGCCGGC CGTCCGAAAC ACATCTACTC
801 CATTTACAAA AAATGGTGA AGAAAAAAGT CAGCTTCGAC GGCCTGTTTC
851 ACATCCGCGC CGTGGCGATT CTGGTCGATA CCGTCCCGGA GTGTTACACC
901 ACCTGGGCGA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGagttCGA
951 cgactACATC GCCAACCCCA AAGgcaACGg ttATAAAAGt TTGCACACCG
1001 TCATCGTcgg cccGGAagaa aaaggtgtgg aagtgcAAAT CCGCACCTTC
1051 GATATGcacc AATTCAaCga ATTCGGTGTC GCCGCCCACT GGCGTTACAA
1101 AGAAGGCGGC AAAGGCGATT CCGCCTACGA AAAAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGACTGGCGC GAAAATATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CCTTCAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAAGTCC TCTCTCTGCC AACGGGCGCA ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGCTG CCGGGGCGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCGGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAGGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCGGCAAGG CCATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGTGTCCA
1551 ACTCGACAAG CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCGGTC
1651 GGACAAGGCG AATTTTCCAA CCGCGCCATC CAAAAAGCCT CGCGCACGCT
1701 GAACGAACCG CCGCCCGTGC CCGTCAGCGC AACCACCATC GTCAAAACAGT
1751 CCAAAATCAA AAAAGGTGGC AAAACCGGCG TGCTCATCGA CGGCGAAGAC
1801 GGCCTTGATG CCACGCTTGC CAAATGCTGC AAACCCGCGC GCCTCCGACG
1851 TATTGCCGGC TTCGTTACCC GCGAGCGCGG CATTTCCGTC CACCGCAAAA
1901 CCTGCCCTCT TTTCCGACAC CTTGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 GAGCGCAAGT GGGCGGCGTT GCAGGAAGGG CAAGTGTTTC CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAATC AACGTTACCG CCGTGCAAAAC CCAGTCCCGC
2101 GACTTGGGAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCCGCGC GTCCTCGCGC GCCTCGGCGA TGTCAAAGGC GTATTAGCGC
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 418; ORF 117-1.ng>:

g117-1.pep

```

1   MTAISPIQDT QSATLQELRE WFD SYCAALP DNDKNLIGTA WSLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VDELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLDILRTELK
251 KYNHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKLS LHTVIVGPPE KGEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTPL GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGOIVPLS TPLENGQORVE IITAKEGHPS VNWLYEGWVK SGKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSATTI VKQSKIKKGG KTGVLIDGED
601 GLMTTLAKCC KPAPPDDIAG FVTRERGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLAGLDGVKG VLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 419>:

m117-1.seq

```

1   ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA

```

```

51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCGG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTTGCTGG CGCAGGAACA TTACCCCGCC
151 GATGCCGCGCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GGCAGCAATG GTTCATGAAC TCGACCTGCT CCCCGATGCC GTCGCCGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301 TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTCACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC CCAGCAGGCA GAAACTATGC GGAAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCAGACAG CCGGAAAAA CGCGCCGTCG
551 CCAAGAAAC CCTCGACATC TTCGCCCGCG TCGCCAACCG TTTGGCGGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAAAGCC
651 CGAAAAATAC CGCGAAATCG CGCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAC TTCCTCAACA TCCTGCGCGG TGAACCAAG
751 AAATACAATG TCCATTTCGA AGTCGCCGCG CGCCGAAAC ACATCTACTC
801 CATTTCACAA AAATGGTGA AGAAAAACT CAGCTTCGAC GGCCTCTTTG
851 ACATCCGCGC CGTGCGAATT CTGGTTGATA CCGTCCCGCA GTGTTACACC
901 ACCTGGGTA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAATCCCA AAGGCAACGG CTATAAAGT TTGCACACCG
1001 TCATCGTCGG CCCGGAAGAC AAAGGCGTGG AAGTACAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCGGTGTC GCCGCCCACT GGCCTTACAA
1101 AGAGGGCGCG AAGGGCGATT CCGCCTACGA ACAGAAATC GCCTGGTTGC
1151 GCCAACTCTT GGACTGGCGC GAAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTGCGCCGCG CCTTCAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCCCTGCC CACGGGCGCG ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCGGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACRAG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCCGGTCCA
1551 ACTCGACAAA CAGTTGCCA AACTCACGCC CAAACCAAC CTGCAAGAGC
1601 TTGCGGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCGGTC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCAACATC GTCAAAAGT
1751 CCAAAATCAA AAAGGCGGC AAAACGCGG TGCTCATCGA CGGCGAAGC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTATCGGC TTCGTTACCC GCGAGCGCGG CATTTAGTGC CACCGCAAAA
1901 CCTGCCCGTC TTTCCAACAC CTCGCCGAAC ACGCGCCCGA AAAAGTGCTG
1951 GACGCAAGCT GGGCGGCATT GCAGGAAGGA CAAGTATTCG CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAATC AACGTTACCG CCGTGCAAC CAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCCGCGC GTCCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGACCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 420; ORF 117-1>:

**m117-1.pep**

```

1  MTAISPIQDT QSATLQELRE WFDYSYCAALP DNDKNLIGTA WLLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLOF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQKPEKY REIALLLDEK RTERLEYIEN FLNILRGELK
251 KYNVHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKGNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQVE IITAKEGHPS VNWLYEGWVK SNKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIDGED
601 GLMTTTLAKCC KPAPPDDIIG FVTRERGISV HRKTCPSFOH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLASLGDVKG VLSVTRL*

```

**m117-1/g117-1** 98.2% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFDYSYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
g117-1	MTAISPIQDTQSATLQELREWFDYSYCAALPDNDKNLIGTAWSLAQEHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120

m117-1.pep	PDHFLGAAQMVHEDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDDEVQK
g117-1	PDHFLGAAQMVDELDPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDDEVQK
	70 80 90 100 110 120
m117-1.pep	130 140 150 160 170 180
	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK
g117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK
	130 140 150 160 170 180
m117-1.pep	190 200 210 220 230 240
	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQKPEKYREIALLLDEKRTTERLEYIEN
g117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQEPEKYREIALLLDEKRTTERLEYIEN
	190 200 210 220 230 240
m117-1.pep	250 260 270 280 290 300
	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
g117-1	FLDILRTELKKYNHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
	250 260 270 280 290 300
m117-1.pep	310 320 330 340 350 360
	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV
g117-1	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEEKGVEVQIRTFDMHQFNEFGV
	310 320 330 340 350 360
m117-1.pep	370 380 390 400 410 420
	AAHWRYKEGGKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH
g117-1	AAHWRYKEGGKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH
	370 380 390 400 410 420
m117-1.pep	430 440 450 460 470 480
	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
g117-1	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
	430 440 450 460 470 480
m117-1.pep	490 500 510 520 530 540
	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
g117-1	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
	490 500 510 520 530 540
m117-1.pep	550 560 570 580 590 600
	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED
g117-1	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSATTIVKQSKIKKGGKTGVLIDGED
	550 560 570 580 590 600
m117-1.pep	610 620 630 640 650 660
	GLMTTLAKCKKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAASWALQEG
g117-1	GLMTTLAKCKKPAPPDDIAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAASWALQEG
	610 620 630 640 650 660
m117-1.pep	670 680 690 700 710 720
	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEVQVNDLPR
g117-1	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEVQVNDLPR
	670 680 690 700 710 720
m117-1.pep	730
	VLASLGDVKGVLSVTRLX
g117-1	VLAGLGDVKGVLSVTRLX
	730

m117-1/RelA



sp|P55133|RELA\_VIBSS GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi|537617 (U13769) ppGpp synthetase I [Vibrio sp.] Length = 744  
Score = 536 bits (1366), Expect = e-151  
Identities = 288/685 (42%), Positives = 432/685 (63%), Gaps = 31/685 (4%)

Query: 74 LDLLPDAVAATLLADI---GRYVPDWNLLVSERCNSTVAELVKGVDVQKLTHFARVDSL 130  
L + D + A LL + G Y D + E + T+ LV+GV+++ ++ ++ S  
Sbjct: 68 LSMADATLIAALLYPLVEGGCYSTD---ALKEEYSGTILHLVQVEQMCAIS---QLKST 121

Query: 131 ATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEKRAVAKETLDI 190  
A +A Q + +R+MLL+MV D R V+IKLA R L+ + + PD +RA A+E +I  
Sbjct: 122 AEETAQAAQVDNIRMLLSMVDDFRCVVIKLAERICNLREVKDQPDDEV-RRAAAQECANI 180

Query: 191 FAPLANRLGVWQLKWQLEDLGRHQKPEKYREIALLLDEKRTERLEYIENFLNIRGELK 250  
+APLANRLG+ QLKW++ED FR+Q P+ Y++IA L E+R +R +YI +F++ L +K  
Sbjct: 181 YAPLANRLGIGQLKWEIEDYAFRYQHPDITYKQIAQLSERRIDREDYITHFVDDLSDAMK 240

Query: 251 KYNVHFVAVGRPKHIYSIYKKMVKKLSFDGLDIRAVRILVDVTPCYTTLGIVHSLWQ 310  
N+ EV GRPKHIYSI++KM KK L FD LFD+RAVRI+ + + +CY LG+VH+ ++  
Sbjct: 241 ASNIRAEVQGRPKHIYSIWRKMQKKSLEFDELFDVRAVRIVAEELQDCYAALGVVHTKYR 300

Query: 311 PIPGEFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTDFMHQFNEFGVAHHWRYKEG- 369  
+P EFDY+ANPK NGY+S+HTV++GPE K +E+QIRT MH+ +E GVAHHW+YKEG  
Sbjct: 301 HLPKEFDDYVANPKNGYQSIHTVVLGPEGKTIEIQTIRKMHHESELGVAHHWRYKEGT 360

Query: 370 --GKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPHGKVLSP 427  
G SAY++KI WLR+LL W+E M++SG ++ +++++F+D +Y TP G V+ LP  
Sbjct: 361 ASGGAQSAYDEKINWLRKLLAQEEMSDSG--EMLDELRSQVFDREVYAF+PKGDVVDLP 418

Query: 428 TGATPIDFAYALHSSIGDRRCGAKVEGQIVPLSTPLENGQVEIITAKEGHPSVNWLYE- 486  
+ ATP+DFAY +HS +G RC GAKVEG+IVP + L+ G +VEIIT KE +PS +WL  
Sbjct: 419 SNATPLDFAYHIHSEVGHRCIGAKVEGRIVPFTYHLQMGDQVEIITQKEPNPSRDWLNPN 478

Query: 487 -GWVKSNAIGKIRAYIRQONADTVREGRVQLDKQLAKL--TPKPNLQELAENLGKYP 543  
G+V S++A K+ A+ R+Q+ D G+ L+ +L K+ T K A+ K P  
Sbjct: 479 LGFVTSSRARAKVHAWFRKQDRDNIIAGKEILEAELVKIHATLKDAQYAAKRFNVKSP 538

Query: 544 EDLYTAVGQGEIS-NRAIQKACGTLNEPPVPVSETTIVKQSKI-----KKGKNGV 594  
E+LY +G G++ N+ I +N+P + + K S+ KK ++ V  
Sbjct: 539 EELYAGIGSGDLRINQVINHINALVNKPTAEEDQQLLEKLSEASNKQATSHKKPQRDAV 598

Query: 595 LIDGEDGLMTTLAKCCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDSW 654  
+++G D LMT LA+CC+P P DDI GFVT+ RGISVHR C + L HAPE+++D W  
Sbjct: 599 VVEGVNDLMTHLARCCQPIPGDDIQGFVTQGRGISVHRMDCEQLEELRHHAPERIIDTVW 658

Query: 655 AALQEGQVFVAVDIEIRAQDRSGLLRDVSALARHKLNVAVQTQ--SRDLEASMRFTLEV 712  
G + + + + A +R+GLL++++ L K+ V ++++ + + M F LE+  
Sbjct: 659 GGGFVGN-YTITVRVTASERNGLLKELTNLMNEKVKVAGMKSRVDYKQMSIMDFEEL 717

Query: 713 KQVNDLPRVLASLGDVKGVLVSVTRL 737

+ L RVL + VK V RL  
Sbjct: 718 TDLEVLGRVLKRIEQVKDVAEAKRL 742

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 421>:

a117-1.seq

```

1   ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCAC CGCGCTGCCG AACACGATA
101 AAAAAGTTGT CTTAGCCGCC CGTTCGCTGG CGGAAGCACA TTACCCCGCC
151 GATGCCGCCA CGCCGTATGG CGAACCGCTG CCCGACCACT TCCTCGGCGC
201 GGCACAAATG GTTCATGAAC TCGACCTGCT CCCGATGCC GTCGCGGCCA
251 CCCTGCTTGC CGACATCGGA CGTACGTCC CCGACTGGAA CCTATTGGTT
301 TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTCACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC CCAGCAGGCA GAAACTATGC GGAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCCAGAAAA CGCGCCGTCG
551 CCAAGAAAC CCTCGACATC TTCGCCCCGC TCGCAACCG TTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAGAAC
651 CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAC TTCCTTAATA TCCTGCGTAC GGAACCAAA
751 AAATACAATA TCCACTTTGA AGTCGCCGCG CGTCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAAGT CAGCTTCGAC GGGTTGTTCG

```

```

851 ACATCCGCGC CGTGCGGATT CTGGTTGATA CCGTCCCCGA GTGTTACACC
901 ACACCTGGGCA TTGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAACCCGA AAGGCAACGG CTATAAAGT TTGCACACCG
1001 TCATCGTCGG CCGGAAGAC AAAGGCGTGG AAGTGCAAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCGGTGTC GCCGCGCACT GCGGTTACAA
1101 AGAGGGCGGC AAAGGCGATT CCGCCTACGA AAAAAAATC GCCTGGTTAC
1151 GCCAACTTTT GGACTGGCGC GAAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTGCGCGCCG CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCCCTGCC CACAGGCGCG ACCCCCATCG
1301 ACTTCGCTTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCGCTCG AAAACGGACA
1401 CGGTGTCGAA ATCATTACCG CCAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGTAC AAAAGCCAG AAGACCTCTA CACCGCGTCT
1651 GGACAAGCGG AAATTTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCATC GTCAACAGT
1751 CCAAAATCAA AAAAGGCGGC AAAACGGCG TGCTCATCGA CGGCGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 CATTGTCGGC TTCGTTACCC GCGATCGCGG CATTCGCTA CACGCGAAAA
1901 CCTGCCCTTC TTCCGACAC CTCGCGGAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGA CAAGTGTTCT CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GTCGCGGCT TTTGCGGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAATC AACGTTACCG CCGTGCAAA CAGTCCCGC
2101 GACTTGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTTACCGA
2151 CCTCCACGC GTCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 422; ORF 117-1.a>:

**a117-1.pep**

```

1  MTAISPIQDT QSATLQELRE WFDSYCTALP NNDKKLVLA RSLAEAHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLNLRTELK
251 KYNIFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKLS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLDWR ENMAESGKED
401 LAAAFTELEF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQORVE IITAKEGHPS VNWLYEGWVK SNKAIGKIRA
501 YIRQQNADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIVG FVTRDRGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVTDLPR VLASLGDVKG VLSVTRL*

```

**a117-1/m117-1** 97.7% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
a117-1	MTAISPIQDTQSATLQELREWFD SYCTALPNNDKKLVLAARS LAEHYPADAATPYGEPL					
	10	20	30	40	50	60
m117-1.pep	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK					
a117-1	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK					
	70	80	90	100	110	120
m117-1.pep	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK					
a117-1	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK					
	130	140	150	160	170	180
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRTLQFLSNAPDSPEK					
a117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRTLQFLSNAPDSPEK					
	190	200	210	220	230	240
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFHQKPEKYREIALLLDEKRTERLEYIEN					
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFHQEPEKYREIALLLDEKRTERLEYIEN					
	190	200	210	220	230	240

	250	260	270	280	290	300
m117-1.pep	FLNILRGELKKYNVHFVAGRPKHIYSIYKKMVKKKLSFDGLFDIRAVRILVDTVP	ECYT				
a117-1	FLNILRTELKKYNIHFVAGRPKHIYSIYKKMVKKKLSFDGLFDIRAVRILVDTVP	ECYT				
	250	260	270	280	290	300
	310	320	330	340	350	360
m117-1.pep	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
a117-1	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m117-1.pep	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLT	PH				
a117-1	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLT	PH				
	370	380	390	400	410	420
	430	440	450	460	470	480
m117-1.pep	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
a117-1	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
	430	440	450	460	470	480
	490	500	510	520	530	540
m117-1.pep	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY					
a117-1	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY					
	490	500	510	520	530	540
	550	560	570	580	590	600
m117-1.pep	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKGGKNGVLIDGED					
a117-1	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKGGKNGVLIDGED					
	550	560	570	580	590	600
	610	620	630	640	650	660
m117-1.pep	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDA	SWAALQEG				
a117-1	GLMTTLAKCKPAPPDDIIGFVTRDRGISVHRKTCPSFRHLAEHAPEKVLDA	SWAALQEG				
	610	620	630	640	650	660
	670	680	690	700	710	720
m117-1.pep	QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVAVQTQSRDLEASMRFTLEV	KQVNDLPR				
a117-1	QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVAVQTQSRDLEASMRFTLEV	KQVNDLPR				
	670	680	690	700	710	720
	730					
m117-1.pep	VLASLGDVKGVLVSVTRLX					
a117-1	VLASLGDVKGVLVSVTRLX					
	730					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 423>:

```

g118.seq
1  ATGTGCGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGCTG GAGAATGATT TAATcgaGGT TAGGAGAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAAATG GGAGCTTTT GAAATTAAG
251 CTTCCCCTTG GTTGCTGAT AGCGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAaCA AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 424; ORF 118.ng>:

```

g118.pep
1  MCEFkdFRrn IPCfEEYDEN SFIgKWYDDG VWDDEEYwKL ENdLIEVRRK
51  YPYpMDIPRD IVIGIGTIID FLMVPnWELF EIKASpWLpD SVGIHERYER
101 FTTMLRYIFT EKdIVNVRFd YYNKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 425>:

```
m118.seq
1  ATGTGTGAGT TCAAGGATAT TATAAGAAAC GTTCCTTATT TTGAGGGGTA
51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGACAT ACCAAGATAT GTTGTCATTG GAATCGGTAC
201 CATTATTGAT TTCTTAATGG TTCCAAATTG GAAACTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 426; ORF 118>:

```
m118.pep
1  MCEFkdIIRN VPYFEGYDEN SFIGKwyDDG VWDDEEYwKL ENdLIEVRKK
51  YPYPMdIPRY VVIGIGTIID FLMVPNwKLF EIKASpWLPD SVGIHERYER
101 FTTMLRYIFT EKdIVNVRFd YYNKK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 118 shows 92.8% identity over a 125 aa overlap with a predicted ORF (ORF 118.ng) from *N. gonorrhoeae*:

```
m118/g118

          10      20      30      40      50      60
m118.pep  MCEFkdIIRNVpYFEGYDENsFIGKwyDDGvWDDEEYwKLEndLIEVRKKYPYPMdIPRY
          |||||: ||:| || |||||
g118       MCEFkdFRRNIPCFEeYDENsFIGKwyDDGvWDDEEYwKLEndLIEVRKKYPYPMdIPRD
          10      20      30      40      50      60

          70      80      90      100     110     120
m118.pep  VVIGIGTIIDFLMVPNwKLFElKASpWLPdSVGIHERYERfTTMLRYIfTEKdIVNVRFd
          :|||||
g118       IVIGIGTIIDFLMVPNwELFEIKASpWLPdSVGIHERYERfTTMLRYIfTEKdIVNVRFd
          70      80      90      100     110     120

m118.pep  YYNKKX
          |||||
g118       YYNKKX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 427>:

```
a118.seq
1  ATGTGTGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAATGAG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 428; ORF 118.a>:

```
a118.pep
1  MCEFkdFRRN IPCFEEYDEN SFIGKwyDDG VWDDEEYwKL ENdLIEVRKK
51  YPYPMdIPRD IVIGIGTIID FLMVPNwELF EIKASpWLPD SVGIHERYER
101 FTTMLRYIFT EKdIVNVRFd YYNKK*
```

m118/a118 93.6% identity in 125 aa overlap

```
m118.pep  MCEFkdIIRNVpYFEGYDENsFIGKwyDDGvWDDEEYwKLEndLIEVRKKYPYPMdIPRY
          |||||: ||:| || |||||
a118       MCEFkdFRRNIPCFEeYDENsFIGKwyDDGvWDDEEYwKLEndLIEVRKKYPYPMdIPRD
          10      20      30      40      50      60
```

	70	80	90	100	110	120
m118.pep	VVIGIGTIIDFLMVPNWKLF EIKAS PWLPDSVGIHERYERFTT MLRYIFTEKDIVNVRFD					
a118	IVIGIGTIIDFLMVPNWE LFEIKAS PWLPDSVGIHERYERFTT MLRYIFTEKDIVNVRFD					
	70	80	90	100	110	120
m118.pep	YYNKXX					
a118	YYNKXX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 429>:

```

g120.seq
1  ATGATGAAGA CTTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAAGGCTACC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGTA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAATCC GGCGGTACGG TTGTCGGCAA TACCCTGCAC CCTGCCTACT
251 ATAAAGACAT ACGCAGGGGC AAACGTGTAT CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTTGTTCA CGCTTGCCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGTCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGCC TGAATAAGGC GGGTACGGGA AAATACAGCA Taggcggcgt
501 gGAAACCGAA GTCGTCAAAT ATCGGGTGCG GC CGCGGCAC GATACGGTAA
551 CGTATTCTTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGAcgaCG GCAAAACCTA TACGCTGAAG CTCAAATCGG TGCAGATCAA
651 CGGACAGGCC GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 430; ORF 120.ng>:

```

g120.pep
1  MMKTFKNIFS AAILSAAALPC AYAARLPQSA VLHYSGSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PAYYKDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DTVTYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 431>:

```

m120.seq
1  ATGATGAAGA CTTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGmACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGTA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GGCGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAACGTGTAT CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTTGTTCA CGCTTGCCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGCG GC CGCGGCAC GATGCGGTAA
551 TGTATTCTTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCG

```

This corresponds to the amino acid sequence <SEQ ID 432; ORF 120>:

```

m120.pep
1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLXYSYSGYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 120 shows 97.3% identity over a 223 aa overlap with a predicted ORF (ORF 120.ng) from *N. gonorrhoeae*:

m120/g120

	10	20	30	40	50	60
m120.pep	MMKTFKNIFS	AAILSAAALPCAYAAGLPQSAVLX	YSGSYGIPATMTFERSGNAYKIVSTIK			
g120	MMKTFKNIFS	AAILSAAALPCAYAARLPQSAVLHYSGSYGIPATMTFERSGNAYKIVSTIK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTY	GKAGESKTEQSPKAM				
g120	VPLYNIRFESGGTVVGNTLHPAYYKDIRRGKLYAEAKFADGSVTY	GKAGESKTEQSPKAM				
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE	VVKYRVRRGD				
g120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE	VVKYRVRRGD				
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA	AKP				
g120	DTVTYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA	AKPX				
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 433>:

a120.seq

```

1  ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AACTGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTTGTTC ACGTTGCTG GCAGTTGGCG GCAAATGACG
401 CGAAATCCC CCCGGGGCTG AAAATCACCA ACGGCAGAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGCGGCGGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 434; ORF 120.a>:

a120.pep

```

1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLHYSGSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNTLH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

m120/a120 99.6% identity in 223 aa overlap

	10	20	30	40	50	60
m120.pep	MMKTFKNIFS	AAILSAAALPCAYAAGLPQSAVLX	YSGSYGIPATMTFERSGNAYKIVSTIK			
a120	MMKTFKNIFS	AAILSAAALPCAYAAGLPQSAVLHYSGSYGIPATMTFERSGNAYKIVSTIK				

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	10	20	30	40	50	60
m120.pep	70	80	90	100	110	120
	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVITYGKAGESKTEQSPKAM					
a120	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVITYGKAGESKTEQSPKAM					
	70	80	90	100	110	120
m120.pep	130	140	150	160	170	180
	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVKYRVRRGD					
a120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVKYRVRRGD					
	130	140	150	160	170	180
m120.pep	190	200	210	220		
	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAKPX					
a120	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAKPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 435>:

g121.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51  GGCGGATGCC GTGCTGGTAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCTGACC GGTTCGCGCG CAAATGTCTG
151 GATTTCAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACTGa cgcggatttT TACCGTCggc gacttcCGCA
401 GCCGCGACCT TGCTGCCGGC GGacaAGGTG CGCCGCTCGT CCCCgcCTTT
451 CACGAAGCCC TGTTCGCGCA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CGCGGGGATT GCCAACATCA GCGTACTCCC CCCCggCGCA CCCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cacTGGcagc TGCCTTACGA CAAAAacggt gcAAAGgcgg cacAAGGCAA
651 catatTGcCg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTCTCAC
701 AACCCcacc aaAAAGCACG GGgcGCGaac TgtttgcccT AAattggctc
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgtat tgcggacgct
801 ttcccgattc accgcgcaaA ccgTttggga cgcgtctca CACGACGCGG
851 CAGATGCCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATttg
1001 cgtggttggc GGCCTGTTGG ATTAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCGACCGGCG CATCCAACC GTGTATTCTG GGCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 436; ORF 121.ng>:

g121.pep

```

1  METQLYIGIM SGTSMGDADA VLVRMDGGKW LGAEGHAFTP YPDLRRLKLL
51  DLQDTGTDEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVWDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 437>:

m121.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTCGCGCG CCAATGTCTG

```

```

151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCCTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxCAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACGCCACCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 438; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCQNLAAPS DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL Axxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
151 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKW LGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKW LGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCQNLAAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
g121	HRSRILSQELSRLYAQTAAELLCQNLAAPCDITALGCHGQTVRHAPHEGYSIQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121.pep	Axx					
g121	AELTRIFTVGDFRSRDLAAGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPFGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	xxxxxxxxxxxxxxxxxxxxxxxxxQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
g121	PAFGFDTPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDAYSHAAADARQMYICDGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAYSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300



345

	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	:					
g121	LMADLAECFGTRVSLHSTAE LNLDPOQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
g121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 439>:

```

a121.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CAAATGCTG
151 GATTGTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACAGCGAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGGCGCGGC GGACAAGGCG CGCCGCTCGT CCCCCTTTT
451 CACGAAGCCC TGTTCGCGCA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTCGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTC ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGCG GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCGC CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 440; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRRLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLA PS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPOQWVEA AFAFWMAACW VNRI PGSPHK
351 ATGASKPCIL GAGYYY*

```

m121/a121 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	:					
a121	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAELLCQNLA PSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	:					
a121	HRSRILSQELSRLYAQTAELLCQNLA PSDITALGCHGQTVRHAPEHSYSVQLADLPLL					
	70	80	90	100	110	120

346

	130	140	150	160	170	180
m121.pep	XX					
		:	:	:	:	:
a121	AERTQIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121.pep	190	200	210	220	230	240
	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
	:	:	:	:	:	:
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121.pep	250	260	270	280	290	300
	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNPV					
	:	:	:	:	:	:
a121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFDVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
m121.pep	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
	:	:	:	:	:	:
a121	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWMAACWVNRI PGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
	:	:	:	:	:	:
a121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 441>:

m121-1.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCC TACCCCGGCA GGTACGCGG CCAATTGCTG
151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCGCGCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATT
351 GCCGCTGCTG GCGGAACGGA CGCGGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGCG GGACAAGGCG CGCCACTCGT CCCC GCCTTT
451 CACGAAGCCC TGTTCGCGCA CAACAGGGAA ACACGCGCGG TACTGAACAT
501 CGCGGGGATT GCCAACATCA GCGTACTCCC CCCC GACGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGACGCGTG GACGCAAGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCCAACC TAAAAGCAGC GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGTTT ACCGCGCAAA CCGTTTGC GA CCGCTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCGC CATCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 442; ORF 121-1>:

m121-1.pep

```

1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLRRLQL
51  DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDVAV HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 95.6% identity in 366 aa overlap

10 20 30 40 50 60

```

m121-1.pep  METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTYPGRRLRRQLLDLQDTGADEL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         METQLYIGIMSGTSMGDADAVLVRMDGGKWLGAEGHAFTYPDRLRRLKLLDLQDTGTDEL
              10      20      30      40      50      60

              70      80      90      100     110     120
m121-1.pep  HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAFEPHGYSIQLADLPLL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         HRSRMLSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAFEPHGYSIQLADLPLL
              70      80      90      100     110     120

              130     140     150     160     170     180
m121-1.pep  AERTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDNRETRAVLNIGGIANISVLPPDA
              || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         AELTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPPGA
              130     140     150     160     170     180

              190     200     210     220     230     240
m121-1.pep  PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
              190     200     210     220     230     240

              250     260     270     280     290     300
m121-1.pep  GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICGGGIRNPV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDVASHAAADARQMYICGGGIRNPV
              250     260     270     280     290     300

              310     320     330     340     350     360
m121-1.pep  LMDLAECFGTRVSLHSTADLNLDQPQVVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         LMDLAECFGTRVSLHSTAE LNLDQPQVVEAAAFWLAACWINRIPGSPHKATGASKPCIL
              310     320     330     340     350     360

m121-1.pep  XAGYYYY
              |||||
g121         GAGYYYY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 443>:

```

a121-1.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGCGATGCC GTACTGATAC GGATGGACGG CCGCAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCGAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGTG ACGCGCAAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCCGACCTT TCGCGCCGGC GGACAAGGCG CGCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCGGACGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGCG AATATGCTGA TGGACGCTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCGG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCTT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTG ACCGCGCAAA CCGTTTTCGA CGCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCGGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 444; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM SGTSMDGADA VLIRMDGGKW LGAEGHAFTP YPGRRLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAFESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWMQA

```

201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL  
 251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV  
 301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK  
 351 ATGASKPCIL GAGYYY\*

m121-1/a121-1 96.4% identity in 366 aa overlap

m121-1.pep	10	20	30	40	50	60
	METQLYIGIMSGTSM	DGADAVLIRMDGGK	WLGAEGHAFTYP	PGRLRRQLLDLQ	DTGADEL	
a121-1	10	20	30	40	50	60
	METQLYIGIMSGTSM	DGADAVLIRMDGGK	WLGAEGHAFTYP	PGRLRRKLLDLQ	DTGADEL	
m121-1.pep	70	80	90	100	110	120
	HRSRILSQELSR	LYAQTAAE	LLCSQNLAPSD	ITALGCHGQT	VRHAP	EHGYSIQLADLPLL
a121-1	70	80	90	100	110	120
	HRSRILSQELSR	LYAQTAAE	LLCSQNLAPSD	ITALGCHGQT	VRHAP	EHHSYSVQLADLPLL
m121-1.pep	130	140	150	160	170	180
	AERTRIFTVGDF	RSRDLAAGG	QGAPLVPAF	HEALFRDN	RETRAVLN	IGGIANISVLP
a121-1	130	140	150	160	170	180
	AERTRIFTVGDF	RSRDLAAGG	QGAPLVPAF	HEALFRDD	RETRAVLN	IGGIANISVLP
m121-1.pep	190	200	210	220	230	240
	PAFGFDTGPGN	MLMDAWTQ	AHWQLPYDK	NGAKAAQGN	ILPQLLDRL	LAHPYFAQPH
a121-1	190	200	210	220	230	240
	PAFGFDTGPGN	MLMDAWTQ	AHWQLPYDK	NGAKAAQGN	ILPQLLDRL	LAHPYFAQPH
m121-1.pep	250	260	270	280	290	300
	GRELFALNWLE	TYLDGGENR	YDVLRTLSR	FTAQTVCD	AVSHAAAD	ARQMYICGGG
a121-1	250	260	270	280	290	300
	GRELFALNWLE	TYLDGGENR	YDVLRTLSR	FTAQTVCD	AVSHAAAD	ARQMYICGGG
m121-1.pep	310	320	330	340	350	360
	LMADLAECFG	TRVSLHST	ADLNLDPQ	WVEAAXFA	WLAAACW	INRIPGSPHK
a121	310	320	330	340	350	360
	LMADLAECFG	TRVSLHST	ADLNLDPQ	WVEAAXFA	WLAAACW	INRIPGSPHK
m121-1.pep						
	XAGYYYX					
a121						
	GAGYYYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 445>:

g122.seq

```

1  ATGGCTTTAC TGAGCATCCG CAAGCTGCAC AAACAATACG GCAGCGTAAC
51  CGCCATCCAA TCCTTAGACT TGGACTTGGA AAAAGGCGAA GtcatCGTAC
101 TGCTGGGCCC gTccggctgc ggCAAATCCA CCTCctgcg ctgctgcaaC
151 GGTTTGGAGC CGCACCaaag cgGCAGCATC GTGATGGAGC GTgtcgGCGA
201 ATTCggcAAA GACGTTTCCT GGCAAACCGC CCGGCAAAaA gtcggtatgg
251 tctttcaaag taacgAactg Tttgcccaca tgaccgtcat cgAaaacatc
301 ttcttAggcC CGGTAAagga aCAAAAcCgc gaccgtgccg aagcaGAGGC
351 gCAAGCCGGC AAactGttgg aacgcgTCGG actgctAGAC CGCAAAAACG
401 CCTATCCGCG CGAACTTTCC GCGCGTCAGA AACAGCGCAT CGCCATTGTC
451 CGCGCCCTGT GCCTGAATCC GGAAGTCATC CTGCTGGAGC AAATCACC GC
501 CGCACTTGAC CCCGAAATGG TCGCGAAGT CTGGAAGTG GTTTTGAAC
551 TCGCCCGCGA AGGGATGAGT ATGCTCATCG TAACCCACGA AATGGGGTTC
601 GCACGCAAAG TTGCCGACCG CATCGTCTTT ATGGACAAAG GCGGCATCGT
651 CGAATCGTCC GACCCGAAA CTTTTTTTC CGACCAAAA AGCGAACGCG
701 CCCGCAATT TCTGGCAGGT ATGGACTACT GA
```

This corresponds to the amino acid sequence <SEQ ID 446; ORF 122.ng>:



1	MALLSIRKLH	KQYGSVTAIQ	SLDLDLEKGE	VIVLLGPSGC	GKSTLLRCVN
51	GLEPHQGGSI	VMDGVGEFGK	DVSQWTARQK	VGMVFQSNEL	FAHMTVIENI
101	FLGPFVKEQR	DRAEAEAAQG	KLLERVGLED	RKNAYPRELS	GGQKQRIAIV
151	RALCLNPEVI	LLDEITAAAL	PEMVEVLELV	VLELAREGMS	MLIVTHEMGF
201	ARKVADRIVF	MDKGGIVESS	DPETFFSAPK	SERARQFLAG	MDY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 447>:

m122.seq

1	GTGTGTCATGA	TTAAATCCG	CAATATCCAT	AAGACCTTTG	GCGAAAACAC
51	TATTTTGC	GGCATCGATT	TGGATGTGTG	CAAAGGGCAG	GTGGTCGTCA
101	TCCTCGGGcC	TTCCGGCTCA	GGCAAAACGA	CGTTTCTGCG	ATGCCTAAAC
151	GCGTTGGAA	TGCCCGAAGA	CGGACAAAC	GAGTTCGACA	ACGAGCGACC
201	GCTGAAATC	GATTTTCTA	AAAAACCAAT	CAAAACGAT	ATTTTGGCAC
251	TGCGCGCAA	ATCAKGCATG	GTGTTTCAAC	AATACAyCT	TTTCCGCGAC
301	AAAACCGCCT	TGGA AACGT	AATGGAAGGA	CCGGTTGCCG	TACAgGGCAA
351	GCCTGCCGCC	CAAGCGCGCG	AAGAGGCTCT	GAAACTGTGT	GAAAAAGTCG
401	GCTTGGGCGA	CAAAAGTGGAT	TTGTATCCCT	ACCAGCTTTT	CGGCGGTCAG
451	CAGCAGCGCG	TCGGCATTTG	CCGCGCATTG	GCGATTTCG	CTGAAGTATG
501	GCTGTTTGAC	GAAACGACTT	CCGCGCTCGA	TCTGAAATTG	GTGCAAGATG
551	TTTTGGATmC	CATGAAGGAA	TTGGCGCAAG	AAGGCTGGAC	CATGGTTGTC
601	GTTACGCATG	AAATCAAGTT	CGCCTTAGAA	GTGGCAACCA	CCGwCGTCGT
651	GATGGACrGC	GGCGTTATTG	TCGAACAAGG	CAGCCCGCAA	GATTTGTTTCG
701	ACCACCCCAA	ACGCAACGG	ACGCGGAGAT	TTTTAAGCCA	AATCCAATCT
751	ACCAAGATT	GA			

This corresponds to the amino acid sequence <SEQ ID 448; ORF 122>:

m122.ppt

1	VVMIKIRNIH	KTFGENTILR	GIDLDVCKQG	VVVLGPGSGS	GKTTFLRCLN
51	ALEMPEDGQI	EFDNERPLKI	DFSKKPSKHD	ILALRRKSXM	VFQQYNLFPH
101	KTALENVMEG	PVAVQGKPAA	QAREEALKLL	EKVG LGDKVD	LYPYQLSGGQ
151	QQRVGIARAL	AIQPELMLFD	EPTSALDPEL	VQDVLDMKE	LAQEGWTMVV
201	VTHEIKFALE	VATTXVMDX	GVIVEQGSQP	DLFDHPKHER	TRRFLSQQS
251	TKI*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 122 shows 47.2% identity over a 246 aa overlap with a predicted ORF (ORF 122.ng) from *N. gonorrhoeae*:

m122/q122

		10	20	30	40	50	60
m122.pep	VVMIKIRNIHKTFGENTILRGIDLDVCKGQVVVLGPSGSgKTTFLRCLNALEMPEDGQI						
	:::: ::    :     :::: ::   :: :: :: ::   :: :: :: ::    :  :						
g122	MALLSIRKLHKQYGSVTAIQSLDLLEKEGEIVLLGGPSGCGKSTLLRCVNGLPEPHQGCSI						
		10	20	30	40	50	60
		70	80	90	100	110	120
m122.pep	EFDNERPLKIDFSKKPSKHDI LALRRKSXmVFQQYNLFPHKTALENVMEGPVAVQGPAA						
	:  : :     : :  ::     : :     :: :: ::      ::						
g122	VMDGVGEGFKDVSQWTA-----RQKVGMVFQSNElFAHMTVIENIFLGPVKQEQRDRRA						
		70	80	90	100	110	
		130	140	150	160	170	180
m122.pep	QAREEALKLLEKVLGDkVDLPYPQLSGGQQRVGIARALAIQPELMlFDEPTSalDPeL						
	:  : :      ::     } :     :     :: :: ::     :: :: ::    }::   ::						
g122	EAEAQAAGKLLERVGLLDRKNAYPRELSGGQKQRIAlVRALCLNPeVILLDeITAlDPeM						
		120	130	140	150	160	170
		190	200	210	220	230	240
m122.pep	VQDVLDxMKELAQEGWTMVVtTHEIKfALEvATTxVMDxGViVEqGSPQDLFDHPKhER						
	:: : :  :: :  :: ::   :  ::           :: :: :: : :  ::						
g122	VREVLEVLELAREGMSMLIVtHEMGfARKvADrIVMDKGgiVeSSDPETffSAPKSE						

350

	180	190	200	210	220	230
	250					
m122.pep	TRRFLSQQSTKIX					
	: : : :					
g122	ARQFLAGMDYX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 449>:

```

a122.seq
1  GTGTGCATGA TTAAATCCG CAATATCCAT AAGACCTTCG GCAAAAATAC
51  CATTTTGC GC CATCAATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
101 TCCTCGGGCC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
151 GCGTTGGAAA TGCCCGAAGA CGGACAAATC GAGTTCGACA ACGAGCGACC
201 GCTGAAAATC GATTTTCTA AAAAACCAAG CAAACACGAT ATTTTGGCAC
251 TGCGCCGCAA ATCAGGCATG GTGTTTCAAC AATACAACCT CTTCCGCAC
301 AAAACCGCCT TGGAAAACGT GATGGAAGGA CCGGTTGCCG TACAGGGCAA
351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTTC CGGCGGTCAG
451 CAGCAGCGCG TCGGCATTGC CCGAGCATTG GCGATTGAGC CCGAGCTGAT
501 GTTGTGTTGAC GAACCCACTT CCGCGCTTGA CCCCAGATTG GTGCAAGACG
551 TGTGTAACGC CATGAAGGAA TTGGCGCGGG AAGGTTGGAC GATGGTCGTC
601 GTTACCCACG AAATCAAGTT CGCGCTGGAA GTTGCCACGA CCGTTGTCGT
651 GATGGACGGC GCGGTTATCG TAGAGCAGGG CAGCCCAGAA GAGTTGTTCC
701 ACCACCCCAA ACACGAACGG ACGCGGAGAT TTTTAAGCCA AATCCAATCT
751 ACCAAGATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 450; ORF 122.a>:

```

a122.pep
1  VVMIKIRNIH KTFGKNTILR GINLDVCKGQ VVVLGPGSGS GKTTLRLCLN
51  ALEMPEDGQI EFDNERPLKI DFKKPSKHD ILALRRKSGM VFQQYNLFPH
101 KTALENVMEG PVAVQKPAQ QAREEALKLL EKVLGDKVD LYPYQLSGGQ
151 QQRVGIARAL AIQPELMLFD EPTSALDPEL VQDVLNAMKE LAREGWTMVV
201 VTHEIKFALE VATTVVVMDG GVIVEQGSPEL ELDHDPKHER TRRFLSQQS
251 TKI*

```

m122/a122 96.0% identity in 253 aa overlap

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKTFFGENTILRGIDLVDCKGQVVVLGPGSGSKTTFLRLCLNALEMPEDGQI					
a122	VVMIKIRNIHKTFFGENTILRGIDLVDCKGQVVVLGPGSGSKTTFLRLCLNALEMPEDGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m122.pep	EFDNERPLKIDFSKKPSKHDILALRRKSGMVVFQQYNLFPHKTALENVMEGPPVAVQKPAQ					
a122	EFDNERPLKIDFSKKPSKHDILALRRKSGMVVFQQYNLFPHKTALENVMEGPPVAVQKPAQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m122.pep	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
a122	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m122.pep	VQDVLDMKELAQEGWMTMVVTHEIKFALEVATTXVMDXGVIVEQGSPELFDHDPKHER					
a122	VQDVLNAMKELAREGWTMVVTHEIKFALEVATTVVMDGGVIVEQGSPELFDHDPKHER					
	190	200	210	220	230	240
	250					
m122.pep	TRRFLSQQSTKIX					

|||||||  
a122 TRRFLS QIQSTKIX  
250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 451>:

g122-1.seq  
1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACCATT  
51 GCGCGGCATC GATTGGATG TGGGCAAAGG GCAGGTGGTC GTCATCCTCG  
101 GGCCTTCCGG CTCGGGTAAA ACAACATTTC TGCGCTGCCT AAACGCGTTG  
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGCGC GGCCGTTACG  
201 CATTGATTTT TCCAAAAAAA CAAGCAAACA CGATATTTTG GCACTGCGCC  
251 GCAAGTCCGG AATGGTATTC CAACAATACA ACCTCTTCCC GCATAAAACC  
301 GTGTTGGAAA ACGTGATGGA AGGGCCGGTT GCCGTACAGG GCAAGCCTGC  
351 CGCCCAAGCG CGCGAAGAGG CTTTGAAGCT GCTGGAAAAA GTCGGCTTGG  
401 GCGATAAAGT GGATTTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG  
451 CGTGTCGGTA TCGCCCGCGC ACTGGCGATT CAGCCTGAAT TGATGCTGTT  
501 TGACGAACCC ACTTCCGCGC TGGACCCCGA GTTGGTGCAA GACGTGTTGG  
551 ACCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC  
601 CACGAAATCA AGTTCACGCT GGAAGTTGCC ACGAACGTCG TCGTGATGGA  
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC  
701 TCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTGCCAAG  
751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 452; ORF 122-1.ng>:

g122-1.pep  
1 MIKIRNIHKT FGENTILRGI DLDVKGQV VILGPSGSGK TFLRCLNAL  
51 EMPEDGQIEF DNARPLRIDF SKKTSKHDIL ALRRKSGMVF QQYNLFPHKT  
101 VLENVMEGPV AVQGKPAAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ  
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA REGWTMVVVT  
201 HEIKFTLEVA TNVVVMDGGV IVEQGSPEL FDHLKHERTR RFLS QIQSAK  
251 I\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 453>:

m122-1.seq  
1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA AACTATT  
51 GCGCGGCATC GATTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG  
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG  
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA  
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC  
251 GCAAATCAGG CATGGTGTTC CAACAATACA ACCTCTTCC GCACAAAACC  
301 GCCTTGAAA ACGTAATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC  
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG  
401 GCGACAAAGT GGATTTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG  
451 CGCGTCGCGA TTGCCCAGC ATTGGCGATT CAGCCTGAAC TGATGCTGTT  
501 TGACGAACCG ACTTCCGCGC TCGATCCTGA ATTGGTGCAA GATGTTTGG  
551 ATACCATGAA GGAATTGGCG CAAGAAGGCT GGACCATGGT TGTGTTTACG  
601 CATGAAATCA AGTTCGCCTT AGAAGTGGCA ACCACCGTCG TCGTGATGGA  
651 CGGCGGCGTT ATTGTCGAAC AAGGCAGCCC GCAAGATTG TTCGACCACC  
701 CCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG  
751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 454; ORF 122-1>:

m122-1.pep  
1 MIKIRNIHKT FGENTILRGI DLDVCKGQV VILGPSGSGK TFLRCLNAL  
51 EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT  
101 ALENVMEGPV AVQGKPAAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ  
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDTMKELA QEGWTMVVVT  
201 HEIKFALEVA TTVVMDGGV IVEQGSQDL FDHFKHERTR RFLS QIQSTK  
251 I\*

m122-1/g122-1 94.8% identity in 251 aa overlap

	10	20	30	40	50	60
m122-1.pep	MIKIRNIHKT FGENTILRGI DLDVCKGQV VILGPSGSGK TFLRCLNALEMPEDGQIEF					
g122-1	MIKIRNIHKT FGENTILRGI DLDVKGQV VILGPSGSGK TFLRCLNALEMPEDGQIEF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 455>:

This corresponds to the amino acid sequence <SEQ ID 456; ORF 122-1.a>:

a122-1/m122-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
a122-1.pep	MIKIRN1HKTFGKNTILRGINLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
m122-1	MIKIRN1HKTFGENTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
a122-1.pep	DNERPLKIDFSKKPSKHDILARRKSGVMVFQQYNLFPHKTALENVMEGPPAVQGGKPAQA					
m122-1	DNERPLKIDFSKKPSKHDILARRKSGVMVFQQYNLFPHKTALENVMEGPPAVQGGKPAQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a122-1.pep	REEALKLEKVGGLGDKVDLPYPYQLSGGQQQRVGRIARALAIQPELMLFDEPTSAIDPELVQ					
m122-1	REEALKLEKVGGLGDKVDLPYPYQLSGGQQQRVGRIARALAIQPELMLFDEPTSAIDPELVQ					



353

	130	140	150	160	170	180
	190	200	210	220	230	240
a122-1.pep	DVLNAMKELAREGWTMVVTHEIKFALEVATTVVMDGGVIVEQGSPELFDHPKHERTR					
	:     :     :     :     :     :     :     :     :     :     :					
m122-1	DVLDTMKELAQEGWTMVVTHEIKFALEVATTVVMDGGVIVEQGSPELFDHPKHERTR					
	190	200	210	220	230	240
	250					
a122-1.pep	RFLSQIQSTKIX					
	:					
m122-1	RFLSQIQSTKIX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 457>:

g125.seq

```

1  ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGGT
51  TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACGCTGC
101 TCGCCCTCTT GGGCTGGCAG CGCGGTCTGG CGGCCCTGCT TTTGGGTCAT
151 GCCGTCGGCG GCGCGCTGTT TTTGCGGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GTGTGCGCCT GTCGTTCCGC AAATGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGTCGGCGC AacggTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACggc gaATCCTTTG TCTGGTGGGC ATTGGCAAAC GGCGCACTGA
401 TCGTGCTGTG GCTGGTTTTC GGCGCACGCA GAACGGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GCTTGCCGTG TTGTGGTTGA GCGTCGAAGT
501 GTTCGCTTCG TCCGGCACAA ACGCCGCGCC CGCCGTTTCA GACGGCATGA
551 CCTTCGGAAC GGCAGTCGAA CTGTCCGCGC TCATGCCGCT TTCCTGGCTG
601 CCGCTGGCCG CCGACTACAC GCGCCAAGCA CGCCGCCCGT TTGCGGCAAC
651 CCTGACGGCA ACGCTCGCCT ATACGCTGAC GGGCTGCTGG ATGTATGCCT
701 TGGGTTTGGC GCGGCTCTG TTTACCGGAG AAACCGACGT GGCGAAAATC
751 CTGTTGGGCG CGGGCTTGGG CATAACGGGC ATTCTGGCAG TCGTCTCTC
801 CACCGTTACC ACAACGTTTC TCGATACCTA TTCCGCGGCG GCGAGTGCAG
851 ACAACATTTT CGCGGTTTTT GCGGAAATAC CCGTCGCTGT CGGCGTTACC
901 CTGatccgca ccgtgcttgc cgtcatgctg cccgttaccg aatataaaaa
951 cttcctgctg cttatccgct cggatatttg gccgatggcg ggtggttttg
1001 attgccgaCT TTTtgtctt AAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 458; ORF 125.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 459>:

m125.seq

```

1  ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCTCCGCCA TCGGGCTGAT
51  TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACGCTGC
101 TTGCGCTTTT GGGCTGGCAG CGCGGTCTGG CGGCTCTACT TTTGGGTCAT
151 GCCGTCGGCG GCGCGCTGTT TTTGCGGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GCGTGCGCCT GTCGTTCCGC AAACGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGCGCG AACGGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATTGGCAAAC GGCGCGCTGA
401 TTGTGCTGTG GCTGGTTTTC GGCGCACGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGGCTGA GTGCCGAAGT
501 CTTTTCACAG GCAGGCAGCA CCGCCGCACA GGTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTGA TGCCGCTTTC CTGGCTGCCG
601 CTTGCCGCGC ACTACACGCG CCACGCGCGC CGCCCGTTTG CGGCAACCCT
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTTGGCAGC GCGGTTGTTT ACCGGAGAAA CCGACGTGGC AAAAATCCTG
751 CTGGGCGCAr GTTTGgGTGC GGCAGGCATT TTGGCGGTCT TCCTCTCCAC
801 CGTTACCACA ACGTTTCTCG ATGCCTATT CCGCGGCGCG AGTGCGAACA

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```
m125.pep
  1  MSGNASSPSS  SSAIGLIWFG  AAVSIAEIST  GTLLAPLWGQ  RGLAALLLGH
51  AVGGALFFAA  AYIGALTGRS  SMSVRLSFG  KRGSVLFWSA  NMLQLAGWTA
101 VMIYAGATVS  SALGKVLWDG  ESFVWWALAN  GALIVLWLVF  GARKTGGLTK
151 VSMLLMLLAV  LWLSAEVFST  AGSTAAQVSD  GMSFGTAVEL  SAVMPLSWLP
201 LAADYTRHAR  RPFAVLTAT  LAYLTLTGCM  YALGLAAALF  TGETDVAKIL
251 LGAXLGAAGI  LAVVLTSTVT  TFLDAYSAGA  SANNISARFA  ETPVAVXVTL
301 IGTVLAVMLP  VTEYENFLLL  IGSVFAPMAG  GFCRLFRLE  TA*
```

ORF 125 shows 92.1% identity over a 343 aa overlap with a predicted ORF (ORF 125.ng) from *N. gonorrhoeae*:

```

m125/g125

      10      20      30      40      50      60
m125.pep  MSGNASSPSSSSAIGLIWFGAAVSI AEISTGTL LAPLGWQRGLAALLLGHAVGGALFFAA
          |||||:||||:|||||
g125      MSGNASSPSSSSAIGLVWFGAAVSI AEISTGTL LAPLGWQRGLAALLLGHAVGGALFFAA
          10      20      30      40      50      60

      70      80      90      100     110     120
m125.pep  AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
          |||||:|||||
g125      AYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWTAVMIYVGATVSSALGKVLWDG
          70      80      90      100     110     120

      130     140     150     160     170     179
m125.pep  ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQ-VS
          |||||:|||||
g125      ESFVWWALANGALIVLWLVFGARRTGGLKTVSMLLMLLAVLWLSVEVFASSGNTNAAPAVS
          130     140     150     160     170     180

      180     190     200     210     220     230     239
m125.pep  DGMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTG CWMYALGLAAAL
          |||:|||||
g125      DGMTFGTAVELSAVMPLSWLPLAADYTRQARRPFAATLTATLAYTLTG CWMYALGLAAAL
          190     200     210     220     230     240

      240     250     260     270     280     290     299
m125.pep  FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT
          |||||:|||||
g125      FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDTSAGASANNISARFAEIPVAVGVT
          250     260     270     280     290     300

      300     310     320     330     340
m125.pep  LIGTVLAVMLPVTEYENFLLIGSVFAPMAGGFDCRLFRLETAX
          |||||:|||||
g125      LIRTVLAVMLPVTEYKNFLLIRSVFGPMAGGFDCRLFLCKTAX
          310     320     330     340

```

```

a125.seq
      1  ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGAT
     51  TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACACTGC
    101  TTGCGCCTTT GGGCTGGCAG CGCGGTCTGG CGGCTCTGCT TTTGGGTTCAT

```

```

151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GCGTGCGCCT GTCGTTCCGGC AAACGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGGCGC AACGGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATTGGCAAAC GGCGCGCTGA
401 TTGTGCTGTG GCTGGTTTTC GGCGCAGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGGCTGA GTGCCGAAGT
501 CTTTTCACAG GCAGGCAGCA CCGCCGCACA GGTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTGA TGCCCGTTTC TTGGCTGCCG
601 CTGGCCGCGC ACTACACGCG CCACGCGCGC CGCCCGTTTG CGGCAACCCT
651 GACGGCAACG CTCGCCACG CTGTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTGGCAGC GGCCTGTTC ACCGGAGAAA CCGACGTGGC AAAAATCCTG
751 CTGGGCGCAG GTTTGGGTGC GGCAGGCATT TTGGCGGTG TCCTGCTGAC
801 CGTTACCACC ACTTTTCTCG ATGCCTACTC CGCCGGCGTA AGTGCCAACA
851 ATATTTCGC CAAACTTTCG GAAATACCCA TCGCCGTTCG CGTCGCCGTT
901 GTCGGCACAC TGCTTGCCGT CCTCCTGCCC GTTACCGAAT ATGAAAACCT
951 CCTGCTGCTT ATCGGCTCGG TATTGCGGCC GATGGCG.GC GGTTTTGATT
1001 GCCGACTTTT TCGTCTGAA ACGGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 462; ORF 125.a>:

```

a125.pep
1  MSGNASSPSS SAAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
51  AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSVA NMLQLAGWTA
101 VMIIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
201 LAADYTRHAR RFFAATLTAT LAYTLTGCMW YALGLAAALF TGETDVAKIL
251 LGAGLGAAGI LAVVLSTVTT TFLDAYSAGV SANNISAKLS EIPIAVAVAV
301 VGTLLAVLLP VTEYENFLLL IGSVFAPMAX GFDCRLFRLE TA*

```

m125/a125 95.6% identity in 342 aa overlap

```

          10      20      30      40      50      60
m125.pep  MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA
          |||
a125      MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA
          10      20      30      40      50      60

          70      80      90      100     110     120
m125.pep  AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
          |||
a125      AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
          70      80      90      100     110     120

          130     140     150     160     170     180
m125.pep  ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQVSD
          |||
a125      ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQVSD
          130     140     150     160     170     180

          190     200     210     220     230     240
m125.pep  GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMWYALGLAAALF
          |||
a125      GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMWYALGLAAALF
          190     200     210     220     230     240

          250     260     270     280     290     300
m125.pep  TGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVTL
          |||
a125      TGETDVAKILLGAGLGAAGILAVVLSTVTTTFLDAYSAGVSANNISAKLSEIPIAVAVAV
          250     260     270     280     290     300

          310     320     330     340
m125.pep  IGTVLAVMLPVTEYENFLLLIGSVFAPMAGGFDCRLFRLETAX
          :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a125      VGTLLAVLLPVTEYENFLLLIGSVFAPMAXGFDCRLFRLETAX

```

310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 463>:

```
g126.seq
1   AtgccgtcTG AAaccCcaaa ggcACGCCGC CGGCTTTCAG ACGGCATCGC
51  GTCCGACAAC CATACCAAAG AATCCATCAT GCTCACCctg tacggcGAAA
101 CTTTCCCTTC GCGGCTGCTg ctcggcacgG cggcctacCC GACCCCTGAA
151 ATCCTCAAAC AATCCGTCCG AACCGCCCGG CCCGCGATGA ttaccGTCTC
201 GCTGCGCCGC ACGGGATGCG GCGGCGAGGC GCACGGTCAG GGGTTTGGT
251 CGCTGCTTCA AGAAACCGGC GTTCCCGTCC TGCCGAACAC GGCAGGCTGC
301 CAAAGCGTGC AGGAAGCGGT AACGACGGCG CAAATGGCGC GCGAAGTGTT
351 TGAAACCGAT TGGATAAAAT TGGAATCAT CGGCGACGAC GACACCTTGC
401 AGCCGGACGT GTTCCAATC GTCGAAGCGG CGGAAATCCT GATTAAAGAC
451 GGCTTCAAAG TGCTGCCTTA TTGCACCGAA GACCTGATTG CCTGCCGCG
501 CCTGCTCGAT GCGGGCTGTC AGGCGTTGAT GCCGTGGGCG GCTCCCATCG
551 GCACGGGTTT GGGGGCGGTT CACGCCTATG CGCTCAAAAT CCTGCGCGAA
601 CGCCTGCCCG ACACGCCGCT GATTATCGAC GCGGGCTTGG GTTTGCCTTC
651 CCAAGCGGCA CAAGTGATGG AATGGGGTTT TGACGGCGTA TTGTTAAACA
701 CCGCCGTTTC CCGCAGCGGC GACCCCGTCA ACATGGCGCG CGCCTTCGCA
751 CTCGCCGTCG AATCCGGACG GCTGGCATTG GAAGCCGGGC CGGTCGAAGC
801 GCGAACCAAA GCCCAAGCCA GCACGCCGAC AGTCGGACAA CCGTTTGGC
851 ATTCGGCGGA ATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 464; ORF 126.ng>:

```
g126.pep
1   MPSETPKARR RLSDGIASDN HTKESIMLTL YGETFPSRL LGTAAYPTPE
51  ILKQSVRTAR PAMITVSLRR TCGGGEAHGQ GFWSLLQETG VPVLPNTAGC
101 QSVQEAHTTA QMAREVFETD WIKLELIGDD DTLQPDVFQL VEAELLIKD
151 GFKVLPYCTE DLIACRRLLD AGCQALMPWA APIGTGLGAV HAYALKILRE
201 RLPDTPLIID AGLGLPSQAA QVMEWGFQDV LLNTAVSRSG DPNMARAFA
251 LAVESGRLAF EAGPVEARTK AQAATPTVQ PFWSAEY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 465>:

```
m126.seq (partial)
1   ..CACTATACAA AGGAACCCAT TATGCTCACC CTATACGGCG AAACCTTTCCC
51  CTGCGGGCTG CTGCTCGGCA CGGCTGCCTA CCCGACCCC GAAATCCTCA
101 AACAAATCCAT CCAAACCGCC CAGCCTGCGA TGATTACCGT CTCGCTGCGC
151 CGCGCGGGAA GCGGCGGGCA GCGCACGGT CAGGGGTTTT GGTGCTGCT
201 TCAAGAAACC GCGGTTCCCG TCCTGCCGAA CACGGCAGGC TGCCAAAGCG
251 TGCAGGAAGC GGTAAACGAC GCGCAAATGG CCGCGAAGT GTTTGAAACC
301 GATTGGATAA AATTGGAAT CATCGGAGAT GACGACACCT TGCAGCCGGA
351 TGTGTTCCAG CTTGTGGAAG CGGCGGAAAT CCTGATTAAA GACGGCTTCA
401 AAGTGCTGCC TTATTGCACC GAAGACCTGA TTGCCTGCCG CCGCCTGCTC
451 GACGCGGGCT GTCAGGCGTT GATGCCGTGG GCGGCCCCGA TCGGCACGGG
501 TTTGGGCGCG GTTACGCCT ACGCGTTGAA CGTCTGCGC GAACGCCTGC
551 CCGACACGCC GCTGATTATC GACGCGGGCT TGGGTTTGCC CTCACAGGCG
601 GCACAAGTGA TGAATGGGG CTTTGACGCG GTGCTTTTGA ATACTGCCGT
651 TTCCCGCAGC GGCATCCCG TCAATATGGC ACGCGCCTTC GCACTCGCCG
701 TCGAATCCGG ACGGCTGGCA TTTGAAGCCG GACCGGTCGA AGCACGCGAC
751 AAAGCGCAAG CCAGCACGCC GACAGTCGGA CAACCGTTTT GGCATTGCGC
801 GGAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 466; ORF 126>:

```
m126.pep (partial)
1   ..HYTKEPIMLT LYGETFPSRL LLGTAAYPTP EILKQSIQTA QPAMITVSLR
51  RAGSGGEAHG QGFWSLLQET GVPVLPNTAG QSVQEAHTT AQMAREVFET
```

```

101 DWIKLELIGD DDTLQPDVFQ LVEAAEILIK DGFKVLPYCT EDLIACRRL
151 DAGCQALMPW AAPIGTGLGA VHAYALNVLR ERLPDTPLII DAGLGLPSQA
201 AQVMEWGFDG VLLNTAVSRS GDPVNMARAF ALAVESGRLA FEAGPVEARD
251 KAQASTPTVG QPFWHSAEY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 126 shows 95.9% identity over a 269 aa overlap with a predicted ORF (ORF 126.ng) from *N. gonorrhoeae*:

m126/g126

```

                                10      20      30      40
m126.pep      .  HYTKPEIMLTLYGETFPSSRLLLGTAAAYPTPEILKQSIQTAQ
                  ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      MPSETPKARRRLSDGIASDNHTKESIMLTLYGETFPSSRLLLGTAAAYPTPEILKQSVRTAR
                  10      20      30      40      50      60

                                50      60      70      80      90      100
m126.pep      PAMITVSLRRAGSGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  ||||| ||||| :| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      PAMITVSLRRTGCGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  70      80      90      100      110      120

                                110      120      130      140      150      160
m126.pep      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  130      140      150      160      170      180

                                170      180      190      200      210      220
m126.pep      APIGTGLGAVHAYALNVLRERLPDTPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
                  ||||| ||||| :| ||||| ||||| ||||| ||||| ||||| |||||
g126      APIGTGLGAVHAYALKILRERLPDTPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
                  190      200      210      220      230      240

                                230      240      250      260      270
m126.pep      DPVNMARAFALAVESGRLA FEAGPVEARDKAQASTPTVGQPFWHSAEYX
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      DPVNMARAFALAVESGRLA FEAGPVEARTKAQASTPTVGQPFWHSAEYX
                  250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 467>:

```

a126.seq
1  TTGTTAATCC ACTATACAAA GGAACCCATT ATGCTCACCC TGTACAGCGA
51  AACTTTCCCT TCGCGGCTGC TGCTCGGCAC AGCCGCCTAC CCGACCCCTG
101 AAATCCTCAA ACAATCCGTC CGAACC GCCCGCGAT GATTACCGTC
151 TCGCTGCGCC GCGCGGGATG CGGCGGCGAG GCGCACGTC AGGGGTTTG
201 GTCGCTGCTT CAAGAAACCG GCGTTCCCGT CCTGCCGAAC ACGGCAGGCT
251 GCCAAAGCGT GCAGGAAGCG GTAACGACGG CGCAAATGGC GCGCGAAGTG
301 TTTGAAACCG ATTGGATTAA ACTCGAACTC ATCGGCGACG ACGACACCTT
351 GCAGCCGAT GTGTTCCAAC TTGTCGAAGC GCGCGAAATC CTGATTAAAG
401 ACGGCTTCAA AGTGCTCCCT TATTGCACCG AAGACCTGAT TGCCTGCCGC
451 CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG ATGCCGTGGG CGGCCCCGAT
501 CGGCACGGGT TTGGGCGCGG TTCACGCCTA CGCGTTGAAC GTCCTGCGCG
551 AACGCCTGCC CGACACGCCG CTGATTATCG ACGCGGGCTT GGGTTTGCCC
601 TCACAGGCGG CACAAGTGAT GGAATGGGGC TTTGACGGCG TGCTTTTGAA
651 TACTGCCGTT TCCCGCAGCG GCGATCCGGT CAATATGGCA CGCGCCTTCG
701 CACTCGCCGT CGAATCCGGA CGGCTGGCAT TTGAAGCCGG ACCGGTCGAA
751 GCACGCGACA AAGCGCAAGC CAGCACGCCG ACAGTCGGAC AACCGTTTGG
801 GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 468; ORF 126.a>:

```
a126.pep
  1  LLIHYTKPEI MLTLYSETFP SRLLLGTAA YPTPEILKQSV RTARPAMITV
 51  SLRRAGCGGE AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV
101  FETDWIKLEL IGDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR
151  RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP
201  SQAAQVMEWG FDGVLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE
251  ARDKAQASTP TVGQPFWHS A_EY*
```

m126/a126 98.1% identity in 269 aa overlap

```

              10      20      30      40      50
m126.pep      HYTKPEIMLTLYGETFP SRLLLGTAA YPTPEILKQSIQTAQPAMITVSLRRAGSGGE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           LLIHYTKPEIMLTLYSETFP SRLLLGTAA YPTPEILKQSVRTARPAMITVSLRRAGCGGE
              10      20      30      40      50      60

              60      70      80      90      100     110
m126.pep      AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD
              70      80      90      100     110     120

              120     130     140     150     160     170
m126.pep      VFQLVEAAEILIKDGFKVLPYCTEDLIACRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           VFQLVEAAEILIKDGFKVLPYCTEDLIACRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              130     140     150     160     170     180

              180     190     200     210     220     230
m126.pep      VLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DGVLNTAVSRSGDPVNMA RAFALAVESG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           VLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DGVLNTAVSRSGDPVNMA RAFALAVESG
              190     200     210     220     230     240

              240     250     260     270
m126.pep      RLAFEAGPVEARDKAQASTPTVGQPFWHS A EYX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           RLAFEAGPVEARDKAQASTPTVGQPFWHS A EYX
              250     260     270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 469>:

```
g126-1.seq
  1  ATGCTCAGCC TGTACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
 51  GGCCGCGTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCAGCC
101  GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCACGGGATG CGGCGGCGAG
151  GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201  CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251  CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAATC
301  ATCGGCGGACG ACGACACCTT GCAGCCGGAC GTGTTCCAAC TCGTCGAAGC
351  GGCGGAAATC CTGATTAAAG ACGGCTTCAA AGTGTGCTT TATTGCACCG
401  AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ATGCGGGCTG TCAGGCGTTG
451  ATGCCGTGGG CGGCTCCCAT CGGCACGGGT TTGGGGGCGG TTCACGCCTA
501  TCGGCTCAA AATCTGCGCG AACGCTGCC CGACACGCCG CTGATTATCG
551  ACGCGGGCTT GGGTTTGCTT TCCCAAGCGG CACAAGTGAT GGAATGGGGT
601  TTTGACGGCG TATTGTAA AACCAGCGTT TCCGCGAGCG GCGACCCCGT
651  CAACATGGCG CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701  TTGAAGCCGG GCCGGTCGAA GCGCGAACCA AAGCCCAAGC CAGCACGCCG
751  ACAGTCGGAC AACCCTTTT GCATTGCGCG GAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 470; ORF 126-1.ng>:

```
g126-1.pep
  1  MLTLYGETFP SRLLLGTAA YPTPEILKQSV RTARPAMITV SLRRTGCGGE
```

```

51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALK ILRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSQDPVNMA RAFALAVESG RLAFEAGPVE ARTKAQASTP
251 TVGQPFWHSA EY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 471>:

m126-1.seq

```

1 ATGCTCACCC TATACGGCGA AACTTTCCCC TCGCGGCTGC TGCTCGGCAC
51 GGCTGCCTAC CCGACCCCGG AAATCCTCAA ACAATCCATC CAAACCGCCC
101 AGCCTGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGAAG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAAGTC
301 ATCGGAGATG ACGACACCTT GCAGCCGGAT GTGTTCCAGC TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCGGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGCG
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCAGCCCG
751 ACASTCGGAC AACCGTTTTG GCATTGCGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 5; ORF 126-1>:

m126-1.pep

```

1 MLTYGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE
51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSQDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWHSA EY*

```

m126-1/g126-1 96.9% identity in 262 aa overlap

	10	20	30	40	50	60
m126-1.pep	MLTYGETFP	SRLLLGTAAY	PTPEILKQSI	QTAQPAMITV	SLRRAGSGGE	AHGQGFWSLL
g126-1	MLTYGETFP	SRLLLGTAAY	PTPEILKQSV	RTARPAMITV	SLRRAGSGGE	AHGQGFWSLL
	10	20	30	40	50	60
m126-1.pep	QETGVPVLP	NTAGCQSVQEA	VTTAQMAREV	FETDWIKLEL	IGDDDTLQPD	VFQVLEAAEI
g126-1	QETGVPVLP	NTAGCQSVQEA	VTTAQMAREV	FETDWIKLEL	IGDDDTLQPD	VFQVLEAAEI
	70	80	90	100	110	120
m126-1.pep	LIKDGFKVLP	YCTEDLIACR	RLLDAGCQAL	MPWAAPIGTG	LGAVHAYALN	VLRERLPDTP
g126-1	LIKDGFKVLP	YCTEDLIACR	RLLDAGCQAL	MPWAAPIGTG	LGAVHAYALK	ILRERLPDTP
	130	140	150	160	170	180
m126-1.pep	LIIDAGLGLP	SQAAQVMEWG	FDGVLLNTAV	SRSQDPVNMA	RAFALAVESG	RLAFEAGPVE
g126-1	LIIDAGLGLP	SQAAQVMEWG	FDGVLLNTAV	SRSQDPVNMA	RAFALAVESG	RLAFEAGPVE
	190	200	210	220	230	240
m126-1.pep	ARDKAQASTP	TVGQPFWHS	AEYX			
g126-1	ARTKAQASTP	TVGQPFWHS	AEYX			
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 473>:

a126-1.seq

```

1 ATGCTCACCC TGTACAGCGA AACTTTCCTT TCGCGGCTGC TGCTCGGCAC
51 AGCCGCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCAGCC
101 GGGCCGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGATG CGGCGGCGAG

```

360

```

151 GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCTCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATTAA ACTCGAACTC
301 ATCGGCGACG ACGACACCTT GCAGCCGGAT GTGTTCCAAC TTGTGCAAGC
351 GCGGGAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTCG CACTCGCGCT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTGT GCATTGCGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 474; ORF 126-1.a>:

a126-1.pep

```

1 MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
51 AHQGGFWSLL QETGVPVLPN TAGCQSVQEA VTQAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQLVAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAQVMWEG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

a126-1/m126-1 98.1% identity in 262 aa overlap

a126-1.pep	10	20	30	40	50	60
	MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE AHQGGFWSLL					
m126-1	MLTLYGETFP SRLLLGTAAY PTPEILKQSI QTAQPMITV SLRRAGSGGE AHQGGFWSLL					
	10	20	30	40	50	60
a126-1.pep	70	80	90	100	110	120
	QETGVPVLPN TAGCQSVQEA VTQAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
m126-1	QETGVPVLPN TAGCQSVQEA VTQAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
	70	80	90	100	110	120
a126-1.pep	130	140	150	160	170	180
	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP					
m126-1	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP					
	130	140	150	160	170	180
a126-1.pep	190	200	210	220	230	240
	LIIDAGLGLP SQAQVMWEG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
m126-1	LIIDAGLGLP SQAQVMWEG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
a126-1.pep	250	260				
	ARDKAQASTP TVGQPFWWSA EYX					
m126-1	ARDKAQASTP TVGQPFWWSA EYX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 475>:

g127.seq

```

1 ATGGAAATAT GGAATATGTT GAACACTTGG CCCGATGCCG TCCCGATACG
51 CGCGGAGGCG GCCGAATCCG TGGCGGCGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAGAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGTTTTTT GGTGCGCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GGCAGCAATT CAAACGCTGG
251 CTTTGTCGAT GTTTGCGGTG GCGGCGGCGG TCGTCTGTGC GACAAAAGAA
301 CTGATTATGT GTCTGTGCGG CAGTATTTTA aggtctGCCA CCCAGCAATA
351 CTCGTCGCGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAATCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCGCGC ACAATATTTT GGGCGACTAT GTCATCCATA

```



```

551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 TCAGCGGTAT TTGGAACG TGCAGGCGGA AAAACTGTTT ATCACGCCCG
701 CCGCCAGGCC GCGCGTTACC CGCGTACCGT ACGACGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCCTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TGCGCGTACA ATACCGCCTG TTAAATCATC
851 CCGCCGgctc cgAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 476; ORF 127.ng>:

g127.pep

```

1 MEIWNMLNTW PDAVPIRAEA AESVAAVAAL LLARALLNI HFRRHPDFGI
51 ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAAVVVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNLLLLSHV VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVs KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 477>:

m127.seq

```

1 ATGGAAATAT GGAATATGTT GGACACTTGG CTCGGTGCCG TCCCGATACG
51 TGCGGAGGCG GTCGAATCCG TGGCGGCGGT TCGCGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAAAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGCGTTTTT GGTGCGCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCGAAATC CAAACGCTGG
251 CTTTGTTCGAT GTTTCGGGTG GCGGCGGCGG TCGTCGTGGC GACGAAGGAA
301 CTGATTATGT GTCTGTGCGG CAGTATTTTA AGGTCTGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAACCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCGCGC ACAATATTTT GGGCGACTAT GTCATCCATA
551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 CCAACGGSAT TTGGAACG TGCAGGCGGA AAAACTGTTT ATCACGCCCG
701 CCGCCAGACC GCGCGTTACC CGCGTGCCGT ACGATGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCTTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TGCGCGTACA ATACCGCCTG TTAAATCACC
851 CCGCCGGCTC CGAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 478; ORF 127>:

m127.pep

```

1 MEIWNMLDTW LGAVPIRAEA VESVAAVAAL LLARALLNI HFRRHPDFGI
51 ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAAVVVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNLLLLSHV VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVs KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 127 shows 97.9% identity over a 290 aa overlap with a predicted ORF (ORF 127.ng) from *N. gonorrhoeae*:

m127/g127

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAAVAALLARALLNIHFRRHPDFGIESKRRFLVAS					
	:         :					
g127	MEIWNMLNTWPDVPIRAEAAESVAAVAALLARALLNIHFRRHPDFGIESKRRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAAVVVATKELIMCLSGSILRSATQQYSVG					
g127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAAVVVATKELIMCLSGSILRSATQQYSVG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
g127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
g127	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
g127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 479>:

```

a127.seq
  1  ATGGAATAT  GGAATATGTT  GGACACTTGG  CTCGGTGCCG  TCCCGATACG
 51  TCGGAGGCG  GTCGAATCCG  TGGCGGTGGT  CGCGGCTTTG  CTGCTGGCGC
101  GCGCCCTTCT  GTTGAATATC  CACTTCAAAC  GGCATCCGGA  TTTCGGCATC
151  GAAAGCAAGC  GCGCGTTTT  GGTGCGCAGC  CGCAATATAA  CGCTGCTTTT
201  GGTGCTGTTT  TCGCTGGCAT  TTATCTGGTC  GCGGCAAATC  CAAACGCTGG
251  CTTTGTGAT  GTTTCGGTG  GCGGCGCGG  TCGTCGTGGC  GACGAAGGAA
301  CTGATTATGT  GTCTGTCGG  CAGCATTTTA  AGGTCTGCCA  CCCAGCAATA
351  CTCGGTCGGC  GACTATATCG  AAATCAACGG  CCTGCGCGGG  CGCGTGGTCG
401  ACATCAACCT  GTTGAACACG  CTGATGATGC  AGGTGCGTCC  GAACCCCTTG
451  GTCGGACAGC  TTGCGGGAAC  CACCGTTTCT  TTCCCAACA  GCCTGTTGTT
501  GAGCCACCCC  GTGCGCGCG  ACAATATTTT  GGGCGACTAC  GTCATCCATA
551  CCGTCGAAAT  CCCGGTCCC  ATCCATTGG  ATTCGGATGA  AGCCGTATGC
601  CGTCTGAAAG  CCGTACTCGA  GCCCTTGTC  GCGCCCTACA  TCCCGGCCAT
651  CCAACGGCAT  TTGAAAACG  TGCAGGCGGA  AAAACTGTTT  ATCAGCCCGC
701  CCGCCAAACC  GCGCGTTACC  CGCGTGCCGT  ACGATGACAA  GGCATACCGC
751  ATCATCGTCC  GCTTCGCCTC  CCCCCTTCA  AAGCGGCTGG  AAATCCAACA
801  GCGGTTATG  GACGAATTT  TCGCGTACA  ATACCGCTG  TAAATTACC
851  CCGCCGGCTC  CGAAACACTT  TAA

```

This corresponds to the amino acid sequence <SEQ ID 480; ORF 127.a>:

```

a127.pep
  1  MEIWNMLDTW  LGAVPIRAEA  VESVAVVAAL  LLARALLNI  HFKRHPDFGI
 51  ESKRRFLVAS  RNITLLLVLF  SLAFIWSAQI  QTLALSMFAV  AAHVVVATKE
101  LIMCLSGSIL  RSATQQYSVG  DYIEINGLRG  RVVDINLLNT  LMMQVGNPL
151  VGQLAGTTVS  FPNLSLLSHP  VRRDNILGDY  VIHTVEIPVP  IHLDSDEAVC
201  RLKAVLEPLC  APYIPAIQRH  LENVQAEKLF  ITPAAKPRVT  RVPYDDKAYR
251  IIVRFASPV  KRLEIQQAVM  DEFLRVQYRL  LNPAGSETL  *

```

m127/a127 98.6% identity in 290 aa overlap

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLNIHFKRHPDFGIESKRRLVAS					
a127	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLNIHFKRHPDFGIESKRRLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAHVVVATKELIMCLSGSILRSATQQYSVG					
a127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAHVVVATKELIMCLSGSILRSATQQYSVG					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
a127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
a127	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRHLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
a127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNYPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 481>:

g128.seq

1	atgattgaca	acgCActgct	ccacttgggc	gaagaaccCC	GTTTtaatca
51	aatccaaacc	gaagACAtca	AACCCGCCGT	CCAAACCGCC	ATCGCCGAAG
101	CGCGCGGACA	AATCGCCGCG	GTCAAAGCGC	AAACGCACAC	CGGCTGGGCG
151	AACACCGTCG	AGCGTCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTGT
201	GGGCGTCGTG	TCCCATCTCA	ACTCCGTCGT	CGACACGCCC	GAAGTCCGCG
251	CCGTCTATAA	CGAACTGATG	CCTGAAATCA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TGGAAGTGA	CAACCGCTTC	AAAACCATCA	AAAATTCCCC
351	CGAATTGCA	ACGCTTTCCC	CCGCACAAAA	AACCAAGCTC	GATCACGACC
401	TGCGCGATTT	CGTATTGAGC	GGCGCGGAAC	TGCCGCCCGA	ACGGCAGGCA
451	GAAGTGGCAA	AACTGCAAAAC	CGAAGGCGCG	CAACTTTCCG	CCAAATTCTC
501	CCAAAACGTC	CTAGACGCGA	CCGACGCGTT	CGGCATTAC	TTTGACGATG
551	CCGCACCGCT	TGCCGGCATT	CCCGAAGACG	CGCTCGCCAT	GTTTGC CGCC
601	GCCGCGCAAA	GCGAAGGCAA	AACAGGTTAC	AAAATCGGCT	TGCAGATTCC
651	GCACTACCTT	GCCGTTATCC	AATACGCGCG	CAACCGCGAA	CTGCGCGAAC
701	AAATCTACCG	CGCCTACGTT	ACCCGTGCCA	GCGAACTTTC	AAACGACGGC
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGAAA	ACGCATTGAA
801	AACCGccaaa	cTGCTCGGCT	TTAAAAATTA	CGCCGAATTG	TCGCTGGCAA
851	CCAAAATGGC	GGACACGCCC	GAACAGGTTT	TAAACTTCCT	GCACGACCTC
901	GCCCGCGCG	CCAAACCCTA	CGCCGAAAAA	GACCTCGCCG	AAGTCAAAGC
951	CTTCGCCCCG	GAACACCTCG	GTCTCGCCGA	CCCGCAGCCG	TGGGACTTGA
1001	GCTACGCGG	CGAAAACTG	CGCGAAGCCA	AATACGCATT	CAGCGAAACC
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGCAAA	GTTCTGGCAG	GCCTGTTCCG
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	CGCCGAAAAA	ACCGTTCCCG
1151	TCTGGCACAA	AGACGTGCGC	TATTTTGAAT	TGCAACAAAA	CGGCAAAACC
1201	ATCGGCGGCG	TTTATATGGA	TTGTACGCA	CGCGAAGGCA	AACGCGGCGG
1251	CGCGTGGATG	AACGActaca	AAGGCCGCGG	CCGCTTTGCC	GACGgcacGC
1301	TGCAACTGCC	CACCGCCTAC	CTCGTCTGCA	ACTTCGCCCC	GCCCGTCGCG
1351	GGCAAAGAAG	CGCGTTTAAG	CCACGACGAA	ATCCTCACCC	TCTTCCACGA
1401	AacCGGCCAC	GGACTGCACC	ACCTGCTTAC	CCAAGTGGAC	GAAGTGGGCG
1451	TGTCCGCAT	CAAcggcgtA	GAATGGGACG	CGGTGCAACT	GCCGACCCAG
1501	TTTATGGAAA	ACTTCGTTTG	GGAATACAAT	GTATTGGCAC	AAATGTCCGC
1551	CCACGAAGAA	AccgGCGAGC	CCCTGCCGAA	AGAACTCTTC	GACAAAATGC
1601	TcgcGCCCAA	AAACTTCCAG	CGCGGTATGT	TCCTCGTCCG	GCAAATGGAG
1651	TTCGCCCTCT	TCGATATGAT	GATTTACAGT	GAAAGCGACG	AATGCCGTCT
1701	GAAAAACTGG	CAGCAGGTTT	TAGACAGCGT	GCGCAAAGAA	GTCGCCGTCA
1751	TCCAACCGCC	CGAATACAAC	CGCTTCGCCA	ACAGCTTCGG	CCacatctTC
1801	GCcggcGGCT	ATTCCGCAGG	CTATTACAGC	TACGCATGGG	CCGAAGTCCT
1851	cAGCACCGAT	GCCTACGCCG	CCTTTGAAGA	AAGcGACGac	gtcGCCGCCA
1901	CAGGCAAACG	CTTCTGGCAA	GAAAtccttg	ccgTcggcgg	ctCCCCGAGC
1951	gcgGCGGAAT	CCTTCAAAGC	CTTCCGCGGA	CGCGAACCGA	GCATAGACGC

2001 ACTGCTGCGC CAAagcggtT TCGACAACGC gGcttgA

This corresponds to the amino acid sequence <SEQ ID 482; ORF 128.ng>:

g128.pep

```

1 MIDNALLHLG EEPFRNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTTGWA
51 NTVERLTGIT ERVGRWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEI SLATKMADTP EQVLNPLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQONGKT
401 IGVVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDDMIYS ESDCRLKNW QQVLDSVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAFAEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR QSGFDNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 483>:

m128.seq (partial)

```

1 ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51 AATCAAAACC GAAGACATCA AACCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AACCGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCG GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAAACTC AACCAC
1 TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51 wGTCAAAAAA TAyTTCcCyG TCGGCAAwGT ATTAACCGGA CTGTTCCGCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGCTC
151 TGGCACAAG ACCTGCGCTA TtkTGAATTG CAACAAAACG GCGAaMCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCGCGCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTAKA ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAATAA TTCGTTTGGG AATACAATGT CTTGGCACA mTGTcAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAaG CGGCATGTT yTsGTCCGGC AAwTGGAGTT
651 CGCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCGTCTGA
701 AAAACTGGCA ACAGGTTTGA GACAGCGTGC GCAAAAAAGT CGCCGTCTATC
751 CAGCCGCCCG AATACAACCG CTTGCCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCGGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGnAT CGCGCAGCGG
951 nGCAGAATCC TTCAAAGCCT TCCGCGGCCG CGAACCGAGC ATAGACGCAC
1001 TCTTGGCCCA CAGCGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 484; ORF 128>:

m128.pep (partial)

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTTGWA
51 NTVEPLTGIT ERVGRWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH
//
1 YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTVPV
51 WHKDVRXYEL QQNGEXIGV YMDLYAREGK RGGAWMNDYK GRRRFSdGTL
101 QLPTAYLVCN FAPPVGGREA RLShDEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMIIYSEDDE GRLKNWQQVL DSVRKKVAI
251 QPPEYNRFAL SFGHIFAGGY SAAXSYAWA EVLSADAYAA FEESDDVAAT

```

301 GKRFWQEILA VGXSRGAES FKAFRGREPS IDALLRHS GF DNAV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng) from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
				340	350	360
g128.pep	YAGEKLREAKYAFSETEVKKYFPVGKVLG					
m128	YASEKLREAKYAFSETXVKKYFPVGKVLNG					
				10	20	30
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQQNGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
m128	GRRRFSGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSEDECLKNWQQVLDVRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDEGLKNWQQVLDVRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRGAESFKAFRGREPS					
	280	290	300	310	320	330

```
          670      679
g128.pep  IDALLRQSGFDNAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 485>:

```
a128.seq
1  ATGACTGACA  ACGCACTGCT  CCATTGGGC  GAAGAACCCC  GTTTTGATCA
51  AATCAAAACC  GAAGACATCA  AACCCGCCCT  GCAAACCGCC  ATTGCCGAAG
101 CGCGCGAACA  AATCGCCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
151 AACACTGTCTG  AACCCTGAC  CGGCATCACC  GAACGCGTCG  CGAGGATTTG
201 GGGCGTGGTG  TCGCACCTCA  ACTCCGTCAC  CGACACGCCC  GAACTGCGCG
251 CCGCTACAA  TGAATTAATG  CCCGAAATTA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAGCTGTA  CAACCGCTTC  AAAACCATCA  AAAACTCCCC
351 CGAGTTCGAC  ACCCTCTCCC  ACGCGCAAAA  AACCAAACTC  AACCACGATC
401 TGCGCGATTT  CGTCCTCAGC  GGCGCGGAAC  TGCCGCCCGA  ACAGCAGGCA
451 GAATTGGCAA  AACTGCAAA  CGAAGGCGCG  CAACTTTCG  CCAAATTCTC
501 CCAAAACGTC  CTAGACGCGA  CCGACGCGTT  CGGCATTTAC  TTTGACGATG
551 CCGCACCGCT  TGCCGGCATT  CCCGAAGACG  CGCTCGCCAT  GTTGGCCGCT
601 GCCGCGCAAA  GCGAAGGCAA  AACAGGCTAC  AAAATCGGTT  TGCAGATTCC
651 GCACTACCTC  GCCGTCATCC  AATACGCCGA  CAACCGCAAA  CTGCGCGAAC
701 AAATCTACCG  CGCCTACGTT  ACCGCGCCA  GCGAGCTTTC  AGACGACGGC
751 AAATTCGACA  ACACCGCCAA  CATCGACCGC  ACGCTCGAAA  ACGCCCTGCA
801 AACCGCCAAA  CTGCTCGGCT  TCAAAAATA  CGCCGAATTG  TCGCTGGCAA
851 CCAAATGGC  GGACACCCCC  GAACAAGTTT  TAAACTTCCT  GCACGACCTC
901 GCCCGCCGCG  CCAAACCCTA  CGCCGAAAA  GACCTCGCCG  AAGTCAAAGC
951 CTTGCGCCCG  GAAAGCCTCG  GCCTCGCCGA  TTTGCAACCG  TGGGACTTGG
1001 GCTACGCCGG  CGAAAACTG  CGCGAAGCCA  AATACGCATT  CAGCGAAACC
1051 GAAGTCAAAA  AATACTTCCC  CGTCGGCAAA  GTATTAAACG  GACTGTTCGC
1101 CCAAATCAA  AAATCTACG  GCATCGGATT  TACCGAAAA  ACCGTCCCCG
1151 TCTGGCACAA  AGACGTGCGC  TATTTTGAAT  TGCAACAAA  CGGCGAAACC
1201 ATAGGCGCG  TTTATATGGA  TTTGTACGCA  CGCGAAGGCA  AACGCGCGG
1251 CGCGTGGATG  AACGACTACA  AAGGCCGCCG  CCGTTTTTCA  GACGGCACGC
1301 TGCAACTGCC  CACCGCCTAC  CTCGTCTGCA  ACTTCACCCC  GCCCGTCGGC
1351 GGCAAAGAAG  CCCGCTTGAG  CCATGACGAA  ATCCTCACCC  TCTTCCACGA
1401 AACCGGACAC  GGCCTGCACC  ACCTGCTTAC  CCAAGTCGAC  GAACTGGCG
1451 TATCCGGCAT  CAACGGCGTA  GAATGGGACG  CAGTCGAACT  GCCCAGTCAG
1501 TTTATGGA  ATTTCTGTTG  GGAATACAAT  GTCTTGGCGC  AAATGTCCGC
1551 CCACGAAGAA  ACCGGCGTTC  CCCTGCCGAA  AGAATCTTTC  GACAAAATGC
1601 TCGCGCCAA  AAATTTCCAA  CGCGAATGT  TCCTCGTCCG  CCAAATGGAG
1651 TTCGCCCTCT  TTGATATGAT  GATTTACAGC  GAAGACGACG  AAGGCCGTCT
1701 GAAAACTGG  CAACAGGTTT  TAGACAGCGT  GCGCAAAGAA  GTCGCCGTCG
1751 TCCGACCGCC  CGAATACAAC  CGCTTCGCCA  ACAGCTTCGG  CCACATCTTC
1801 GCAGGCGGCT  ATTCCGCAGG  CTATTACAGC  TACGCGTGGG  CGGAAGTATT
1851 GAGCGCGGAC  GCATACGCCG  CCTTTGAAGA  AAGCGACGAT  GTCGCCGCCA
1901 CAGGCAAACG  CTTTGGCAG  GAAATCCTCG  CCGTCGGCGG  ATCGCGCAGC
1951 GCGGCAGAAT  CCTTCAAAGC  CTTCCGCGGA  CGCGAACCGA  GCATAGACGC
2001 ACTCTTGCGC  CACAGCGGCT  TCGACAACGC  GGCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 486; ORF 128.a>:

```
a128.pep
1  MTDNALLHLG  EEPFDQIKT  EDIKPALQTA  IAEAREQIAA  IKAQHTGWA
51  NTVEPLTGIT  ERVGRWGVV  SHLNSVTDTP  ELRAAYNELM  PEITVFTEI
101  GDIELYNRF  KTIKNSPEFD  TLSHAQKTKL  NHDLRDFVLS  GAELPPEQQA
151  ELAKLQTEGA  QLSAKFSQNV  LDATDAFGIY  FDDAAPLAGI  PEDALAMFAA
201  AAQSEKGTGY  KIGLQIPHYL  AVIQYADNRK  LREQIYRAYV  TRASELSDDG
251  KFDNTANIDR  TLENALQTAK  LLGFKNYAEL  SLATKMADTP  EQVLNLFHDL
301  ARRAKPYAEK  DLAEVKAFAR  ESLGLADLQP  WDLGYAGEKL  REAKYAFSET
351  EVKKYFPVGK  VLNGLFAQIK  KLYGIGFTEK  TVPVWHKDVR  YFELQONGET
401  IGGVYMDLYA  REGKRGGAWM  NDYKGRRRFS  DGTLLQLPTAY  LVCNFTPPVG
451  GKEARLSHDE  ILTLFHETGH  GLHLLTQVD  ELGVSGINGV  EWDAVELPSQ
501  FMENFVWEYN  VLAQMSAHEE  TGVPLPKELF  DKMLAAKNFQ  RGMFLVRQME
```

551 FALFDMMIYS EDDEGRILKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF  
 601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS  
 651 AAESFKAFRG REPSIDALLR HSGFDNAA\*

m128/a128 66.0% identity in 677 aa overlap

	10	20	30	40	50	60
m128.pep	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQTHGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQTHGTWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m128.pep	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130					
m128.pep	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAAQSEGKTYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVINFLHDL					
	250	260	270	280	290	300
				140	150	
m128.pep	-----YASEKLREAKYAFSETXVKKYFPVGX					
	:					
a128	ARRAKPYAEKDLAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
	160	170	180	190	200	210
m128.pep	VLNGLFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
	220	230	240	250	260	270
m128.pep	NDYKGRRRFSDGTLQLPTAYLVCNFPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
	280	290	300	310	320	330
m128.pep	ELGVSGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
	340	350	360	370	380	390
m128.pep	XGMFXVRQXEFALFDMMIYSEDDEGRILKNWQQVLDSVRKKVAVIQPPEYNRFRALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGRILKNWQQVLDSVRKEVAVVRPPEYNRFRANSFGHIF					
	550	560	570	580	590	600



```

400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRG
          |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
          610      620      630      640      650      660

460      470
m128.pep  REPSIDALLRHSGFDNAVX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      REPSIDALLRHSGFDNAAX
          670

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 487>:

g128-1.seq (partial)						
1	ATGATTGACA	ACGCACTGCT	CCACTTGGGC	GAAGAACCCC	GTTTTAATCA	
51	AATCAAAACC	GAAGACATCA	AATCCGCGCT	CCAAACCCGC	ATGCCCGAAG	
101	CGCGCGGACA	AATCGCGGCC	GTCAAAGCGC	AAACGCACAC	CGGCTGGGCG	
151	AACACCGTCG	AGCGTCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG	
201	GGCGTCGTG	TCCCATCTCA	ACTCCGTCGT	CGACACGCCCT	GAACTGCGCG	
251	CCGTCATATA	CGAACTGATG	CTTGAAATCA	CCGTCTTCTC	CACCGAAATC	
301	GGACAAGACA	TGGAACGTGA	CAACCGCTTC	AAACCATCA	AAAATTTCCC	
351	CGAATTTGCA	ACGCTTTCCC	CCGCACAAA	AACCAAGCTC	GATCAGGACC	
401	TGCGCGATTT	CGTATTGAGC	GGCGCGGAAC	TGCGCGCCGA	ACGGCAGGCA	
451	GAAC TGCCAA	AACTGCAAA	CGAAGGCGCG	CAACTTTCCG	CCAAATTTCT	
501	CCAAAAAGTC	CTAGACGCGA	CCGACGCGTT	CGGCAATTAC	TTTGACGATG	
551	CGCACCCTCT	TGCCGGCATT	CCCGAAGACG	CGCTCGCCAT	GTTTGCCGCC	
601	GCCGCGCAAA	GCGAAGGCAA	AACAGGTTAC	AAAATCGGCT	TGCAGATTCC	
651	GCACTACTTT	GCCGTTATCT	AATACGCGCG	CAACCGCGAA	CTGCGCGGAA	
701	AAATCTACCG	CGCTACGTT	ACCGCTGCCA	CGGAACTTTC	AAACGACGGC	
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGAAA	ACGCATTGAA	
801	AACCGGCCAA	TGCTCGGCT	TTAAAAATTA	CGCGGAATTG	TCGCTGGCAA	
851	CCAAAATGCG	GGACACGCC	GAACAGGTTT	TAAACTTCTC	GCACGACCTC	
901	GCCCGCGCG	CCAAACCTTA	CGCGGAAAA	GACCTCGCCG	AAGTCAAAGC	
951	CTTCGCCCGC	GAACACCTCG	GTCTCGCCGA	CCCGCAGCCG	TGGGACTTGA	
1001	GCTACGCGCG	CGAAAAACTG	CGCGAAGCCA	AATACGATT	CAGCGAAACC	
1051	GAACTCAAAA	AAACTTTCCC	GCTCGGCAAA	GTTCTGGCAG	CCCTGTTCCG	
1101	CCAAATCAAA	AATACTACG	GATCGCGATT	CGCGGAAAA	ACGCTTCCCG	
1151	TCTGGCACAA	AGACGTGCGC	TATTTTGAAT	TGCAACAAA	CGGCAAAACC	
1201	ATCGCGCGCG	TTTATATGGA	TTTGATCGCA	CGCGAAGGCA	AACGCGGCGG	
1251	CGCGTGGATG	AACGACTACA	AAGGCGCGCG	CGCTTTTGCC	GACGCGACGG	
1301	TGCAACTGCC	CACCGCCTAC	CTCGTCTGCA	ACTTCGCCCC	GCCCGTCGGC	
1351	GGCAAGAAG	CGGTTTAAAC	CCACGACGAA	ATCCTCACCC	TCTTCCACGA	
1401	AACCGGCCAC	GGACTGCAC	ACCTGCTTAC	CCAAGTGAC	GAAC TGGGCG	
1451	TGTCGCGCAT	CACCGCGCTA	AAA			

This corresponds to the amino acid sequence <SEQ ID 488; ORF 128-1.ng>:

g128-1.pep (partial)		g128-2.pep (partial)		g128-3.pep (partial)		g128-4.pep (partial)	
1	MIDNALHLHG	EPRFNQIKT	EDIKPAVQTA	IAEARGQIAA	VKAQTHTWGA		
51	NTVERLTGIT	ETVGRINGVV	SHLSNVVDTP	ELRAVYINAA	PEITVFTTTEI		
101	GQDIELYNRF	KRKNSPEFA	TLSPAQTKTL	DHDLRDFVLS	GAEILPPERQA		
151	ELAKLQTEGA	QLSAKFSQNV	LDATDAFGIY	FDDAAPLAGI	PEDALAMFAA		
201	AAQSEKGTGY	KIGLQIPHYL	AVIQYAGNRE	LREQIYRADY	TRASELSNDG		
251	KFDNTANIDR	TLENALKTAK	LLGFKNYAEL	SLATKMADTP	EQVLNLFHDL		
301	ARRAKPYAEK	DLAEVKAFAR	EHGLGLADPQ	WDLSYAGEKL	REAKYAFSET		
351	EVKKYPFVGK	VLAGLFGAAM	KLYGIGPAEK	TVPVWHKDVY	YFELQQNGKT		
401	IGGVYMDLYA	REGKRGGAWK	NDYKGRRRFA	DGTLQLPTAR	LVCNFAPPVG		
451	GKEARLSHDE	ILTLFHETGH	GLHHLLTOVD	ELGVSGINGV	K		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 489>:

```

ml28-1.seq
      1  ATGACTGACA  ACGCACTGCT  CCATTGGGC  GAAGAACCCC  GTTTTGATCA
     51  AATCAA AAC  GAAGACATCA  AACC CGCCT  GCA AACCGCC  ATCGCCGAAG
    101  CGCGCGAA CA  AATCGCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
    151  AACACTGT CG  AACCCCTGAC  CGGCATCACC  GAACCGCTCG  CAGGATTTTG

```



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201 GGGCGTGGTG TCGCACCTCA ACTCCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAAA AACCAAATC AACACGATC
401 TGCGCGATT TCGTCTCAGC GCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAACTGGCAA AACTGCAAC CGAAGGCGCG CAACTTTCG CCAAATTCCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGT CGGCATTTC TTGACGATG
551 CCGCACCCTG TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCGCGCAAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 AACTACCTC GCCGTATCC AATACGCCGA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCTTACGTT ACCCGCGCCA GCGAATTTT AGACGACGCG
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCGCGCGCG CCAAAACCTA CGCCGAAAAA GACCTCGCGG AAGTCAAAGC
951 CTTCGCGCGC GAAAGCCTGA ACCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCAG CGAAAACTG CGCGAAGCCA AATACGCGTT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGCGC TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CCGTTTTTCA GACGCGACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTCGCCCC ACCCGTCGGC
1351 GGCAGGGAAG CCCGCTGAG CCACGACGAA ATCCTCATCC TCTTCCACGA
1401 AACCGGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TATCGGGCAT CAACGGCGTA GAATGGGACG CGGTGGAAT GCCCAGCCAG
1501 TTTATGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCAC AAATGTCAGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCGGCCAA AAATCTCAA CGCGCATGT TCCTCGTCCG GCAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAAAA GTCGCCGTC
1751 TCCAGCGGCC CGAATACAAC CGCTTCGCTT TGAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGCAAAACG CTTTGGGAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGCG CGCGAACCGA GCATAGACGC
2001 ACTCTGCGC CACAGCGGTT TCGACAACGC GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 490; ORF 128-1>:

m128-1.pep.

```

1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVEPLTGIT ERVGRWGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLANALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLPQ WDLGYASEKL REAKYAFSET
351 EVKXYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDAVEPLPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRKKNW QQVLDSVRKK VAVIQPPEYN RFALSFHGIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAV*

```

m128-1/g128-1 94.5% identity in 491 aa overlap

```

          10      20      30      40      50      60
g128-1.pep MIDNALLHLGEEPRFNQIKTEDIKPAVQTAAEARGQIAAVKAQTHTGWANTVERLTGIT
          |||
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90     100     110     120
g128-1.pep ERVGRWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
          |||
m128-1      ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90     100     110     120

```

370

	130	140	150	160	170	180
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
	190	200	210	220	230	240
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV					
	190	200	210	220	230	240
	250	260	270	280	290	300
g128-1.pep	TRASELSNDGKFDNTANIDRTLLENALKTAKLLGFKNYAELSLATKMDTPEQVLNFLHDL					
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMDTPEQVLNFLHDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPWDLSYAGEKLREAKYAFSETEVKKYFPVVK					
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPQWDLGVAEKLREAKYAFSETEVKKYFPVVK					
	310	320	330	340	350	360
	370	380	390	400	410	420
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWM					
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
	490					
g128-1.pep	ELGVSGINGVK					
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 491>:

a128-1.seq

```

1  ATGACTGACA  ACGCACTGCT  CCATTGGGCG  GAAGAACCCC  GTTTTGATCA
51  AATCAAAACC  GAAGACATCA  AACCCGCCCT  GCAAACCGCC  ATTGCCGAAG
101 CGCGCGAACA  AATCGCCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
151 AACACTGTGC  AACCCCTGAC  CGGCATCACC  GAACGCGTCG  GCAGGATTTC
201 GGGCGTGGTG  TCGCACCTCA  ACTCCGTCAC  CGACACGCC  GAACTGCGCG
251 CCGCTACAA  TGAATTAATG  CCCGAAATTA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAGCTGTA  CAACCGCTTC  AAAACCATCA  AAAACTCCCC
351 CGAGTTCGAC  ACCCTCTCCC  ACGCGCAAAA  AACCAAATC  AACCACGATC
401 TGCGCGATTT  CGTCTCAGC  GGCGCGGAAC  TGCCGCCCGA  ACAGCAGGCA
451 GAATTGGCAA  AACTGCAAA  CGAAGGCGCG  CAACTTTCG  CCAAATTCTC
501 CCAAAACGTC  CTAGACGCGA  CCGACGCGTT  CGGCATTTC  TTTGACGATG
551 CCGCACCGCT  TGCCGGCATT  CCCGAAGACG  CGCTCGCCAT  GTTTGCCGCT
601 GCCGCGCAAA  GCGAAGGCAA  AACAGGCTAC  AAAATCGGTT  TGCAGATTCC
651 GCACTACCTC  GCCGTATCC  AATACGCCGA  CAACGCAAAA  CTGCGCGAAC
701 AAATCTACCG  CGCCTACGTT  ACCCGCGCCA  GCGAGCTTTC  AGACGACGGC
751 AAATTCGACA  ACACCGCCAA  CATCGACCGC  ACGCTCGAAA  ACGCCCTGCA
801 AACCGCAAAA  CTGCTCGGCT  TCAAAACTA  CGCCGAATG  TCGCTGGCAA
851 CCAAAATGGC  GGACACCCCC  GAACAAGTTT  TAAACTTCCT  GCACGACCTC
901 GCCCGCCGCG  CCAAACCTTA  CGCCGAAAAA  GACCTCGCCG  AAGTCAAAGC
951 CTTGCGCCCG  GAAAGCCTCG  GCCTCGCCGA  TTTGCAACCG  TGGGACTTGG
1001 GCTACGCCGG  CGAAAAATG  CGCGAAGCCA  AATACGCATT  CAGCGAAACC
1051 GAAGTCAAAA  AATACTTCCC  CGTCGGCAAA  GTATTAAACG  GACTGTTTCG
1101 CCAATCAAAA  AAACCTTACG  GCATCGGATT  TACCGAAAAA  ACCGTCCCCG
1151 TCTGGCAGAA  AGACGTGCGC  TATTTTGAAT  TGCAACAAAA  CGGCGAAACC
1201 ATAGGCGGCG  TTTATATGGA  TTTGTACGCA  CGCGAAGGCA  AACCGGCGCG

```

```
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACGCGCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCCTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAACCTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGC GC CACAGCGGCT TCGACAACGC GGCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 492; ORF 128-1.a>:

a128-1.pep

```
1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWGA
51 NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV EWDAVELP SQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRKKNW QQVLDVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*
```

m128-1/a128-1 97.8% identity in 677 aa overlap

```
10 20 30 40 50 60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
|||||
m128-1 MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
10 20 30 40 50 60

70 80 90 100 110 120
a128-1.pep ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
|||||
m128-1 ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
70 80 90 100 110 120

130 140 150 160 170 180
a128-1.pep TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
|||||
m128-1 TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
130 140 150 160 170 180

190 200 210 220 230 240
a128-1.pep FDDAAPLAGI PEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
|||||
m128-1 FDDAAPLAGI PEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
190 200 210 220 230 240

250 260 270 280 290 300
a128-1.pep TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
|||||
m128-1 TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
250 260 270 280 290 300

310 320 330 340 350 360
a128-1.pep ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
|||||
```

```

m128-1      ARRAKPYAEKDLAEVKAFARESLNLADLQPWDLGYASEKLREAKYAFSETEVKKYFPVGK
              310      320      330      340      350      360

              370      380      390      400      410      420
a128-1.pep  VLNGLFAQIKKLYGIGFTEKTPVWVKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
              |||
m128-1      VLNGLFAQIKKLYGIGFTEKTPVWVKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
              370      380      390      400      410      420

              430      440      450      460      470      480
a128-1.pep  NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
              |||
m128-1      NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHLHLLTQVD
              430      440      450      460      470      480

              490      500      510      520      530      540
a128-1.pep  ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              |||
m128-1      ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              490      500      510      520      530      540

              550      560      570      580      590      600
a128-1.pep  RGMFLVRQMEFALFDMMIYSEDDDEGRLLKNWQQVLDVRKEVAVVRPPEYNRFANSFGHIF
              |||
m128-1      RGMFLVRQMEFALFDMMIYSEDDDEGRLLKNWQQVLDVRKKVAVIQPPEYNRFALSFGHIF
              550      560      570      580      590      600

              610      620      630      640      650      660
a128-1.pep  AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              |||
m128-1      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660

              670      679
a128-1.pep  REPSIDALLRHSGFDNAAX
              |||
m128-1      REPSIDALLRHSGFDNAVX
              670

```

## a128-1/ P44573

sp|P44573|OPDA\_HAEM OLIGOPEPTIDASE A >gi|1075082|pir||C64055 oligopeptidase A (prlc) homolog  
- Haemophilus influenzae (strain Rd KW20)  
>gi|1573174 (U32706) oligopeptidase A (prlc) [Haemophilus influenzae Rd] Length = 681  
Score = 591 bits (1507), Expect = e-168  
Identities = 309/677 (45%), Positives = 415/677 (60%), Gaps = 4/677 (0%)

```

Query: 4  NALLHLGEBEPRFDQIKTEDIKPALQTXXXXXXXXXXXXXTHTGWANTVEPLTGITERV 63
          N LL++ P F QIK E I+PA++ H W N + PLT +R+
Sbjct: 5  NPLLNIQGLPPFSQIKPEHIRPAVEKLIQDCRNTIEQVLKQPHFTWENFILPLTETNDRL 64

Query: 64 GRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFDTLS 123
          R W VSHLNSV ++ ELR AY +P ++ + T +GQ LYN + +KNS EF S
Sbjct: 65 NRAWSPVSHLNSVKNSTELREAYQTCLPLLSEYSTWVGQHKGLYNAYLALKNSAEFADYS 124

Query: 124 HAQKTKLNHDLRDFVLSGAELPPEQQABELAKLQTEGAQLSAKFSQNVLDATDAFGIYFDD 183
          AQK + + LRDF LSG L E+Q ++ ++L+++FS NVLDAT + ++
Sbjct: 125 IAQKKAIENSLRDFELSGIGLSEKQQRGYEIVARLSELNSQFSNVLDATMGWEKLIEN 184

Query: 184 AAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHVLAVIQYADNRKLREQIYRAYVTRA 243
          A LAG+PE AL +A+S+G GY+ L+IP YL V+ Y +NR LRE++YRAY TRA
Sbjct: 185 EAELAGLPESALQAAQQAESKGLKGYRFTLEIPSYLPVMTYCENRALREEMYRAYATRA 244

Query: 244 SELSDD-GKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDLAR 302
          SE + GK+DN+ ++ L ++ AKLLGF Y ELSLATKMA+ P+QVL+FL LA
Sbjct: 245 SEQGPNGAKWDNSKVMEEILTLRVELAKLLGFNTYTELSLATKMAENPQQVLDLDFDLHAE 304

Query: 303 RAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGKVL 362
          RAKP EK+L E+K + + G+ +L PWD+G+ EK ++ YA ++ E++ YFP +V+
Sbjct: 305 RAKPQGEKELQELKGYCEKEFGVTELAPWDIGFYSEKQKQHLAYAINDEELRPYPENRVI 364

```

Query: 363 NGLFAQIKKLYGIGFTE-KTVPVWHKDVRYFEL-QQNETIGGVYMDLYAREGKRGAWM 420  
 +GLF IK+++ I E K V WHKDVR+F+L +N + G Y+DLYARE KRGAWM  
 Sbjct: 365 SGLFELIKRIFNIRAVRKGVDTWKDVRFDLIDENDQLRGSFYLDLYAREHKRGAWM 424

Query: 421 NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEIXXXXXXXXXXXXXXQVD 480  
 +D GR+R DG+++ P AYL CNF P+G K A +H+E+ Q+D  
 Sbjct: 425 DDCIGRKRKLDGSIETPVAYLTCNFNAPIGNKPALFTHNEVTTLFHEFGHGIHMLTQID 484

Query: 481 ELGVSGINGVENDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ 540  
 V+GINGV WDAVELPSQFMEN+ WE LA +S H ETG PLPKE ++L AKNFQ  
 Sbjct: 485 VSDVAGINGVPWDAVELPSQFMENWCWEEALAFISGHYETGEPLPKEKLTQLLKAKNFQ 544

Query: 541 RGMPLVRQMEFALFDMMIYSEDDEGRLEKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF 600  
 MF++RQ+EF +FD ++ D + L SV+ +VAV++ ++ R +SF HIF  
 Sbjct: 545 AAMFILRQLEFGIFDFRLHHTFDAEKTNIQILDTLKSQVAVIKGVWDWARAPHFSHF 604

Query: 601 XXXXXXXXXXXXXWAEVLSADAYAAFEESDDV-AATGKRFWQEILAVGGSRSAAESFKAFR 659  
 WAEVLSADAY+ FEE TKG F EIL GGS E FK FR  
 Sbjct: 605 AGGYAAGYYSYLWAEVLSADAYSRFEEGIFNPITGKSFLDEILTRGGSSEPMELFKRFR 664

Query: 660 GREPSIDALLRHSGFDN 676  
 GREP +DALLRH G N  
 Sbjct: 665 GREPQLDALLRHKGIMN 681

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 493>:

g129.seq  
 1 ATGCTTTCAC CTCCTCGGCG TAAACGGCG GCACATCAAT CAAGCCGTCT  
 51 TTCATTGCG TCGGAAAAA ATGCGCGGTG TTGCCGTGAT CAAAATCAAT  
 101 ATCGTGCAGC ATCCAGCCCA AATCGCGGTT TGCCTCGCTT TCCGATAACG  
 151 CCGACGGCGG CAGCGGTTCA CCCTTATCCG CGCTTTCGCC ATTTGCCCTT  
 201 TCAGGCTGCG GGCATAGGGG CGGAACAGGC GCGGTCGAA TCCTGTTTCA  
 251 TCCGGACAAA CGCGTTGGCA GTCGAAAAAT CCGGCCGGCC GTGTCAAATA  
 301 ATGCGTTACT TTGGCCGGGT CTTGTCCTTT GTAAGCGGCG GTCTTTTTTT  
 351 GCGCGCCATC CGCATCTGTT TGGGCGCATG GCAAACGGCG GCTGCCGTAC  
 401 AATCAAAATG TTTGGCGATT TCATGCAGAC AGGCATCCGG ATGCCGCCCG  
 451 ACATATCGAG CCGGTTTTTG CCTATCCGAT TTGGCGGCAT TTAGGCCGGT  
 501 AACTTGA

This corresponds to the amino acid sequence <SEQ ID 494; ORF 129.ng>:

g129.pep  
 1 MLSPPRRKA AHQSSRLSFA CGKNAACCRD QNQYRAASSP NRGLPRFPIT  
 51 PTAAAVHPYP RFRHLPFQAA GIGAEQAAVE SCFIRTNALA VGKSGRPCQI  
 101 MRYFGRVLSF VSGGLFLRAI RICLGAWQTA AAVQSKCLAI SCRQASGCRP  
 151 TYRAGFCLSD LAAFRPVT\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 495>:

m129.seq (partial)  
 1 ..TATCTGCGCT TTTACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA  
 51 ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG  
 101 GAAAATTCGG CCGGCTGTGT CAAATAATGC GTTACTTTGG CCGGTCCTTG  
 151 TTCTTTGTAA GTGGTGGTCT TTTTTCGCG GTTATCCCA TCTGTTTGAG  
 201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTCAT  
 251 GCAGATAGGC ATCCGGGTGT TGCCCAACAT ATTGAGCCGG TTTTGCCTA  
 301 TCCGATTGTA CGGCATTTAG ACCGTAAC TGA

This corresponds to the amino acid sequence <SEQ ID 496; ORF 129>:

m129.pep (partial)  
 1 ..YLRPHYLPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGRLC QIMRYFGRVL  
 51 FTVSGGLFLR VIPICLSAXQ MVAAVQSKCL AISCRXASGC CPTYXAGFCL  
 101 SDLTAFRPVT \*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 129 shows 79.1% identity over a 110 aa overlap with a predicted ORF (ORF 129.ng) from *N. gonorrhoeae*:

m129/g129

```

m129.pep                                10      20      30
                                         YLRFHLYLPFQAAGIGTEQVAVKSCFIQINT
                                         | | | : | | | | | : | | : | | : | :
g129  RDQNQYRAASSPNRGLRPFPIPTPTAAAVHPYPRFRHLFPQAAGIGAEQAAVESCFTRTNA
      30      40      50      60      70      80

      40      50      60      70      80      90
m129.pep  LVVGKFGRLCQIMRYFGRVLFFVSGGLFLRVPICLSAXQMVAAVQSKCLAISCRXASGC
      | : | | | | | | | | | | | | | | | : | | | : | | : | | | | | | | | | |
g129  IAVGKSGRPCQIMRYFGRVLSFVSGGLFLRAIRICLGAWQTAAAVQSKCLAISCRQASGC
      90     100     110     120     130     140

      100     110
m129.pep  CPTYXAGFCLSDLTAFRPVTX
      | | | | | | | : | | | | |
g129  RPTYRAGFCLSDLAAFRPVTX
      150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 497>:

```

a129.seq (partial)
1 TATCTGCGCT TTTCACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA
51 ACAGGATAGCG GTCAAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
101 GAAAATTTCGG CCAGCTGTGT CAAATAATCG GTTACTTTGG CCGGGTCTTG
151 TTCTTTGTAA GTGGTGGTCT TTTTTTGC GC GTTATCCCCA TCTGTTTGAG
201 TGCATAGCAA ATGGTGCGT CCGTACAAT AAAATGTTG GCGATTTTCA
251 GCAGATAGGC ATCCTGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCGCTA
301 TCCGATTTGA CGGCATTTAG ACCGGTAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 498; ORF 129.a>:

a129.pep (partial)

1	YLRFHYLPFQ	AAGIGTEQVA	VKSCFIQINT	LVVGKFGQLC	QIMRYFGRVL
51	FFVSGGLEFLR	<u>VIPICLSA</u> *Q	MVAAVQSKCL	AISCR*ASWC	CPTY*AGFCL
101	SDLTAFRPVT	*			

**m129/a129** 98.2% identity in 110 aa overlap

	10	20	30	40	50	60
m129.pep	YLRFHYPFQAAGIGTEQVAVKSCFIQINTLVVGKFGRLCQIMRYFGRVLFVVGGLFLR					
a129	YLRFHYPFQAAGIGTEQVAVKSCFIQINTLVVGKFGQLCQIMRYFGRVLFVVGGLFLR					
	10	20	30	40	50	60
	70	80	90	100	110	
m129.pep	VIPICLSAXQMVAAVQSKCLAISCRXASGCCPTYXAGFCLSDLTAFRPVTX					
a129	VIPICLSAXQMVAAVQSKCLAISCRXASWCCPTYXAGFCLSDLTAFRPVTX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 499>:

g130.seq

```
1 ATGAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCT
51 TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAAGC
101 TGGCGGGGAC TGGATCGTTG GGCAGTGTGC ATGCCACTAC GGAAGCGGCA
151 ACGCAGACCC GCATCCAGCC TGTCGGACAA TTGACGATGG GTGACGGCAG
201 CCCCCTCGGC GAACGCCAAG CGCAACAGAT TTTCGGCAAA ATCTGTATCC
```

```

251 AATGCCACGC GCGGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGACT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCGA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGCAG
401 ACCTGACCGA TCAGGAAGCTC AAACGGGCGA TTACCTACAT GGCGAATAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAGGTG TGCCACGGCG GTTCGATTCC
651 CCGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGCAC AAACATGCCC TTGAAGGCTT TAACGCGATG
751 CCGGCCAAAG GCGGCAATGC AGTTTGTAGC GATGACGAAG TCAAAGCGGC
801 TGTTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 500; ORF 130.ng>:

```

g130.pep
  1 MKQLRDNKAQ GSALFTLVSG IVIVIAVLVF LIKLAGSGSF GDVDATTEAA
 51 TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFQHAL NGFNAMPAKG GAADLTDQEL KRAITYMANK
151 SGGSPNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAAPAVGVGD
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKKGKETH KHALEGFNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 501>:

```

m130.seq (partial)
  1 ..GGCGAACAGA TTTTCGGCAA AATCTGTATC CAATGCCACG CGGCGGACAG
 51 CAATGTGCCG AACGCTCCGA AACTGGAACA CAACGGCGAT TrGGCACCGC
101 GTATCGGCAA GGCTTCGATA CCTTGTTCGA ACACGCGCTG AACGGCTTTA
151 ACGCCATGCC TGCAAAGGC GGTGCGGCAG ACCTGACCGA TCAGGAAGCTT
201 AAACGGGCGA TTACTTACAT GGCGAACAAA AGCGGCGGTT CTTTCCCGAA
251 TCCTGATGAG GCTGCGCCTG CCGACAATGC CGCTTCAGGA ACAGCTTCTG
301 CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG CGAAGGCAGA AGACAAGGGT
351 GCGGCACCCC TGCGGTCGGC GTTGACGGTA AAAAAGTCTT CGAAGCAACC
401 TGTCAGGTGT GCCACGGCGG TTCGATTCCC GGTATTCCCG GCATAGGCAA
451 AAAAGACGAT TGGGCACCGC GTATCAAAAA AGGCAAAGAA ACCTTGCACA
501 AACACGCCCT TGAAGGCTTT AACGCGATGC CTGCCAAAG CGCAATGCA
551 GGTTTGAGCG ATGACGAAGT CAAAGCGGCT GTTGACTATA TGGCAAACCA
601 ATCCGGTGCA AAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 502; ORF 130>:

```

m130.pep (partial)
  1 ..GEQIFGKICI QCHAADSNVP NAPKLEHNGD XAPRIQGFDL LQHALNGFN
 51 AMPAKGGAAD LTDQELKRAI TYMANKSGGS FPNPDEAAPA DNAASGTASA
101 PADSAPAEAE KAEDKGAAPA VGVDGKKVFE ATCQVCHGGS IPGIPGIGKK
151 DDWAPRIKKG KETLHKHALE GFNAMPKXG NAGLSDDEVK AAVDYMANKS
201 GAKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 130 shows 98.1% identity over a 206 aa overlap with a predicted ORF (ORF 130.ng) from *N. gonorrhoeae*:

```

m130/g130
      10      20      30
m130.pep      GEQIFGKICIQCHAADSNVPNAPKLEHNGD
                |||
g130      DATTEAATQTRIQPVGQLTMDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
           50      60      70      80      90     100

      40      50      60      70      80      89
m130.pep      XAPRI-QGFDTLFQHALNGFNAMPAKGAADLTDQELKRAITYMANKSGGSFPNPDEAAP
                |||
g130      WAPRIAQGFDTLFQHALNGFNAMPAKGAADLTDQELKRAITYMANKSGGSFPNPDEAAP
           110     120     130     140     150     160

```

376

```

          90      100      110      120      130      140
m130.pep  ADNAASGTASAPADSAAPEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||
g130       ADNAASGTASAPADSAAPEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130.pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDEVKAAVDYMANQSGAKFX
          |||
g130       KKDDWAPRIKKGKETLHKHALEGFNAMPKGGNAGLSDEVKAAVDYMANQSGAKFX
          230      240      250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 503>:

```

a130.seq
1  ATGAAACAAC  TCCGCGACAA  CAAAGCCCAA  GGCTCTGCAC  TGTTTACCCT
51  TGTGAGCGGT  ATCGTTATTG  TTATTGCAGT  CCTTTATTTC  CTGATTAAGC
101 TGGCGGGCAG  CGGCTCGTTC  GGCATGTCTG  ATGCCACTAC  GGAAGCAGCA
151 ACGCAGACCC  GTATCCAGCC  TGTCGGACAA  TTGACGATGG  GCGACGGCAT
201 CCCCCTCGGC  GAACGCCAAG  GCGAACAGAT  TTTCCGGCAA  ATCTGTATCC
251 AATGCCACGC  GCGGCAGAGC  AATGTGCCGA  ACGCTCCGAA  ACTGGAACAC
301 AACGGCGATT  GGGCGCGCG  TATCGCGCAA  GGCTTCGATA  CCTTGTTCCT
351 ACACGGCTG  AACGGCTTTA  ACGCCATGCC  TGCCAAAGGC  GGTGCGGTAG
401 ACCTGACCGA  TCAGGAACCT  AAACGGGCGA  TTAATTACAT  GCGCAACAAA
451 AGCGGCGGTT  CTTTCCCGAA  TCCTGATGAG  GCTGCGCCTG  CCGACAATGC
501 CGCTTCAGGA  ACAGCTTCTG  CTCCTGCCGA  TAGTGAGCT  CCGGCAGAAG
551 CGAAGGCAGA  AGACAAGGGT  GCGGCAGCCC  CTGCGGTCGG  CGTTGACGGT
601 AAAAAAGTCT  TCGAAGCAAC  CTGTCAGGTG  TGCCACGGCG  GTTCGATTCC
651 CCGTATTCCC  GGCATAGGCA  AAAAAGACGA  TTGGGCACCG  CGTATCAAAA
701 AAGGCAAAGA  AACCTTGCAC  AAACACGCC  TTGAAGGCTT  TAACGCGATG
751 CCTGCCAAG  GCGGCAATGC  AGGTTTGAGC  GATGACGAAG  TCAAAGCGGC
801 TGTGACTAT  ATGGCAAACC  AATCCGGTGC  AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 504; ORF 130.a>:

```

a130.pep
1  MKQLRDNKAQ  GSALFTLVSG  IVIVIAVLVF  LIKLAGSGSF  GDVDATTEAA
51  TQTRIQPVGQ  LTMGDGIPVG  ERQGEQIFGK  ICIQCHAADS  NVPNAPKLEH
101 NGDWAPRIAQ  GFDTLFQHAL  NGFNAMPAKG  GAVDLTDQEL  KRAITYMANK
151 SGGSFNPNDE  AAPADNAASG  TASAPADSAA  PAEAKAEDKG  AAAPAVGVDG
201 KKVFEATCQV  CHGGSIPGIP  GIGKKDDWAP  RIKKGKETLH  KHALEGFNAM
251 PAKGGNAGLS  DDEVKAAVDY  MANQSGAKF*

```

m130/a130 97.6% identity in 206 aa overlap

```

          10      20      30
m130.pep  GEQIFGKICIQCHAADSNVPNAPKLEHNGD
          |||
a130       DATTEAATQTRIQPVGQLTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
          50      60      70      80      90      100

          40      50      60      70      80      89
m130.pep  XAPRI-QGFDTLFQHALNGFNAMPAKGGADLTDQELKRAITYMANKSGGSFNPDEAAP
          |||
a130       WAPRIAQGFDTLFQHALNGFNAMPAKGGAVDLTDQELKRAITYMANKSGGSFNPDEAAP
          110      120      130      140      150      160

          90      100      110      120      130      140
m130.pep  ADNAASGTASAPADSAAPEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||
a130       ADNAASGTASAPADSAAPEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130.pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDEVKAAVDYMANQSGAKFX

```



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|||||  
a130 KKDDWAPRIKKGKETLHKHALEGFNAMPAGGNAGLSDDDEVKAAVDYMANQSGAKFX  
230 240 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 505>:

g132.seq  
1 ATGGAAGCCT TCAAAACCCCT AATTTGGATT ATTAATATTA TTTCCGCTTT  
51 GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG  
101 GCGCGACCTT CGGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT  
151 GCCGCAACG CCAACTTcct CAgccGCTCG AccGccGTTG CAGCAACAtt  
201 tttcttTGca acctgcAtgg gctatggTgt atattcacac CCACACGACA  
251 AAACACGGTT TGGACTtcag caacataCGA CAGACTCAGC AagcACCCAA  
301 ACCcgtAAGC AATACCGAAC CTTCTGCCCC TGTTCCCTCAG CAGCAGAAAT  
351 AACagtTTTT CAAATgccga caTGgtga

This corresponds to the amino acid sequence <SEQ ID 506; ORF 132.ng>:

g132.pep  
1 MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS  
51 AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QHTTDSASTQ  
101 TRKQYRTFCP CSSAAEITVF QMPTW\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 507>:

m132.seq (partial)  
1 ATGGAACCCT TCAAAACCTT AATTTGGATT GTTAATTAA TTTCCGCTTT  
51 GGCCGCTCTC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG  
101 GCGCGACTTT CGGA...

This corresponds to the amino acid sequence <SEQ ID 508; ORF 132>:

m132.pep (partial)  
1 MEAFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 132 shows 89.5% identity over a 38 aa overlap with a predicted ORF (ORF 132.ng) from *N. gonorrhoeae*:

m132/g132

	10	20	30	
m132.pep	MEPFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG			
	: :     :			
g132	MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSGSGSAQGVFGSAGNANFLSRS			
	10	20	30	40 50 60

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 509>:

a132.seq  
1 ATGGAAGCCT TCAAAACCCCT AATTTGGATT GTTAATATAA TTTCCGCTTT  
51 GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG  
101 GCGCGACTTT CGGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT  
151 GCCGCAACG CTAACCTCCT CAGCCGCTCG ACCGCCGTTG CAGCAACATT  
201 TTTCTTTGCA ACCTGCATGg GCTATGGTGT ATATTACAC CCACACGACA  
251 AAACACGGTT TGGACTTCAG CAACGTACAA CAACTCAGC AAGCACCCTAA  
301 ACCCGTAAGC AATACCGAAC CTTCTGCCCC TGTTCCCTCAG CAGCAGAAAT  
351 AACAGTTTTT CAAATGCCGA CATGGTGA

This corresponds to the amino acid sequence <SEQ ID 510; ORF 132.a>:

a132.pep  
1 MEAFKTLIWI VNIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS  
51 AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QRTTNSASTQ  
101 TRKQYRTFCP CSSAAEITVF QMPTW\*

m132/a132 92.1% identity in 38 aa overlap

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```

          10      20      30
m132.pep  MEPFKTLIWIIVNLISALAVFVLVLLQHGKGADAGATFG
          || |||||:|||||:|||||
a132      MEAFKTLIWIIVNIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFGSAGNANFLSRS
          10      20      30      40      50      60

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 511>:

```

g134.seq
1  ATGTCCCAAG AAATCCTCGA CCAAGTGC GC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCGATGCGG GTAAAACCA C GCTGACCGAA AACTGCTGC
101 TGTTCGCGG  CGCGATTCAA AGCGCAGGCA CGGTGAAAGG TAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGA TGCAGTTGCA CTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CAGTGGACAG CGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCGATA
401 CGCCGATTGT TACCTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCT
451 TTGGAACCTT TGGACGAAGT GGAAGACATC CTGCAAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTCAAGGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCCTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATAAAC AATCCCGAAT TGGAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGACGG
701 CGGCTTCCAA CGAATTTAAT CTCGacgaAT TTCTCGccgG CGAACTCACG
751 CCAGTGTCTT TCGGCTCTGC GATTAACAAC TTCGGCATTC AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CACCCGCACC GAAACCGCGC GACGCGACCA
851 TGCGCATGGT CGGGCCGGAC GAGCCGAAAT TTTCCGGATT TATCTTTAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATCG CCTTCTTGCG
951 CGTCTGTCTC GGTAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTAG TAACCTTCAT GTCGCACGAC
1051 CGCGAACTGG CGGAAGAAGC CTACGCCGGC GACATCATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGG
1151 CGTTTACCGG CATCCCATTC TTCGCGCCCG AACTGTTCCG CAGCGTCCGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAAC TG CAAAAGGTT TGCAACAAC T
1251 CGGCGAAGAA GGTGCGGTTT AAGTATTC AA ACCGATGAGC GGC GCGGATT
1301 TGATTTTGGG TCGGTCGCGC GTGTTGCA GT TTGAAGTCGT AACCTCACGC
1351 CTCGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAATG GCGGAATTG
1451 AAAAAGCCAA CGCAGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTTGGGG TTGACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCAACA TTCGGTCAAA CTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 512; ORF 134.ng>:

```

g134.pep
1  MSQEILDQVR RRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51  GKFATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDPPIVTFM NKYDREVRDS
151 LELLDEVEDI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKGIN NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLEGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATMRMVGPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELAEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL OKGLQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 513>:

```

m134.seq
1  ATGTCCCAAG AAATCCTCGA CCAAGTGC GC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCTGACGCAG GTAAAACCA C GTTGA CTGAA AACTCTTGC
101 TGTTCGCGG  CGCGATTCA GAGCGGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACTCCGA CTGGATGGAA ATCGAGAAGC AGCGCGGCAT

```

```

201 TTCCGTGGCA TCAAGTGTGA TGCAGTTCGA TTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CCGTGGACAG CGCATTAATG GTCATCGACG CGGCAAAAGG
351 CGTGGAAGCG CAAACCATCA AGCTCTTAAA CGTCTGCCGC CTGCGCGATA
401 CACCGATTGT TACGTTTATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAAC TTT TGGACGAAGT GGAAAACATT TTA AAAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA TGAATTTTAT CTCTTTGAAG CTGGCGGCGA ACGCCTGCCG
601 CACGAGTTTC ACATCATCAA AGGCATCGAT AATCCTGAAT TGGAAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTTAAT CTCGACGAAT TCCTCGCCGG CGAACTCACG
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CGCCCGCGCC GAAACCGCGC GACGCGACCG
851 TACGTATGGT CGAGCCGGAC GAGCCGAAGT TTTCCGGATT TATCTTCAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CTTTCTTGCG
951 CGCTGCTCC GGCAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TTACCTTCAT GTCGCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGG
1151 CGTTCACCGG CATCCCATTC TTCGCACCCG AACTGTTCCG CAGCGTACGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAACG CAAAAAGGCT TGCAACAGCT
1251 CGGCGAAGAA GGCGCGGTGC AGGTGTTCAA ACCGATGAGC GGCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTGTCAGT TTGAAGTCGT TACCTCGCGC
1351 CTCGCCAAGC AATACGGCGT AGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAAGT GCTGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACGCGT GAATTGGA CTCACGCAAG AACGTTGGCC
1551 GGACATCGTG TTCCACGAAA CACGCGAACA TTCGGTCAAA CTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 514; ORF 134>:

m134.pep

```

1 MSQEILDQVR RRRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWME IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSED TYR
101 VLTAVDSALM VIDAAGVEA OTIKLLNVCR LRDTPIVTFM NKYDREVRDS
151 LELLDEVENI LKIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKID NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLOFEVVTSR
451 LANEYGVEAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 134 shows 98.7% identity over a 531 aa overlap with a predicted ORF (ORF 134.ng) from *N. gonorrhoeae*:

m134/g134

```

          10      20      30      40      50      60
m134.pep MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
          |||
g134      MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD
          10      20      30      40      50      60

          70      80      90      100     110     120
m134.pep IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSED TYRVLTA VDSALMVIDAAKGVEA
          |||
g134      IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSED TYRVLTA VDSALMVIDAAKGVEA
          70      80      90      100     110     120

          130     140     150     160     170     180

```

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m134.pep	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVENILKIRCAPVTWPIGMGKNFKG
g134	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVEDILQIRCAPVTWPIGMGKNFKG
	130 140 150 160 170 180
m134.pep	VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
g134	VYHILNDEIYLF EAGGERLPHEFDIIKGINNPELEQRFPLEIQQLRDEIELVQAASNEFN
	190 200 210 220 230 240
m134.pep	LDEFLAGELTPVFFGSAINNFGIOEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
g134	LDEFLAGELTPVFFGSAINNFGIOEILNSLIDWAPAPKPRDATMRMVGPEPKFSGFIFK
	250 260 270 280 290 300
m134.pep	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHDRELVEEAYAG
g134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHDRELAEAYAG
	310 320 330 340 350 360
m134.pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
g134	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
	370 380 390 400 410 420
m134.pep	GAVQVFKPMSGADLILGAVGVLFQFEVVTSRLANEYGV EAVFDSASIWSARWVSCDDKKKL
g134	GAVQVFKPMSGADLILGAVGVLFQFEVVTSRLANEYGV EAVFDSASIWSARWVSCDDKKKL
	430 440 450 460 470 480
m134.pep	AEFEKANAGNL AIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
g134	AEFEKANAGNL AIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
	490 500 510 520 530

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 515>:

```

a134.seq
1  ATGTCCAAG AAATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCCAC CCGTACGCAG GTAAAACCAC GTTGACTGAA AAACCTCTGC
101 TGTTTTCAGG TCGGATTCAA AGCGCGGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGA TGCAGTTCGA CTATAAAGAC CACACCGTCA
251 ACCTTTTGGA CAGCCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTGACCG CCGTCGATAG TGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCAATA
401 CGCCGATTGT TACGTTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAATTGC TGGACGAAGT GGAAAACATC CTGCAAATCC GCTGCGCGCC
501 CGTAACCTGG CCGATCGGCA TGGGCAGAAA CTTCAAAGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCTTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCCGAAT TGAACACAG
651 CTTTCCGTTA GAAATACAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTCAAT CTCGACGAAT TCCTCGCCGG CGAACTACG
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGAATGGG CGCCCGCGCC GAAACCACGC GATGCGACCG
851 TCGTATGGT CGAGCCGGAC GAGCCGAAGT TTTCCGATT TATCTTCAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGCG

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951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAAATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TAACCTTCAT GTCCCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GTATCCCAAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGA
1151 CGTTTACCGG CATCCCATTG TTCGCGCCCG AACTGTTCCG CAGCGTTCGC
1201 ATCAAAAACC CGCTGAAAAT CAAGCAACTG CAAAAAGGTT TGCAACAGCT
1251 TGGCGAAGAA GGTGCGGTGC AGGTGTTCAA ACCAATGAGC GGCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTGTCAGT TTGAAGTCGT TACCTCGCGC
1351 CTTGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAACG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAACTG GCGGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCGGGCGG CAACCTCGCC
1501 TACCTCGCCC CTAACCGCGT GAATCTGGGA CTCACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAGCA TTCGGTCAAA CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 516; ORF 134.a>:

```

a134.pep
1 MSQEILDQVR RRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFSATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGGVEA QTIKLLNVCR LRNTPIVTFM NKYDREVRDS
151 LELLDEVENI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKGID NPELEQRFPL EIQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IEWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLTFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVEAV FDNASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

m134/a134 98.9% identity in 531 aa overlap

	10	20	30	40	50	60
m134.pep	MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFSATSDWME					
a134	MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFSATSDWMD					
	10	20	30	40	50	60
m134.pep	70	80	90	100	110	120
	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDLSALMVIDAAGGVEA					
a134	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDLSALMVIDAAGGVEA					
	70	80	90	100	110	120
m134.pep	130	140	150	160	170	180
	QTIKLLNVCRLRDTPIVTFMKNYDREVRDSLELLDEVENILKIRCAPVTWPIMGKNFKG					
a134	QTIKLLNVCRLRDTPIVTFMKNYDREVRDSLELLDEVENILQIRCAPVTWPIMGKNFKG					
	130	140	150	160	170	180
m134.pep	190	200	210	220	230	240
	VYHILNDEIYLFEGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
a134	VYHILNDEIYLFEGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
	190	200	210	220	230	240
m134.pep	250	260	270	280	290	300
	LDEFLAGELTPVFFGSAINNFGIQLNSLIDWAPAPKPRDATVRMVEPDPEPKFSGFIFK					
a134	LDEFLAGELTPVFFGSAINNFGIQLNSLIEWAPAPKPRDATVRMVEPDPEPKFSGFIFK					
	250	260	270	280	290	300
m134.pep	310	320	330	340	350	360
	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHRELVEEAYAG					
a134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHRELVEEAYAG					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m134.pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
a134	DIIGIPNHGNIQIGDSFSEGEQLTFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m134.pep	GAVQVFKPMSGADLILGAVGLQFEVVTSRLANEYGVEAVFDSASIWSARWVSCDDKKKL					
a134	GAVQVFKPMSGADLILGAVGLQFEVVTSRLANEYGVEAVFDNASIWSARWVSCDDKKKL					
	430	440	450	460	470	480
	490	500	510	520	530	
m134.pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
a134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 517>:

g135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCG
51  TTCGGACgGC AGCCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCTG CAGGGTTCGG CGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAAATATAC GGCAAACTTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GTGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGATTCCC ATCATCAATG
401 AAAACGACAC GGTTCGGTT GAGGAGTTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCAGC GGCGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCACTCAA ACCCGATTCA TTGGCCGAAG CCGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTcccCcg tgCCAAAGGT TTGCGGACAC AGAAGCAATG
801 GctggCGTTC TATTcggaaa gcggGgag cggtTatgtg gacgaaagtg
851 cggaacacgc tTgtccgaa caagggaaa cctgCTGA

```

This corresponds to the amino acid sequence <SEQ ID 518; ORF 135.ng>:

g135.pep

```

1  MKYKRIVFKV GTSSITRSDG SLSRGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRRAIP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGPNPS NPDAVRLDKI EHNHEIEM
201 AGGSGSANGT GGMLTKIKAA TIAESGVPV YICSSLKPDs LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESGGSVYV DESAEHALSE QGKAC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 519>:

m135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCTGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAAATATAC GGCAAACTTG TCTTCAGACG GCATCGTGTC CGCGCAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT

```

```

501 GACCGACATA GACGGTCTTT ACACGGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AACGGGCACG GCGGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CTGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCGAAA GCCGGGGCAG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGGAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGACAG
951 CAAGGCAACC AACAGCCCC TGGGCAAAGG GCGCGTCCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATCGCGTA AGGCGAAAGG CGTGTTTCATC
1051 CATCGGGACG ACTGGATTTC CATCACGCCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 520; ORF 135>:

```

m135.pep
1  MKYKRIVFKV GTSSITHSDG SLSRGKIQTI TCQLAALHHA GHLEVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAVP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGPNPS NPDAVRLDKI EHNHEIEM
201 AGGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDA LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGSVYV DEGAEHALSE QGKSLLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KSRKAKGVFI
351 HRDDWISITP EIRLLLTEF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 135 shows 97.6% identity over a 294 aa overlap with a predicted ORF (ORF 135.ng) from *N. gonorrhoeae*:

```

m135/g135
      10      20      30      40      50      60
m135.pep  MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g135      MKYKRIVFKVGTSSITRSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG
          10      20      30      40      50      60

      70      80      90      100     110     120
m135.pep  FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g135      FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL
          70      80      90      100     110     120

      130     140     150     160     170     180
m135.pep  SVLLQRRAVPIINENDTVSVEELKIGDNDTLAQVAAMIQADLLVLLTDIDGLYTGPNPS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g135      SVLLQRRRAPIINENDTVSVEELKIGDNDTLAQVAAMIQADLLVLLTDIDGLYTGPNPS
          130     140     150     160     170     180

      190     200     210     220     230     240
m135.pep  NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g135      NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDS
          190     200     210     220     230     240

      250     260     270     280     290     300
m135.pep  LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRGSVYVDEGAEHALSEQGKSLLMSGI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g135      LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESGSVYVDESAEHALSEQGKACX
          250     260     270     280     290

      310     320     330     340     350     360

```

m135.pep AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFSGSAAEDLLKSRKAKGVFIHRDDWISITP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 521>:

```
a135.seq
1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTCGGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGCTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACA GGCGGTATGC TGAATAAAAT
651 CAAAGCGGCG ACGATTGCGA CCGAGTCCGG CGTACCGGTC TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTGCGGAAG CGGCAGATAA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCCGAAA GCAGGGGCGG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGAAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCTT TGGGCAAAGG GCGAGTCTTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATTGCGTA AGGCGAAAGG CGTGTTTCATC
1051 CATCGGACG ACTGGATTTC CATCACGCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTAG
```

This corresponds to the amino acid sequence <SEQ ID 522; ORF 135.a>:

```
a135.pep
1  MKYKRIVFKV GTSSITHSDG SLRSGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGPNPS NPDAVRLDKI EHNHEIIEIM
201 AGGSGSANGT GGMLTKIKAA TIATESGVPV YICSSLKPPA LAEADNQAD
251 GSFFVPRAKG LRTQKQLAF YSESRGGVYV DEGAEHALSE QKSLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAEDLL KLRKAKGVFI
351 HRDDWISITP EIRLLLTEF*
```

m135/a135 98.4% identity in 369 aa overlap

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLRSGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
a135	MKYKRIVFKVGTSSITHSDGSLRSGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
a135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNPS					
a135	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNPS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHNHEIIEMAGGSGSANGTGGMLTKIKAATIAESGVVPYICSSLKPPA					
a135	NPDAVRLDKIEHNHEIIEMAGGSGSANGTGGMLTKIKAATIAESGVVPYICSSLKPPA					
	190	200	210	220	230	240



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	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRGSVYVDEGAEHALSEQGKSLLMSGI					
a135	LAEAADNQADGSFFVPRAKGLRTQKQWLAFYSESRGGVYVDEGAEHALSEQGKSLLMSGI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m135.pep	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAAEDLLKSRKAGVFIHRDDWISITP					
a135	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAAEDLLKLRKAGVFIHRDDWISITP					
	310	320	330	340	350	360
	370					
m135.pep	EIRLLLTEFX					
a135	EIRLLLTEFX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 523>:

g136.seq

1	ATGGAAATCC	GGTTTCAGAC	AGCATTTT	CGTTTGTTTC	AGatgaAAAC
51	AAACGCTtca	aTTCTtaccg	caACACGCCT	TGTATTTCCT	GccgCTGCCG
101	CACGGACAGG	GATCGTTCCT	GCCGgtTTTT	TCCCCCTCCC	TGCGGACGGT
151	TTGCGGTTTG	TTGATGACCG	CCTGCCAGTA	GCGGTAGATG	Tctgccagcg
201	cgTAAGGCag	tTCGGAcgca	agttccgcca	gctcgccctc	ggTGAATTGC
251	AGgcgataa	cgccgtttTC	CTCTTCGTCg	taaagtccgc	ccactgccat
301	cacgGGGTAA	AACAGCTCTT	CAAACGCTTC	ATCATCGGCG	GCTTCAAACC
351	AATCGGTCGG	CACAATGTCC	AAACCGTAAA	GATAGGCGTT	GCACCAAGTG
401	TAAAAATCGC	TGCCGCCCTC	GCCGTCGTCG	TAGAGCCACA	AATCGGGCAG
451	CTTTTATCC	GACATCGCGG	CGGTTGTTC	CATCGCCATT	GCCAAAACCA
501	GCCGTTTCGAT	TTCGGAACGT	TCGGCGGCGG	TAAATGCGA	TTGTCGCCCC
551	AACACTTCGG	GCAGCCAGTC	GAGCGGTGCC	AATTTGTCCG	GCCCGCTCAA
601	CAGCGCCGTC	ATAAAACCTT	GAACCTCGTC	GCAACGCATC	GTGTTGCCTT
651	GTTCGCTTTT	GGCATCCAAT	AA		

This corresponds to the amino acid sequence <SEQ ID 524; ORF 136.ng>:

g136.pep

1	MEIRFQTAFL	RLVQMKTNAS	ILTATRLVFP	AAAARTGIVP	AGFFFPFPADG
51	LRFVDDRLPV	AVDVCQRVRQ	FGRKFRQLAF	GELQADNAVF	LFVVNAAHCH
101	HGVKQLFKRF	IIGGFKPIGR	HNVTQVKIGV	APSVKIAAAL	AVVVEPQIGQ
151	LFIRHRGGCF	HRHCQNPFD	FGTFGGGKLR	FVAQHFGQPV	ERCQFVRPAQ
201	QRRHKTLNLV	ATHRVALFAF	GIQ*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 525>:

m136.seq

1	ATGGAAACAA	ACGCTTCAAT	TCTTACCGCA	ACACGCCTTG	TATTTTCTGC
51	CGCTGCCGCA	CGGACAGGGA	TCGTTCCCTGC	CTGTTTTTTC	GCCTTCCTCG
101	CGGACGGTTT	GCGGTTTGTT	GATGACTGCC	TGCCAGTAGC	GGTAGATATC
151	CGCCAATGCA	TAAGGCAACT	CGGATTCCAG	TTCCGCCAGC	TCGCCTTCTG
201	TGAATTGCAG	ACGGATAGCG	CCGTTTTCTC	CTTCGTCGTA	AATACCGCCC
251	AATGCCATGA	TGGGATAAAA	CAACTCTTCA	AACGCTTCAT	CATCGACGGC
301	TTCAAACCAA	TCGGTCGGCA	CAATATCCAA	ACCGTAAAGA	TAAGCATTGC
351	ACCATGTGTA	AAAATCGCTG	CCGCCGTCTT	CGTTTTTCATA	CAGCCACAAA
401	TCGGGCAGTT	TTTTATCCGA	CATCGCGGCG	GTTGTTTCCA	TCGCCATTGC
451	CAAAACCAGC	CGTTCGATTT	CGGAACGTTC	GGCGGCGGTA	AATTGCGATT
501	CGTCGCCCAA	CACTTCGGGC	AGCCAGTCGA	GCGGTGTCAA	TTGTCCGGC
551	CCGCTCAACA	GCGCCGTCAT	AAAACCTTGA	ACCTCGTCGC	AACGCATCGT
601	GTTGCCCTTGT	TCGCTTTTGG	CATCCAACAA	TTCGCTCAAC	CGCCGTTTGG
651	ATGCTTCGGT	AAATTTTCGG	GAATCCATCA	TTTTCCTTTT	CAAATGGGTT
701	TTGCGCCCTA	TTATCGCCGC	AATGCCGTCT	GA	

This corresponds to the amino acid sequence <SEQ ID 526; ORF 136>:

m136.pep

```

1  METNASILTA TRLVFSAAAA RTGIVPACFF AFPADGLRFV DDCLPVAVDI
51  RQCIRQLGFQ FRQLAFCELQ TDSAVFLFVV NTAQCHDGIK QLFKRFIIDG
101 FKPIGRHNIQ TVKISIAPCV KIAAAVFVFI QPQIGQFFIR HRGGCFHRHC
151 QNQPFDFGTF GGGKLRFVAQ HFGQPVERCQ FVRPAQQRH KTLNLVATHR
201 VALFAFGIQQ FAQPPFGCFG KFSGIHHFPF QMGFAPYYRR NAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 136 shows 85.6% identity over a 209 aa overlap with a predicted ORF (ORF 136.ng) from *N. gonorrhoeae*:

m136/g136

	10	20	30	40
m136.pep	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPV			
g136	MEIRFQTAFLRLVQMKTNASILTATRLVFPAAAAARTGIVPAGFFFPADGLRFVDDRLPV			
	10	20	30	40
	50	60	70	80
m136.pep	AVDIRQCIRQLGFQFRQLAFCELQ TDSAVFLFVVNTAQCHDGIKQLFKRFIIDGFKPIGR			
g136	AVDVCQVRQFGRKFRQLAFGELQADNAVFLFVVNAAHCHHGKQLFKRFIIGGFKPIGR			
	70	80	90	100
	110	120	130	140
m136.pep	HNIQTVKISIAPCVKIAAAVFVFIQPQIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
g136	HNVQTVKIGVAPSVKIAAALAVVVEPQIGQLFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
	130	140	150	160
	170	180	190	200
m136.pep	FVAQHFGQPVERCQFVRPAQQRHKTNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIH			
g136	FVAQHFGQPVERCQFVRPAQQRHKTNLVATHRVALFAFGIQX			
	190	200	210	220
	230	240		
m136.pep	HFPFQMGFAPYYRRNAVX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 527>:

a136.seq

```

1  ATGGAACAA ACGCTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC
51  CGCTGCCGCA CGGACAGGGA TCGTTCCTGC CTGTTTTCCT GCCTTCCCTG
101 CGGACGGTTT GCGGCTTGTT GATGACCGCC TGCCAGTAGC GGTAGATATC
151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCCTTCTG
201 TGAATTGCAG ACGGATAGTG CCGTTGTCCT CTTGCTCGTA AATACCGCCC
251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC
301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTGC
351 ACCATGTGTA AAAATCGCTG CCGCCGTCTT CGTTTTCATA CAGCCACAAA
401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTCCTA TCGCCATTGC
451 CAAAACCAGC CGTTCGATT TCGGAACGTT GCGGCGGGA AATTGCGATT
501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTTGTCCGGC
551 CCGCTCAACA GCGCGTCAT AAAACCTTGA ACCTCGTCGC AACGCATCGT
601 GTTGCTTGT TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCCGTTTGG
651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTTCCTTTT CCAATGGGTT
701 TTGCGCCCTA TTATAGTGGA TTAAATTTAA ATCAGGACAA GGCGACGAAG
751 CCGCAGACAG TACAAATAGT ACGGCAAGGC GAGGCAACGC CGTACTGGTT
801 TAAATTTAAT CCACTATATC GCCGCAATGC CGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 528; ORF 136.a>:

a136.pep

```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRLV  DDRLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVVLFV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVFI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQQRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFPF  PMGFAPYYS  LNLNQDKATK
251 PQTQIVRQG  EATPYWFKFN  PLYRRNAV*

```

m136/a136 98.3% identity in 238 aa overlap

```

m136.pep      10      20      30      40      50      60
METNASILTATRLVFSAAAARTGIVPACFFAFPADGLRFVDDCLPVAVDIRQCIRQLGFQ
|||||
a136          10      20      30      40      50      60
METNASILTATRLVFSAAAARTGIVPACFFAFPADGLRLVDDRPLPVAVDIRQCIRQLGFQ

m136.pep      70      80      90      100     110     120
FRQLAFCELOTD SAVVLFVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV
|||||
a136          70      80      90      100     110     120
FRQLAFCELOTD SAVVLFVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV

m136.pep     130     140     150     160     170     180
KIAAAVFVFIQPIQIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ
|||||
a136         130     140     150     160     170     180
KIAAAVFVFIQPIQIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ

m136.pep     190     200     210     220     230     240
FVRPAQQRHKTNLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPFPMGFAPYYRR
|||||
a136         190     200     210     220     230     240
FVRPAQQRHKTNLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPFPMGFAPYYSG

m136.pep      NAVX
a136          LNLNQDKATKPQTQIVRQGEATPYWFKFNPLYRRNAVX
                250      260      270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 529>:

```

g137.seq
1  ATGATTATCC  ATCACcaatt  CGATCCCGTC  CTCATCAGTA  TCGGCCCGCT
51  TGCCGTCCGC  TGGTATGCCT  TAAGCTACAT  CCTCGGATTT  ATTCTTTTAA
101 CCTTTCTCGG  CAGAAGGCGC  ATCGCGCAAG  GCTTGTCGGT  TTTTACCAAA
151 GAATCGCTCG  ACGACTTCCT  GACATGGGGC  ATTTTGGGCG  TGATTTTGGG
201 CGGACGCTTG  GGCTATGTCC  TGTTTTACAA  ATTCTCCGAC  TACCTCGCCC
251 ATCCGCTTGA  TATTTTCAAG  GTATGGGAAG  GCGGAATGTC  GTTCCACGGC
301 GGCTTTTGGG  GTGTAGTTAT  TGCCATATGG  TTGTTTCAGCC  GCAAGCACGG
351 CATCGGCTTC  CTCAAAGTGA  TGGACACGGT  CGCGCCGCTC  GTTCCGCTGG
401 GTCTCGCTTC  GGGACGTATC  GGCAACTTTA  TCAACGGCGA  ACTTTGGGGA
451 CGCATTACCG  ACATTAACGC  ATTTTGGGCA  ATGGGCTTCC  CGCAAGCGCA
501 TTACGAAGAT  GCCGAAGCCG  CCGGCACAA  TCCGCTTTGG  GCAGAATGGC
551 TGCAACAATA  CGGTATGCTG  CCGCGTCATC  CCTCGCAGCT  TTATCAGTTT
601 GCCCTTGAAG  GCATCTGCCT  GTTCGCCGTC  GTTTGGCTGT  TTTCCAAAAA
651 ACCGCGCCCG  ACCGGGCAGA  CTGCGCGCT  TTTTCTCGGC  GGCTACGGCG
701 TGTTCGCTT  TATTGCCGAA  TTTGCGCGCC  AACCAGACGA  CTATCTCGGG
751 CTGCTGACCT  TGGGGCTGTC  GATGGGGCAA  TGGTTGAGCG  TCCCGATGAT
801 TGTTTTGGGT  ATCGTCGGCT  TTGTCCGGTT  CGGCATGAAA  AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 530; ORF 137.ng>:

g137.pep

```

1  MIIHHQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSY YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIW LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RITDINAFWA MGFPQAHYED AEAHAHNPLW AEWLQOYGML PRHPSQLYQF
201 ALEGICLFAV VWLFSKKPRP TGQTAALFLG GYGVRFRFAE FARQPDYDLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 531>:

```

m137.seq
1  ATGATTACCC ATCCCAATT CGATCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCCGC TGGTATGCCC TAAGCTACAT CCTCGGATTT ATTCTTTTAA
101 CCTTTCTCGG CAGAAGGCGC ATCGCGCAAG GCTTGTCCGT TTTTACCAAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGGG GTGTAGTTAT TGCCATACGG TTGTTCGGCC GCAAACACGG
351 CATCGGCTTC CTCAAAGTGA TGGATACGGT CGCACCGCTC GTTCCGCTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAT GCCGAAGCCG CCGCGCACAA TCCGCTTGGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTCAACGTC ATTTGGCTGT TCTCTAAAAA
651 ACAGCGGTCG ACCGGACAAG TCGCCTCGCT CTTCTCTGGC GGCTACGGCA
701 TATTCGCTT CATTGCCGAA TTCGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 532; ORF 137>:

```

m137.pep
1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSY YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIR LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RVTDINAFWA MGFPQARYED AEAHAHNPLW AEWLQOYGML PRHPSQLYQF
201 ALEGICLFTV IWLFSKKQRS TGQVASLFLG GYGIFRFAE FARQPDYDLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 137 shows 95.4% identity over a 283 aa overlap with a predicted ORF (ORF 137.ng) from *N. gonorrhoeae*:

```

m137/g137
      10      20      30      40      50      60
m137.pep  MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW
          |||||
g137      MIIHHQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW
          10      20      30      40      50      60

      70      80      90      100     110     120
m137.pep  ILGVILGGRLGYVLFYKFSYLAHPLDIFKVWEGGMSFHGGFLGVVIAIRLFGRKHGIGF
          |||||
g137      ILGVILGGRLGYVLFYKFSYLAHPLDIFKVWEGGMSFHGGFLGVVIAIWLFGRKHGIGF
          70      80      90      100     110     120

      130     140     150     160     170     180
m137.pep  LKLMDTVAPLVPLGLASGRIGNFINDELWGRVTDINAFWAMGFPQARYEDAEAAHNPLW
          |||||
g137      LKLMDTVAPLVPLGLASGRIGNFINDELWGRITDINAFWAMGFPQAHYEDAEAAHNPLW
          130     140     150     160     170     180

      190     200     210     220     230     240
m137.pep  AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGIFRFAE

```

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```

|||||
g137  AEWLQQYGMLPRHPSQLYQFALEGICLFAVVWLFSSKKPRPTGQTAALFLGGYGVFRFIAE
      190      200      210      220      230      240

      250      260      270      280
m137.ppep FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX
|||||
g137  FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX
      250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 533>:

```

a137.seq
1  ATGATTACCC ATCCCCAATT CGACCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCCGC TGGTATGCCC TAAGCTACAT CCTCGGATTT ATTCTTTTAA
101 CCTTTCTCGG CAGAAGGCGC ATCGCGCAAG GCTTGTCGGT TTTTACCAAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTACGTCCT TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGGG GTGTAGTTAT TGCCATATGG TTGTTCCGGT GCAAACACGG
351 CATCGGCTTC CTCAACTGA TGGACACGGT CGCACCGCTC GTTCCACTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAC CTCGAAGCCG CCGCGCACAA TCCGCTTGGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTGAAG GCATCTGCCT GTTCGCGCTC GTTTGGCTGT TCTCTAAAAA
651 ACAGCGGCCG ACCGGACAAG TCGCCTCACT CTTCTCGGC GGCTACGGCA
701 TATTCCGCTT CATTGCCGAA TTGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCAGATGAT
801 TGTTTGGGT ATCGTCGGCT TTGTCGGGT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 534; ORF 137.a>:

```

a137.ppep
1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGR L GYVLFYKFS YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIW LFGRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RVTDINAFWA MGFPOARYED LEAAAHNPLW AEWLQQYGML PRHPSQLYQF
201 ALEGICLFAV VWLFSSKQRP TGQVASLFLG GYGIFRFIAE FARQPDDYL
251 LTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

m137/a137 98.2% identity in 283 aa overlap

```

      10      20      30      40      50      60
m137.ppep MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW
|||||
a137  MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW
      10      20      30      40      50      60

      70      80      90     100     110     120
m137.ppep ILGVILGGR LGYVLFYKFS DYLAHPLDIFK VWEGGMSFHG GFLGVVIAIR LFGRKHGIGF
|||||
a137  ILGVILGGR LGYVLFYKFS DYLAHPLDIFK VWEGGMSFHG GFLGVVIAIR LFGRKHGIGF
      70      80      90     100     110     120

      130     140     150     160     170     180
m137.ppep LKLMDTVAPLVPLGLASGRIGNFINDELWGRVTDINAFWAMGFPOARYEDAEAAAHNPLW
|||||
a137  LKLMDTVAPLVPLGLASGRIGNFINDELWGRVTDINAFWAMGFPOARYEDLEAAAHNPLW
      130     140     150     160     170     180

      190     200     210     220     230     240
m137.ppep AEWLQQYGMLPRHPSQLYQFALEGICLFTVIWLFSSKKQRPSTGQVASLFLGGYGIFRFIAE
|||||
a137  AEWLQQYGMLPRHPSQLYQFALEGICLFAVVWLFSSKKQRPSTGQVASLFLGGYGIFRFIAE

```

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	190	200	210	220	230	240
	250	260	270	280		
m137.pep	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFMGKKQHX					
a137	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFMGKKQHX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 535>:

```

g138.seq
1  ATGGAGTTTG AAAACATTAT TTCCGCCGCC gaCAAGGCGC GTATCCTTGC
51  CGAAGCACTG CCTTACatcc gccgGTTTTT CCGTTCCGGT GCCGTCATCA
101 AGTATGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GCGAATTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGAC GATGGATATT
301 GTCGAAATGG TATTGGGCGG GCACGTCAAC AAGGAAATCG TGTCGATGAT
351 TAACACATAT GGAGGGCACG CGGTCGGCGT GAGCGGGCGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGGTCGATA CGCCCGAACA GAATAGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGCGGCT GCATCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT GGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAAtatcgc
651 cgGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACTC acgCCGAAAC
701 GGATTGATGG GCTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCcgccgtc aACGGTGTGA AAGCCACGCA
801 CATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTCGATG ATTTTAGGCA GAGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 536; ORF 138.ng>:

```

g138.pep
1  MEFENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKETMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LVDTPEQNSV
151 DIGQVGTVES IDTGLVKGLI ERGCIPVVP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMTNIAAGVM DKTGNLLTKL TPKRIDGLIA DGTLYGMLP
251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGRGEDA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 537>:

```

m138.seq
1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGTTTTTC CCGTTCCGGT GCCGTCATCA
101 AATACGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGGC GATGGATATT
301 GTCGAAATGG TGTTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACTC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCCGTC AACGGTGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTCGATG ATTTTGGGCG GTGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 538; ORF 138>:

```

m138.pep
1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA

```

51 RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAMDI  
 101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV  
 151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK  
 201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP  
 251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGGGEDA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 138 shows 98.0% identity over a 298 aa overlap with a predicted ORF (ORF 138.ng)  
 from *N. gonorrhoeae*:

m138/g138

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
g138	MEFENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKAMDIVEMVLGGHVNKEIVSMINTY					
g138	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKETMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
g138	GGHAVGVSGRDDHFIKAKKLLVDTPEQNSVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
g138	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDGLIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
g138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGRGEDAX					
	250	260	270	280	290	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 539>:

a138.seq

```

1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51 CGAAGCGCTG CCTTACATCC GCCGTTTTC CGGTTCCGTC GCCGTCATCA
101 AATACGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAGAGAGC GATGGATATT
301 GTCGAAATGG TGTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAAGC ATCGATACCG GTTTGGTTAA
501 AGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACTC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCCGTC AACGCGGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGGTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGTAT CGGTTGCATG ATTTTGGGCG GTGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 540; ORF 138.a>:

```
a138.pep
  1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
 51  RDVVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAEMDI
101  VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151  DIGQVGTVES IDTGLVKGLI ERGCIPVVAP VGVGEKGEAF NINADLVAGK
201  LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251  KIASAVEAAV NGVKATHIID GRVPNALLLE IFTDAGIGSM ILGGGEDA*
```

m138/a138 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
a138	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKAEMDIVEMVLGGHVNKEIVSMINTY					
a138	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKAEMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
a138	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
a138	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
a138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRVPNALLLEIFTDAGIGSMILGGGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 541>:

```
g139.seq
  1  ATGCGAACCA CCTCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
 51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGgc ggcggcggag
101  gcGGCACTTC TGCTCCCGAC TTTAATGCAG GCGGCACCGG TATCGGCAGC
151  AACAGCAGGG CAACGATAGC GGAATCAGCA GCAGTATCTT ACGCCGGTAT
201  AAAAAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCCGGATG
251  ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAAAGCCCC CCGAATCTGC
301  ATACCGGAGA CTTTTCAAAC CCAAATGACC AATATTAAGA ATATGATCAA
351  CCTCAAACCT GCAATTGAAG CAGGCTATAC AGGACGCGGG GTAGAGGTAG
401  GTATCGTCGA TACAGGCGAA TCCGTCGGCA GCATATCCTT TCCCGAAGTG
451  TATGGCAGAA AAGAACACGG CTATAACGAA AATTACAAAA ACAAATTACA
501  AAAACTATAC GGCGTATATG CGGAAGGAAG CGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 542; ORF 138.ng>:

```
g139.pep
  1  MRTTSTFPTK TFKPAAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
 51  NSRATIAESA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKIKAPRIC
101  IPETFQTQMT NIKNMINLKP AIEAGYTGRG VEVGIVDTGE SVGSISFPPEL
151  YGRKEHGYNE NYKNKLQKLY GVYAEGSA*
```



The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 543>:

```
m139.seq
1  ATGCGAACGA  CCCCAACCTT  CCCTACAAAA  ACTTTCAAAC  CGACTGCCAT
51  GCGGTTAGCT  GTTGCAACAA  CACTTTCTGC  CTGCTTAGGC  GCGGCGCGAG
101 GCGGCACTTC  TGCGCCCGAG  TTCAATGCAG  GCGGTACCGG  TATCGGCAGC
151 AACAGCAGAG  CAACAACAGC  GAAATCAGCA  GCAGTATCTT  ACGCCGGTAT
201 CAAGAACGAA  ATGTGCAAAG  AGAAGACGAT  CAGTCTGTGC  GGTGCGGATG
251 ACGTTGCGGT  TACAGACAGG  GATGCCAAAA  TCAATGCCCC  CCCCCGAATC
301 TGCATACCGG  AGACTTTCCA  AATCCAAATG  ACGCATtACA  AGAATTTGAT
351 CAACCTCAAA  CCTGCAATTG  AAGCAGGCTA  TACAGGACGC  GGGGTAGAGG
401 TAGGTATCGT  GCAGCAGGC  GAATCCGTGC  GCAGCATATC  CTTTCCCGAA
451 CTGTATGGCA  GAAAAGAA  CAGCTATAAC  GAAAATTACG  AAAAATATA
501 CGCGGTATAT  GCGGAAGGAA  GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 544; ORF 138>:

```
m139.pep
  1  MRTTPTFPTK  TFKPTAMALA  VATTLSACLG  GGGGGSAPD  FNAGGTGIGS
51  NSRATTAKSA  AVSYAGIKNE  MCKDRSMLCA  GRDDVAVTDR  DAKINAPPRI
101 CIPETFQTQM  THYKNLNLK  PAIEAGYTG R  GVEVGIVDTG  ESVGSI SFP E
151 LYGRKEHGYN  ENYEKLYGVY  AEGSA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 138 shows 92.2% identity over a 179 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

```

m139/g139

                10         20         30         40         50         60
m139.pep  MRTTPTFPKTFKPTAMALAVATTLSACLGGGGGGSAPDFNAGGTGIGNSRATTAKSA
           ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
g139      MRTTSTFPKTFKPAAMALAVATTLSACLGGGGGGSAPDFNAGGTGIGNSRATTIAESA
           10         20         30         40         50         60

                70         80         90        100        110        120
m139.pep  AVSYAGIKNEMCKDRSMLCAGRDDVAVTTDRDAKINAPPRICIPETFQTMTHYKNLINLK
           ||||| ||||| ||||| ||||| ||||| ||||| : ||||| ||||| : |||||
g139      AVSYAGIKNEMCKDRSMLCAGRDDVAVTTDRDAKIKAP-RICIPETFQTMNIKNMINLK
           70         80         90        100        110

                130        140        150        160        170
m139.pep  PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENY----EKLYGVYAEGSAX
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| |||||
g139      PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENYKNKLQKLYGVYAEGSAX
           120        130        140        150        160        170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 545>:

al39.seq

```
1 ATGCGAACGA CCCCACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
51 GGCCTTAGCT GTTGCAACAA CACTTCTGCT CTGCTTAGGC GCGGCGGAG
101 GCGGCACTTC TGCGCCCGAC TTCAATGCAG GCGGCACCGG TATCGGCAGC
151 AACACGACGG CAACAACAGC GAAATCAGCA GCAATATCTT ACGCGGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCAGATC
301 TGCATACCGG AGACTTTACA AACCCTAATG ACGCAT.ACA AGAATTTGAT
351 CAACCTCAAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT GCACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTAC. AAAAATATA
501 CGGCGTATAT GCGGAAGGAA CGGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 546; ORF 139.a>:

1 MRTTPTEPTK TEKPAAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS

394

51 NSRATTAKSA AISYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI  
 101 CIPETLQTQM THXKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSISFPE  
 151 LYGRKEHGYN ENYXKLYGVY AEGSA\*

m139/a139 97.1% identity in 175 aa overlap

	10	20	30	40	50	60
m139.pep	MRTTPTFP	TKFTKPTAMALAVAT	TL	SACLG	GGGGG	TSAPDFNAGGTGIGSNSRATTAKSA
a139	MRTTPTFP	TKFTKPAAMALAVAT	TL	SACLG	GGGGG	TSAPDFNAGGTGIGSNSRATTAKSA
	10	20	30	40	50	60
	70	80	90	100	110	120
m139.pep	AVSYAGIKNEMCKDRSMLCAGR	DDVAVTDRDAKINAPPRI	CIPET	FQTQMTHYKNLINLK		
a139	AISYAGIKNEMCKDRSMLCAGR	DDVAVTDRDAKINAPPRI	CIPET	LQTQMTHXKNLINLK		
	70	80	90	100	110	120
	130	140	150	160	170	
m139.pep	PAIEAGYTGRGVEVGIVDTGESVGSISFPE	LYGRKEHGYNENYKLYGVYAEGSAX				
a139	PAIEAGYTGRGVEVGIVDTGESVGSISFPE	LYGRKEHGYNENYXKLYGVYAEGSAX				
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 547>:

g140.seq

1	Atgtcggcac	gCGCAAGGG	GGCAGgctat	ctcAACAGTA	CCGGACGACa
51	TGTTCCCTTC	CTGAGTGCCG	CCAAAATCGG	GCAGGATTAT	TCTTTCTTCA
101	AAAATATCAA	AACCGACGGC	GGTCTGCTGG	CTTCCCTCGA	CAGCGTCGAA
151	AAAACAGCGG	GCAGTGAAGG	CGACACGCCG	TCCTATTATG	TCCGTCGCGG
201	CAATGCGGCA	CGGACTGCTT	CGGCAGCGGC	ACAATTCGCG	CCCGCCGGTC
251	TGAAACACGC	CGTAGAACAG	GGCGGCAGCA	ATCTGGAATA	CCTGATGGTC
301	GAGCTGGATG	CCTCCGAATC	ATCCGCAACA	CCCAGACGCG	TTGAAACTGC
351	GGTCGCCGAC	CGCACAGATA	TGCCGGGCAT	CCGCCTACGG	CGCACAACTT
401	TCCGCACAGC	GGCAGCCGTA	CAGCATGCGA	ATACCGCCGA	CGGCGTACGc
451	aTCTTcaaCA	GTCTCGCCGC	TAccgTCTAt	GccgACAGTG	CCGCGCCCA
501	TGccgATATG	CAGGGACGCC	GCCTGAAAGC	CGTATCGGAC	GGGTTGGACC
551	ACAACGGTAC	GGGTCTGCGC	GTCATCGCGC	AAACCCAACA	GGACGGTGGA
601	ACGTGGGAAC	AGGGCGGTGT	CGAAGGCAAA	ATGCGCGGCA	GTACCCAAAC
651	TATCGGCATT	GCCGCGAAAA	CCGGCGAAAA	TACGACAGCA	GCCGCCACAC
701	TGGGCATAGG	ACGAGCACA	TGGAGCGAAA	ACAGTGCAAA	TGCAAAAACC
751	GACAGCATTa	GTCTGTTTGC	AGGCATACGG	CACGATGTGG	GCGATATCGG
801	CTATCTCAAA	GGCCTGTTCT	CctaCGGACG	CTACAAAAAC	AGCATCAGCC
851	GCAGCACCGG	TGCGGATGAA	TATGCGGAAG	GCAGCGTCAA	CGGCACGCTG
901	ATGCAGCTGG	GCGCACTGGG	TGGTGTCAAC	GTTCCGTTTG	CCGCAACGGG
951	AGATTTGACG	GTTGAAGGCG	GTCTGCGCCA	CGACCTGCTC	AAACAGGATG
1001	CATTCGCCGA	AAAAGGCagt	GCTTTGGGCT	GGAGCGGCAA	CAGCCTCACT
1051	GAAGGCACAC	TGGTCGGACT	CGCGGGTCTG	AAACTGTCTG	AACCTTTGAG
1101	CGATAAAGCC	GTCTGTCTTG	CGACGGCGGG	CGTGGAACGC	GACCTGAACG
1151	GACGCGACTA	CGCGGTAACG	GGCGGCTTTA	CCGGCGCGGC	TGCAGCAACC
1201	GGCAAGACGG	GTGCACGCAA	TATGCCGCAC	ACCCGCCGGG	TTGCCGGTCT
1251	GGGGGTGGAT	GTGGAATTCT	GCAACGGCTG	GAACGGCTTG	GCACGTTACA
1301	GCTACACCGG	TTCCAAACAG	TACGGCAACC	ACAGCGGACA	AATCGGCGTA
1351	GGCTACCGGT	TCTGA			

This corresponds to the amino acid sequence <SEQ ID 548; ORF 140.ng>:

g140.pep

1	MSARGKGAGY	LNSTGRHVPF	LSAAKIGQDY	SFFKNIKTDG	GLLASLDSVE
51	KTAGSEGDTP	SYVVRGNAA	RTASAAHSA	PAGLKHAVEQ	GGSNLENLMV
101	ELDASESAT	PETVETAVAD	RTDMPGIRLR	RTTFRTAAY	QHANTADGVR
151	IFNSLAATVY	ADSAAAHADM	QGRRLKAVSD	GLDHNGTGLR	VIAQTQQDGG
201	TWEQGGVEGK	MRGSTQTIGI	AAKTGENTTA	AATLGIGRST	WSENSANAKT

251 DSISLFAGIR HDVGDIGYLYK GLFSYGRYKN SISRSTGADE YAEGSVNGTL  
 301 MQLGALGGVN VPFAATGDLT VEGGLRHDLK QDAFAEKGS ALGWSGNSLT  
 351 EGTLVGLAGL KLSQPLSDKA VLSATAGVER DLNGRDYAVT GGFTGAAAAT  
 401 GKTGARNMPH TRRVAGLGVD VEFNGWNGL ARYSYTGSKQ YGNHSGQIGV  
 451 GYRF\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 549>:

m140.seq

1 ATGTCGGCAC GCGGCAAGGG GGCAGGCTAT CTCAACAGTA CCGGACGACG  
 51 TGTTCCTTC CTGAGTGCCG CAAAATCGG GCAGGATTAT TCTTTCTTCA  
 101 CAAACATCGA AACCGACGGC GGCCTGCTGG CTTCCCTCGA CAGCGTGGAA  
 151 AAAACAGCGG GCACTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG  
 201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCGGTC  
 251 TGAAACACGC CGTAGAACAG GGCAGCAGCA ATCTGGAAAA CCTGATGGTC  
 301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC  
 351 GGCAGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCCTAC GGCAGCAACTT  
 401 TCCGCGCAGC GGCAGCCGTA CAGCATGCCA ATGCCGCCGA CGGTGTACGC  
 451 ATCTTCAACA GTCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCGCCCA  
 501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC  
 551 ACAACGGCAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGGA  
 601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC  
 651 CGTCGGCATT GCCGCGAAAA CCGCGAAAA TACGACAGCA GCCGCCACAC  
 701 TGGGCATGGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC  
 751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG  
 801 CTATCTCAA GGCCTGTTCT CCTACGGACG CTACAAAAAC AGCATCAGCC  
 851 GCAGCACCGG TCGGACGAA CATGCGGAAG GCAGCGTCAA CCGCACGCTG  
 901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTTCCGTTTG CCGCAACGGG  
 951 AGATTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG  
 1001 CATTCGCCGA AAAAGGCAGT GCTTGGGCT GGAGCGGCAA CAGCCTCACT  
 1051 GAAGGCACGC TGGTCGGACT CGCGGTCTG AAGCTGTGCG AACCTTGAG  
 1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGGAAACG GACCTGAACG  
 1151 GACGCGACTA CACGGTAACG GCGCGCTTTA CCGGCGCGAC TGCAGCAACC  
 1201 GGCAAGACGG GGCACGCAA TATGCCGCAC ACCCGTCTGG TTGCCGGCCT  
 1251 GGCAGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA  
 1301 GCTACGCCGG TTCCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA  
 1351 GGCTACCGGT TCTGA

This corresponds to the amino acid sequence <SEQ ID 550; ORF 140>:

m140.pep

1 MSARGKGAGY LNSTGRRVPF LSAKIGQDY SFFTNIETDG GLLASLDSVE  
 51 KTAGSEGDITL SYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV  
 101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR  
 151 IFNSLAATVY ADSTAAHADM QGRRLKAVSD GLDHNGTGLR VIAQTQDGG  
 201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGRST WSENSANAKT  
 251 DSISLFAGIR HDAGDIGYLYK GLFSYGRYKN SISRSTGADE HAEGSVNGTL  
 301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL QDAFAEKGS ALGWSGNSLT  
 351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT  
 401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV  
 451 GYRF\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 140 shows 94.5% identity over a 454 aa overlap with a predicted ORF (ORF 140.ng) from *N. gonorrhoeae*:

m140/g140

	10	20	30	40	50	60
m140.pep	MSARGKGAGYLNSTGRRVPFLSAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL					
g140	MSARGKGAGYLNSTGRRHVPFLSAKIGQDYSFFKNIKTDGGLLASLDSVEKTAGSEGDTF					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m140.pep  SYYVRRGNAARTASAAHSAPAGLKHAVEQGGSNLENLMVELDASESSATPETVETAAAD
          |||||||
g140      SYYVRRGNAARTASAAHSAPAGLKHAVEQGGSNLENLMVELDASESSATPETVETAVAD
          |||||||
          70      80      90      100     110     120

          130     140     150     160     170     180
m140.pep  RTDMPGIRPYGATFRAAAVQHANAADGVRIFNSLAATVYADSTAAHADMQGRRLLKAVSD
          |||||||
g140      RTDMPGIRLRRTTFRATAAVQHANTADGVRIFNSLAATVYADSAAAHADMQGRRLLKAVSD
          |||||||
          130     140     150     160     170     180

          190     200     210     220     230     240
m140.pep  GLDHNGTGLRVIAQTQDDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST
          |||||||
g140      GLDHNGTGLRVIAQTQDDGGTWEQGGVEGKMRGSTQTIGIAAKTGENTTAAATLGI GRST
          |||||||
          190     200     210     220     230     240

          250     260     270     280     290     300
m140.pep  WSENSANAKTDSISL FAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL
          |||||||
g140      WSENSANAKTDSISL FAGIRHDVGDIGYLKGLFSYGRYKNSISRSTGADEYAEGSVNGTL
          |||||||
          250     260     270     280     290     300

          310     320     330     340     350     360
m140.pep  MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
          |||||||
g140      MQLGALGGVNVFPAATGDLTVEGGLRHDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
          |||||||
          310     320     330     340     350     360

          370     380     390     400     410     420
m140.pep  KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD
          |||||||
g140      KLSQPLSDKAVLSATAGVERDLNGRDYAVTGGFTGAAAATGKTGARNMPHTRRVAGLGVD
          |||||||
          370     380     390     400     410     420

          430     440     450
m140.pep  VEFNGWNGLARYSYAGSKQYGNHSGRVGVGYRFX
          |||||||
g140      VEFNGWNGLARYSYTGSKQYGNHSGQIGVGYRFX
          |||||||
          430     440     450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 551>:

```

a140.seq
1  ATGTCGGCAG GCGGTAAGGG GGCAGGCTAT CTCAACCGTA CCGGACAACG
51  TGTTCCCTTC CTGAGTGCCG CCAAAATCGG GCGGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGTCTGCTGG CTCCCTCGA CAGCGTCGAA
151 AAAACAGCGG GTAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAAACACGC CGTAGAACAG GCGGCAGCA ATCTGGAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTTAC GGCGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CCGGTGTACG
451 ATCTTCAACA ATCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGCTAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAC
651 CGTCGGCATT GCCGCGAAAA CCGCGAAAA TACGACAGCA CGCGCCACAC
701 TGGGCATGGG ACACAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTA GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CCGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CCGTGTCAAC GTTCCGTTTG CCGCAACGGG

```

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951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTCGCCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCATCACT
1051 GAAGGCACAC TGGTCGGACT CGCGGGTCTG AAGCTGTCGC AACCTTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGCTTTA CCGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGCCTGG TTGCGGGTCT
1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACGCCGG TTCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 552; ORF 140.a>:

```

a140.pep
  1 MSAGGKGAGY LNRTGQRVFP LSAAKIGRDY SFFTNIETDG GLLASLDSVE
 51 KTAGSEGDTL SYYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNNLAATVY ADSTAAHADM QGRRKAVSD GLDHNATGLR VIAQTQODGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGHST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLG GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSIT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

m140/a140 98.2% identity in 454 aa overlap

	10	20	30	40	50	60
m140.pep	MSARGKGAGYLNSTGRRVPFLSAAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDTL					
a140	MSAGGKGAGYLNRTGQRVFPFLSAAKIGRDYSFFTNIETDGGLLASLDSVEKTAGSEGDTL					
	10	20	30	40	50	60
m140.pep	70	80	90	100	110	120
	SYYVRRGNAAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
a140	SYYVRRGNAAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
	70	80	90	100	110	120
m140.pep	130	140	150	160	170	180
	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLSLAATVYADSTAAHADMQGRRKAVSD					
a140	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLSLAATVYADSTAAHADMQGRRKAVSD					
	130	140	150	160	170	180
m140.pep	190	200	210	220	230	240
	GLDHNATGLRVIAQTQODGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST					
a140	GLDHNATGLRVIAQTQODGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGHST					
	190	200	210	220	230	240
m140.pep	250	260	270	280	290	300
	WSENSANAKTDSISLFAGIRHDAGDIGYLGKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
a140	WSENSANAKTDSISLFAGIRHDAGDIGYLGKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
	250	260	270	280	290	300
m140.pep	310	320	330	340	350	360
	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVGLAGL					
a140	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVGLAGL					
	310	320	330	340	350	360
m140.pep	370	380	390	400	410	420
	KLSQPLSDKAVLFLATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					
a140	KLSQPLSDKAVLFLATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					

398

	370	380	390	400	410	420
	430	440	450			
m140.pép	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYREFX					
a140	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYREFX					
	430	440	450			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 553>:

g141.seq

```

1  atgagcttca aAAccgATGC CGAAACCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAGCTG
151 CCGCAAAAAC AAGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GGC GGCGCAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTTCG GCGTGAAAGG CGGCGCGGCA GCGGCGGGCT ACGCGCAAGT
351 TCCGAAGTGA GAAGACATCA ACCTGCACTT CACCGCGGAC TTCCACGCCA
401 TCGGTGCGGC GAATAACCTC CTCGCCGCCA TGCTCGACAA CCATATCTAC
451 CAAGGTAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GGCGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGTATGGGCA
551 AGCCTGTtga cggCGTGATG CGtcccGACG GCTTCGACAT CACCGTCGCC
601 TCCGAAGTga tggcgGTATT CTGCCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTtt gGCAATATTC TCGTCGCCTA CGCCAAAGAC GGCAGCCCGC
701 TTTACGCCAA AGATTGAAG GCACACGGCG CGATGGCGGC ATTGCTAAAA
751 GATGCGATTA AGCCCAATTT GGTGCAAACC ATCGAAGGCA CTCCGGCCTT
801 TGTACACGGC GGCCCCTTCG CCAACATCGC CCACGGCTGC AACTCCGTTA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG TGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCAGT CGTCGTGGCG ACTGTCCGCG
1001 CCCTGAAATA CAACGGCGGC GTGGAACGCG CCAACCTTGG TGAAGAAAC
1051 CTCGAAGCCT TGGCAAAGG TTTGCCAAC CTGTTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCGGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GCGGCGGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA TGCCATCGAC AACCAACCTA
1301 ATAACCTCGG TTTCGCCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCAAAAAGT GTACGGCGCG GAAGATGTCG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CCTCGCTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATATT CATTGAGCGA CAACGCCAAA
1501 CTCTTGGGCT GCGCGAAGG CTTCCGCATC GCCGTACGCG GTATCACTGT
1551 TTCCGCCGGC GCGGGCTTCA TCGTTGCGTT GTGCGGCAAT ATGATGAAAA
1601 TGCCGGGCCT GCCGAAAGT CCGGCTGCCG AGAAAAATCGA TGTGGACGAA
1651 CACGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 554; ORF 141.ng>:

g141.pép

```

1  MSFKTDAETA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFVGKGGAA GGGYAQVLPD EDINLHFTGD PHAIGAANL LAAMLNHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNID GMGKPDVDM RPDGFDITVA
201 SEVMVAFCLA KDISDLKERF GNILVAYAKD GSPVYAKDLK AHGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 DFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKNGG VERANLGEEN
351 LEALAKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WGKGGAGGAD LARKVVNAID NQPNNFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPGPFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDE
551 HGVHGLF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 555>:

m141.seq

```

1  ATGAGCTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTTGGTCT GAATGCCGAC AACATTGAGC
101 CTTACGGTCA TTACAAGGCG AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GCGGGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCGTTGC
251 GCCACATCGG CAAAGATGCC GTGATTGCCG TGCGCGAACC TTCTCTGGGG
301 CCGGTGTTCC GCGTGAAAGG CGGCGCGGCA GCGGCGGGCT ATGCCCAAGT
351 AGAGCGTTTG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTGCGCGCA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GCGGCGCGCT
501 GGTTCGATAT AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGTA
551 AACCCGTTGA CCGCGTGATG CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCGG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCGCGCTT
801 CGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGTGCG AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CTTTCCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGCGCGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACGC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTCCCTT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CCGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACCTCGG TTTGCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCCTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCGCGATC GCGGTGCGCG GCATCACCGT
1551 TTCCGAGGCG GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCTT GCCCAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 556; ORF 141>:

m141.pep

```

1  MSFKTDAEIA QSSTMRPIGE IAAKLGLNAD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDA VIALREPSLG
101 PVFVGKGGAA GGGYAQVLPD EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNID GMGKPDVDM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDADAE LAMIEKACAE
401 HGVEVSLTEV WGKGGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVIHGLF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 141 shows 97.5% identity over a 558 aa overlap with a predicted ORF (ORF 141.ng) from *N. gonorrhoeae*:

m141/g141

```

m141.pep      10      20      30      40      50      60
               MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKL
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g141          10      20      30      40      50      60
               MSFKTDAETAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKL

```

400

m141.pep	70	80	90	100	110	120
	TAINPTPAGEGKTTVTITGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYAQVLP					
g141	TAINPTPAGEGKTTVTITGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYAQVLP					
	70	80	90	100	110	120
m141.pep	130	140	150	160	170	180
	EDINLHFTGDFHAIGAANNLLAAMLNDNHIYQGNELNIDPKRVLWRRVVDMMNDRQLRNIID					
g141	EDINLHFTGDFHAIGAANNLLAAMLNDNHIYQGNELNIDPKRVLWRRVVDMMNDRQLRNIID					
	130	140	150	160	170	180
m141.pep	190	200	210	220	230	240
	GMGKPVDPGMRPDGFDITVASEVMAVFLAKDISDLKERLGNILVAYAKDGSVPYAKDLK					
g141	GMGKPVDPGMRPDGFDITVASEVMAVFLAKDISDLKERFGNILVAYAKDGSVPYAKDLK					
	190	200	210	220	230	240
m141.pep	250	260	270	280	290	300
	ANGAMAALLKDAIKPNLVQTIETGPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
g141	AHGAMAALLKDAIKPNLVQTIETGPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
m141.pep	310	320	330	340	350	360
	GFGADLGAEKFCDIKRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
g141	GFGADLGAEKFCDIKRLAGLKPDAVVVATVRALKYNGGVERANLGEENLEALAKGLPN					
	310	320	330	340	350	360
m141.pep	370	380	390	400	410	420
	LLKHISNLKNVFGLPVVVALNRFVSDADAEIAMI EKACAEHGVESL TEVWGKGGAGGAD					
g141	LLKHISNLKNVFGLPVVVALNRFVSDSDAEIAMI EKACAEHGVESL TEVWGKGGAGGAD					
	370	380	390	400	410	420
m141.pep	430	440	450	460	470	480
	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
g141	LARKVVNAIDNQPNFGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
m141.pep	490	500	510	520	530	540
	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
g141	LDKMPICMAKTQYSLSDNAKLLGCPGEGFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
m141.pep	550	559				
	PAAEKIDVDAEGVIHGLFX					
g141	PAAEKIDVDEHGVHGLFX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 557>:

a141.seq

1	ATGAGTTTCA	AAACCGATGC	CGAAATCGCC	CAATCCTCCA	CCATGCGCCC
51	GATTGGCGAA	ATTGCCGCCA	AGCTGGGTTT	GAACGTTGAC	AACATTGAGC
101	CTTACGGTCA	TTACAAAGCC	AAAATCAATC	CTGCCGAAGC	GTTCAAAC TG
151	CCGCAAAAAC	AGGGCAGGCT	GATTTTGGTT	ACCGCCATCA	ACCCGACTCC



```

201 GGC GGCGCGAA GGTAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTTC GCGTGAAAGG CGGCGCGGCA GCGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GCGGCGCGCT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGCA
551 AGCCTGTTGA CGGCGTGATG CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCTCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCCGCTT
801 CGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAA
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCGTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGCGGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAATTTCGG TTTCGCTTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCAAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCGT
1551 TTCCGAGGCG GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCGT GCCCAAAGTT CCGGCTGCCG AGAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 558; ORF 141.a>:

```

a141.pep
1 MSFKTDAEIA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51 PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFGVKGGA GGGYAQVLPM EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVD MNDRLRNII GMGKPDGVM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNNG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRVFVSDSAE LAMIEKACAE
401 HGVEVSLTEV WGKGAGGAD LARKVNAIE SQTNNGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TOYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVHGLF*

```

m141/a141 99.5% identity in 558 aa overlap

```

          10      20      30      40      50      60
m141.pep MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKL PQKQGRILIV
|||||
a141      MSFKTDAEIAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKL PQKQGRILIV
          10      20      30      40      50      60

          70      80      90     100     110     120
m141.pep TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGGAAGGGYAQVLPM
|||||
a141      TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGGAAGGGYAQVLPM
          70      80      90     100     110     120

          130     140     150     160     170     180
m141.pep EDINLHFTGDFHAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVVD MNDRLRNII
|||||
a141      EDINLHFTGDFHAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVVD MNDRLRNII
          130     140     150     160     170     180

```

m141.pep	190	200	210	220	230	240
	GMGKPV DGVMR PDGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
a141	GMGKPV DGVMR PDGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
	190	200	210	220	230	240
m141.pep	250	260	270	280	290	300
	ANGAMAALLKDAIKPNLVQTIIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
a141	ANGAMAALLKDAIKPNLVQTIIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
m141.pep	310	320	330	340	350	360
	GFGADLGA EKFC DIKCR LAGLKPDA AVV VATVRALKYNGGVERANLGEENLDALEKGLPN					
a141	GFGADLGA EKFC DIKCR LAGLKPDA AVV VATVRALKYNGGVERANLGEENLDALEKGLPN					
	310	320	330	340	350	360
m141.pep	370	380	390	400	410	420
	LLKHISNLKNV FGLPVVVALNR FVSDADAELAMIEKACAEHGVEVSLTEVWGKGAGGAD					
a141	LLKHISNLKNV FGLPVVVALNR FVSDADAELAMIEKACAEHGVEVSLTEVWGKGAGGAD					
	370	380	390	400	410	420
m141.pep	430	440	450	460	470	480
	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
a141	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
m141.pep	490	500	510	520	530	540
	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
a141	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
m141.pep	550	559				
	PAAEKIDVDAEGVIHGLFX					
a141	PAAEKIDVDAEGVIHGLFX					
	550					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 559>:

```

g142.seq
1  ATGCGTGCCG  ATTCATGTT  TGCCGACAAT  ATGCCCCTGC  AGGTGCGCCA
51  ACGCGCCTTC  TATTTCAAGT  TGTCCCCTTT  TGCCGCGATG  CCAAATATGG
101 TAGGCAAAACC  GCTCTTCGGG  CGACAGGCCG  GTCAGCCCGG  CAAAATGTTT
151 GGCAACATCC  TGATGTTTCG  CCGCCAGCAT  ATTGATGCAG  AGGCTGCCGT
201 TTCCGACAG  GATcggaATG  AttcgCGCAC  TCCGGTTTAT  GCACAGCATC
251 ACGGTCGGCG  GCTCGTCGGT  AACCGGCGCA  ACCGCCGTCA  TTGTAATGCC
301 GTAACGCCCT  GCCGCACCGT  CTGTCGTGAT  GACATGAACG  CCTGCCGCAC
351 AGGATGCCAT  CGCATCACGG  AACGAAGTTT  GAAAAGTTT  CTGCAAATCC
401 GCCATTTTTC  CCCTTTAAAC  CGTCCCTTAT  ATAAGAATGC  TGCACACAAG
451 GCATCCCCC  ATGTGCAGCA  GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 560; ORF 142.ng>:

```

g142.pep
1  MRADFMFADN  MPVQVRQRAF  YFKLSRFAAM  PNMVGKPLFG  RQAGQPGKMF
51  GNILMFVRQH  IDAEAAVFRQ  DRNDSRTPVY  AQHHGRRLVG  NRRNRHNCNA
101 VTPCRTVCRD  DMNACRTGCH  RITERSLKSF  LQIRHFSPLN  RPLYKNAAHK
151 ASPHVQOF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 561>:

```
m142.seq
  1 ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCCTGC AGGTGCGCCA
  51 ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
 101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTT
 151 GGCAACATCC TGATGTTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
 201 TTTCCGACAG GATCGGAATG ATTCGCGCAC TCCGGTTGAT GCACAGCATC
 251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCG ACCGCCGTCA TTGTAATGCC
 301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
 351 AAGATGCCAT CGCATCACGG AACGAAGTTT GAAAATTTT CTGCAAATCC
 401 GCCATTTTTC CCTTTTAAAC TGCCCCCTAT ATAAGAATGC TGCACACAAG
 451 GCATCCCCcC ATGTGCAGCA GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 562; ORF 142>:

```
m142.pep
  1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
  51 GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLVG NRRDRRHCA
 101 VTPCRTVCRD DMNACRARCH RITERSLKIF LQIRHFSPLN CPLYKNAAHK
 151 ASPHVQOF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 142 shows 93.7% identity over a 158 aa overlap with a predicted ORF (ORF 142.ng) from *N. gonorrhoeae*:

```
m142/g142
      10      20      30      40      50      60
m142.pep MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFNLMFVRQR
|||||
g142      MRADFMFADNMPVQVRQAFYFKLSRFAAMPNMVVGKPLFGRQAGQPGKMFNLMFVRQH
      10      20      30      40      50      60

      70      80      90     100     110     120
m142.pep IDAEAAVFRQDRNDSRTPVDAQHHGRRLVGNRRDRRHCAVTPCRTVCRDDMNACRARCH
|||||
g142      IDAEAAVFRQDRNDSRTPVYAQHHGRRLVGNRRNRHCAVTPCRTVCRDDMNACRTGCH
      70      80      90     100     110     120

      130     140     150     159
m142.pep RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX
|||||
g142      RITERSLKSLQIRHFSPLNRPPLYKNAAHKASPHVQQFX
      130     140     150
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 563>:

```
a142.seq
  1 ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCCTGC AGGTGCGCCA
  51 ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
 101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTT
 151 GGCAACATCC TGATGTTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
 201 TTTCCGACAG GATCGGAATG ATTCGCGCAC TCCGGTTGAT GCACAGCATC
 251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
 301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
 351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
 401 GCCATTTTTC CCTTTTAAAC TGCCCCCTAT ATAAGAATGC TGCACACAAG
 451 GCACCCCCCA TGTGCAGCAG TTCTGATTCA AAAAGCCGTC GGTCCGACAT
 501 TTCCGCGCGT TACGGCGTAT TACGAGTTCA ACGCATCCTC GATTTTGGCA
 551 AGTTCTGCCA ACAGGTCTTT AAGCAGCAGC ATTTTCTCGC GGGCCAGCAC
 601 TTCCTCGATA GCGTCGTAAC GTCGTCCAC TTCTTCGCGG ATTTCCTCAT
 651 ACAGCTTCTC GCCCTCGGCA GTCAGCTTCA GAAAAACACG TCGTTGGTGC
 701 TTGGAAGGTT TCAGGCGGAC AACCAAACCC GCTTTTTCAG GCGGGGTCTAG
 751 GATACCGGTC AGGCTGGGGC GCAAAATGCA CGCCTGATTC GCCAAATCTT
```

801 GAAAGTCCAG CGTGCCGTTT TCCGCCAAAA GACGGATAAT CCGCCATTGC  
 851 TGATCGGTAA TATTCGCCTG ATTCAGAATA GGCCTGAATT GGGTCATCAG  
 901 GGCTTCCCTT GCCTGTATCA GACCGATATT GATAGACGCA TGTTTTGA

This corresponds to the amino acid sequence <SEQ ID 564; ORF 142.a>:

a142.pep  
 1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF  
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLLVR NRRNRHRCNA  
 101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN CPLYKNAAHK  
 151 APPMCSSSDS KSRRSDISAR YGVLVRQIL DFGKFCQOVF KQQHFLAAQH  
 201 FLDSVVTLVH FFADFLIQLL ALGSQLOKNT SLVVGRFQAD NQTRFFKAGQ  
 251 DTGQAGAQNA RLIRQILKVQ RAVFRQKTDN PELLIGNIRL IQNRPELGHQ  
 301 GFPCLYQTDI DRRMF\*

m142/a142 96.1% identity in 153 aa overlap

	10	20	30	40	50	60
m142.pep	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFGNILMFVRQR					
a142	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFGNILMFVRQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m142.pep	IDAEAAVFRQDRNDSRTPVDAQHHGRRLLVGNRRDRHRCNAVTPCRTVCRDDMNACRARCH					
a142	IDAEAAVFRQDRNDSRTPVDAQHHGRRLLVNRNRHRCNAVTPCRTVCRDDMNACRTGCH					
	70	80	90	100	110	120
	130	140	150	159		
m142.pep	RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX					
a142	RITERSLKSFQIRHFSPLNCPPLYKNAAHKAPPMCSSSDSKSRRSDISARYGVLVRQIL					
	130	140	150	160	170	180
a142	DFGKFCQOVFKQQHFLAAQHFLDSVVTLVHFFADFLIQLLALGSQLOKNTSLVVGRFQAD					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 565>:

g143.seq  
 1 ATGTTGAGCT TCGGCTATCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG  
 51 CTCGCAGATG AGCGCATT TTCAAACGCT AGGCGCAGAC CCGCACAATT  
 101 TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CGGGGATGCT GGTTCAGCCG  
 151 ATAGTGgGCT ACTACTCAGA CCGCACTTGG AAGCCGCGCT TGGGCGGCCG  
 201 CCGCCTGCCG TATCTGCTTT ACGGCACGCT GATTGCGGTC ATCGTGATGA  
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG  
 301 GCCTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTGGACG TGTGTCGAA  
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGATATG GTCAACGAGG  
 401 AGCAGAAAAG CTACGCCTAC GGGATTCAAA GTTCTTAGC GAATACGGAC  
 451 GCGGTTGTGG CAGCGATTCT GCCGTTTGTG TTcgcgata TCGGTTTGGC  
 501 GAACACTGCC GAGAAAGGCG TTGTGCCACA AACCGTGGTC GTAGCATCTCT  
 551 ATGTGGGTGC GCGGTTACTG ATTATTACCA GTGCGTTTAC AATCTCCAAA  
 601 GTCAAAGAAT ACGACCCGGA AACCTACGCC CGTTACCACG GCATCGATGT  
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGTT CGAACTCTTA AAAACCGCGC  
 701 CTAAAGTGTT TTGGACGGTT ACTCCGGTAC AGTTTTCTG CTGGTTCGCC  
 751 TTCCGGTATA TGTGGACTTA CTCGGCAGGC GCGATTGCAG AAAACGCTG  
 801 GCACACTACC GATGCGTCTT CCGTAGGCCA TCAGGAGGCG GGCAACCGGT  
 851 ACGGCGTTTT GGCGGCGGTG TAGTCGGTTG CGGCGGTGAT TTGTTCTGTT  
 901 ATTCTGGCAA AAGTACCGAA TAAATACCAT AAGGCGGGTT ATTTCCGCTG  
 951 TTTGGCTTTG GGCGCGCTCG GTTCTTCTC TATCTTCTC ATCTACAATC  
 1001 AATACGCACT CATCCTGTCT TATATCTTAA TCGGCATCGC TTGGGCGGGC  
 1051 ATTATCACTT ATCCGCTGAC GATTGTGGCC AACGCTTTGT CGGGCAAACA  
 1101 CATGGATACT TATTTGGGCC TGTttaacgg ctctgtCTGT ATGCcgcaaa  
 1151 tcgTcgctTC GctgttgAGT TTCGTGCTTT TCCCAGTGCT GGGCGGCCAT

1201 CAGGCAACCA TGTCTTGGT TGCAGGCGCA GTCTTGCTGC TGGGAGCCTT  
 1251 CTCAGTCTGT CTGATTAAAG AGATCCACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 566; ORF 143.ng>:

g143.pep  
 1 MLSFGYLGVO TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP  
 51 IVGYSDRTW KPRLGRRRLP YLLYGTLIAV IVMILMPNSG SFGFGYASLA  
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKSYAY GIOSFLANTD  
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL IITSFTISK  
 201 VKEYDPETYA RYHGIDVAAN QEKANWFELL KTAPKVFVTV TPVQFFCWFA  
 251 FRYMWTYSAG AIAENVWHTT DASSVGHQEA GNRYGVLAHV \*SVAAVICSF  
 301 ILAKVPNKYH KAGYFGCLAL GALGFFSIFV IYNQYALILS YILIGIAWAG  
 351 IITYPLTIVA NALSGKHMMDT YLGLFNGSVC MPQIVASLLS FVLFPMLGGH  
 401 QATMFLVAGA VLLLGAFSVC LIKEIHGGV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 567>:

m143.seq  
 1 ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG  
 51 CTCGCAAATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT  
 101 TGGGCTGGTT TTTCATCCTG CCGCGCTGG CCGGGATGCT GGTGCAGCCG  
 151 ATTGTGGGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG  
 201 CCGTCTGCGG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA  
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG  
 301 GCTTTGTCTG TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCGTCAAA  
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCAACGAGG  
 401 AGCAGAAAGG CTACGCCTAC GGGATTCAAA GTTCTTAGC AAATACGGGC  
 451 GCGGTCGTGG CCGCGATTCT GCCGTTTGTG TTTGCGTATA TCGGTTTGGC  
 501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGGTC GTGGCGTTTT  
 551 ATGTGGGTGC GCGTTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAAA  
 601 GTGAAGGAAT ACGATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT  
 651 CGCGCGAAT CAGGAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCGC  
 701 CTAAGGCGTT TTGGACGTT ACTTTGGTGC AATTCTTCTG CTGGTTCGCC  
 751 TTCCAATATA TGTGACTTA CTCGGCAGGC GCGATTGCGG AAAACGCTCTG  
 801 GCACACCAAC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACTGGT  
 851 ACGGCGTTTT GCGGCGGGTG CAGTCGGTTG CCGCGGTGAT TTGTTGTTTT  
 901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGCGGGTT ATTTGCGCTG  
 951 TTTGGCTTTG GCGCGCTCG GCTTTTCTC CGTTTTCTTC ATCGGCAACC  
 1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC  
 1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CCGGCAAGCA  
 1101 TATGGGCACT TACTTGGGCT TGTAAACGG CTCTATCTGT ATGCCTCAAA  
 1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCTATGCT GGGCGGCTTG  
 1201 CAGGCCACTA TGTCTTGGT AGGGGCGGTC GTCTGCTGC TGGGCGCGTT  
 1251 TTCCGTGTTC CTGATTAAAG AAACACACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 568; ORF 143>:

m143.pep  
 1 MLSFGFLGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP  
 51 IVGHYSRTW KPRLGRRRLP YLLYGTLIAV IVMILMPNSG SFGFGYASLA  
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKGYAY GIOSFLANTG  
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSFTIFK  
 201 VKEYDPETYA RYHGIDVAAN QEKANWIELL KTAPKAFVTV TLVQFFCWFA  
 251 FQYMWYSAG AIAENVWHTT DASSVGYQEA GNWYGVLAHV QSVAAVICSF  
 301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG  
 351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGL  
 401 QATMFLVGGV VLLLGAFSVF LIKEIHGGV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m143 / g143 93.9% identity in 429 aa overlap

10 20 30 40 50 60

m143.pep	MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW
g143	MLSFGYLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGYYSDRTW
	10 20 30 40 50 60
m143.pep	70 80 90 100 110 120
	KPRLGRRRLPYLLYGTLIATIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
g143	KPRLGRRRLPYLLYGTLIATIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
	70 80 90 100 110 120
m143.pep	130 140 150 160 170 180
	QPFKMMVGDVNEEQKGYAYGQSFLANTGAVVAAILPFVFAYIGLANTAEGVVPQTVV
g143	QPFKMMVGDVNEEQKSYAYGQSFLANTDAVVAAILPFVFAYIGLANTAEGVVPQTVV
	130 140 150 160 170 180
m143.pep	190 200 210 220 230 240
	VAFYVGAALLVITSFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV
g143	VAFYVGAALLIITSFTISKVKEYDPETYARYHGIDVAANQEKANWFELLKTAPKVFWTV
	190 200 210 220 230 240
m143.pep	250 260 270 280 290 300
	TLVQFFCWFQYMWYTSAGAIAENVWHTTDASSVGYQEAGNWWYGVLAQVQSVAAVICSF
g143	TPVQFFCWFQYMWYTSAGAIAENVWHTTDASSVGHQEAGNRYGVLAQVXSVAAVICSF
	250 260 270 280 290 300
m143.pep	310 320 330 340 350 360
	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
g143	ILAKVPNKYHKAGYFGCLALGALGFFSIFFIYNQYALILSYILIGIAWAGIITYPLTIVA
	310 320 330 340 350 360
m143.pep	370 380 390 400 410 420
	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLQATMFLVGGVLLLGAFSVF
g143	NALSGKHMDTYLGLFNGSVCMQIVASLLSFVLPMLGGHQATMFLVAGAVLLLGAFSVC
	370 380 390 400 410 420
m143.pep	430
	LIKETHGGVX
g143	LIKEIHGGVX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 569>:

a143.seq

1	ATGCTCAGTT	TCGGCTTTCT	CGGCGTTCAG	ACGGCCTTTA	CCCTGCAAAG
51	CTCGCAGATG	AGCCGCATCT	TCCAGACGCT	CGGTGCCGAT	CCGCACAGCC
101	TCGGCTGGTT	CTTTATCCTG	CCGCCGCTGG	CGGGGATGCT	GGTGCAGCCG
151	ATTGTCGGCC	ATTACTCCGA	CCGCACTTGG	AAGCCGCGTT	TGGGCGGCCG
201	CCGTCTGCCG	TATCTGCTTT	ATGGCACGCT	GATTGCGGTT	ATTGTGATGA
251	TTTTGATGCC	GAACTCGGGC	AGCTTCGGTT	TCGGCTATGC	GTCTGCTGGCG
301	GCTTTGTCTG	TCGGCGCGCT	GATGATTGCG	CTGTTAGACG	TGTCGTCAAA
351	TATGGCGATG	CAGCCGTTTA	AGATGATGGT	CGGCGACATG	GTCAACGAGG
401	AGCAGAAAGG	CTACGCCTAC	GGGATTCAAA	GTTTCTTAGC	GAATACGGGC
451	GCGGTCTGTT	CGGCGATTCT	GCCGTTTGTG	TTTGCCTATA	TCGGTTTGGC
501	GAACACCGCC	GAGAAAGGCG	TTGTGCCGCA	GACCGTGGTC	GTGGCGTTTT
551	ATGTGGGTGC	GGCGTTGCTG	GTGATTACCA	GCGCGTTCAC	GATTTTCAAA
601	GTGAAGGAAT	ACAATCCGGA	AACCTACGCC	CGTTACCACG	GCATCGATGT
651	CGCCGCGAAT	CAGGAAAAAG	CCAACTGGAT	CGAACTCTTG	AAAACCGCGC
701	CTAAGGCGTT	TTGGACGGTT	ACTTTGGTGC	AATTCTTCTG	CTGGTTCGCC

```

751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGGT
851 ACGGCGTTTT GCGGCGGGTG CAGTCGGTTG CCGCGGTGAT TTGTTGTTTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTGCGCTG
951 TTTGGCTTTG GCGGCGCTCG GCTTTTCTC CGTTTCTTC ATCGGCAACC
1001 AATACGCGCT GGTGTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCC TGTTTAACGG CTCTATCTGT ATGCCGCAAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 570; ORF 143.a>:

```

a143.pep
1  MLSFGLGVQ TAFTLQSSQM SRIFQTLGAD PHSLGWFFIL PPLAGMLVQP
51  IVGHYSDRTW KPRLGGRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA
101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKGYAY GIQSFLANTG
151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
201 VKEYNPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251 FQYMWYSAG AIAENVHHTT DASSVGYQEA GNWYGVLAIV QSVAAVICSF
301 VLAQVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGL
401 QATMFLVGGV VLLLGAFSVF LIKETHGGV*

```

m143/a143 99.5% identity in 429 aa overlap

	10	20	30	40	50	60
m143.pep	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
a143	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
	10	20	30	40	50	60
m143.pep	70	80	90	100	110	120
a143	KPRLGGRRLPYLLYGTLIIVIMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
	70	80	90	100	110	120
m143.pep	130	140	150	160	170	180
a143	QPFKMMVGDMVNEEQKGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKVPQTVV					
	130	140	150	160	170	180
m143.pep	190	200	210	220	230	240
a143	VAFYVGAALLVITSAFTIFKVKEYNPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
	190	200	210	220	230	240
m143.pep	250	260	270	280	290	300
a143	TLVQFFCWFAFQYMWYSAG AIAENVHHTT DASSVGYQEA GNWYGVLAIV QSVAAVICSF					
	250	260	270	280	290	300
m143.pep	310	320	330	340	350	360
a143	VLAQVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT					
	310	320	330	340	350	360
m143.pep	370	380	390	400	410	420
a143	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMLGGLQATMFLVGGVVLLLGAFSVF					

```

a143      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          370      380      390      400      410      420
          NALSGKHMGTYLGLFNFSICMPQIVASLLSFVLFPMLGGLQATMFLVGGVVLLGAFSVF

          430
m143.pep  LIKETHGGVX
          |||||||||
a143      LIKETHGGVX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 571>:

```

g144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGTGC GTCTTCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC CCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGTAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTTCGAC GGGCTGGCCG TTACCcgtTT
351 CAACGCGGTG GCGGCAGACG GccgacggtT atCCCAACGA TTTGGatAtT
401 TCctaccgCT TGGACGAGGA CGGCCGGCTT ACCGTtacct ATCGCGCCAC
451 CGCgctCGGC GACACGGTGT TCGACCCGAC GCTGCACATT TACTGGCGGC
501 TGGACGCGGG CCTGCACGAT GCGGTTCTGC ATATTCCGCA GGGCGGACAT
551 ATTCCGCGCG ATGCCGAAAA ACTGCCCGTC TTAACGGTTT CAGACGGCCT
601 CGAAGTATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 572; ORF 144.ng>:

```

g144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTC VFVLDLGGIV QEFVSLADGV
51  RENPVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRRLSQR FGYFLPLGRG RPAYRYLSRH
151 RARRHGVRPD AAHLLAAGRG PARCGSAYSA GRTYSGRCRK TARLNGFRFP
201 RSI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 573>:

```

m144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGTCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGATGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAAC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTTCGAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTTCGGT GGTGCTGCGC AGCCGCGTGC
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGGG ATATTTCCTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TAcCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATGCC
601 GGCCGATGCC GAAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 574; ORF 144>:

```

m144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFVSLADGV
51  RENLVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLATVGRRR SQRFGEFYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAAHL AAGRGPARGC SAYSAGRITYA
201 GRCRKTARLN GFRRPRSI*

```

Computer analysis of this amino acid sequence gave the following results:



Homology with a predicted ORF from *N. gonorrhoeae*

m144 / g144 91.3% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
g144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTCVFVLDLGGIVQEFSVLADGVRENPFVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
g144	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m144.pep	AADGRSVVLRSLATVGRRLSQRFQYFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL					
g144	AAD-----GRRLSQRFQ--YFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL					
		130	140	150	160	
	190	200	210	219		
m144.pep	AAGRGPARCGSAYSAGRTYAGRCRKRTARLNGFRPRSIX					
g144	AAGRGPARCGSAYSAGRTYSGRCRKRTARLNGFRPRSIX					
	170	180	190	200		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 575>:

```

a144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGTGACACG CGGTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTGCGT GGTGCTGCGC AGCCGCCTG.
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGGA ATATTTCCTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TACCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTGAC CCGACGCTGC ACATTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATTCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 576; ORF 144.a&gt;:

a144.pep	1	MSDTPATRDF	GLIDGRAVTG	YVLSNRRGTR	VCVLDLGGIV	QEFSVLADGV
	51	RENLVVSFDD	AASYADNPFQ	INKQIGRVAG	RIRGAAFDIN	GRTYRVEANE
	101	GRNALHGGSH	GLAVTRFNAV	AADGRSVVLR	SRLXTVGRR	SQRFQFGYFL
	151	PLGRGRPAYR	YLSRHRARRH	GVRPDAAHLL	AAGRGPARCG	SAYSAGRTYS
	201	GRCRKRTARLN	GFRPRSIX*			

m144/a144 99.1% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
a144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					

410

```

a144      |||||
          AASYADNPFOINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
          70      80      90      100     110     120

          130     140     150     160     170     180
m144.pep  AADGRSVVLRSLATVGRRLSQRFGFGYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL
          |||||
a144      AADGRSVVLRSLXTVGRRLSQRFGFGYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL
          130     140     150     160     170     180

          190     200     210     219
m144.pep  AAGRGPARCGSAYSAGRTYAGRCRKRTARLNGFRRPRSIX
          |||||
a144      AAGRGPARCGSAYSAGRTYSGRCRKRTARLNGFRRPRSIX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 577>:

```

gl46.seq
1   ATGAAGCAAA TCCCCCTCCG CCTTCTCCAG GTCGTCATTG ACCACGACAA
51  AGTCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAa ctTCCCGACT GTCCGTCCCG CGCcttTTGA GGCGCGCGGC
151 AAGCACGTCTG AAAGAAGGCG GCAGGATAAA GATACCGACA GCTTCCGGCA
201 GCGCGTTGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTCACG CCCTCCGTGC TTGTGCCGTA
301 ATAGTTGCCG AATACGTCTG CGTATTCCAA AAAAGCCTCC TGCGCGATAA
351 GCGATTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGGGCG CGTCGTATGC GACACGGAAG CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTG CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAA CCGATTGTAT CACAACGGAC ACCCTATTTT
601 ATATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 578; ORF 146.ng>:

```

gl46.pep
1   MKQIPLRLIQ VVIDHDKVEQ YGLFDEMPCL RQPPLDNFPT VRPAPEARG
51  KHVERRRQDK DTDSEFRQVA NLRRLNVDF QNHVIACRRQ RIHALRACAV
101 IVAEYVCVFQ KSLLRDKRFK LFFGNKVIMY AVCFAFTRRA RMRHGNNAQT
151 VMVCQQRHQ  RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPYF
201 IFADAHILPL LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 579>:

```

m146.seq
1   ATGGCGCAAA TCCTCCTCCG CTCGCGCCAA GTCGTCATTG ACCACGACAA
51  AGTCAAACAA TACGGACTGC TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCTCGACT GTCCGTCCCG CGTCCGTTGA GGCGCGCGGC
151 AAGTACGTCTG AAAGAAGGCG GCAGGATAAA GATGCCGACG GCTTCCGGCA
201 GCGCGTCGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTCACA CCCTCCGCGC CTGTGCCGTA
301 ATAGTTGCCA AATACGTCTG CGTATTCCAA AAAAGCTTCC TGCGCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGGGCG CGTCGTGTGC GACACGGAAG CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTG CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAATGGAC ACCCAGTTTC
601 CTATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 580; ORF 146>:

```

m146.pep
1   MAQILLRSRQ VVIDHDKVKQ YGLLDEMPCL RQPPLDNFPT VRPASVEARG
51  KYVERRRQDK DADGFGQVA NLRRLNVDF QNHVIACRRQ RIHTLRACAV
101 IVAKYVGVFQ KSLFLDKRLK LFFGNKVIMY AVCFAFTRRA RVRHGNNAQT
151 VMVCQQRHQ  RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQWTPSF
201 LFADAHILPL LF*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m146 / g146 90.1% identity in 212 aa overlap

		10	20	30	40	50	60
m146.pep		MAQILLRSRQVV	IDHDKVKQYGL	LDFMPCLRQPP	LDNFPTVRPAS	VEARGKYVERR	RQDK
g146		MKQIPLRLLQV	VIDHDKVEQYGL	FDFMPCLRQPP	LDNFPTVRPAP	FEARGKHVERR	RQDK
		10	20	30	40	50	60
		70	80	90	100	110	120
m146.pep		DADGFGQQRV	ANLRRALNVDF	QNHVIACRRQR	IHTLRACAVIV	AKYVGVFQKS	SFLRDKRLK
		:   :					
g146		DTDSFRQQRV	ANLRRALNVDF	QNHVIACRRQR	IHALRACAVIV	AEYVCVFQKS	LLRDKRFK
		70	80	90	100	110	120
		130	140	150	160	170	180
m146.pep		LFFGNKVIMY	AVCFAFTRRR	ARRVRHGNQA	QTMVCQQPRH	QRGFARAGSG	RNDKDVAFSIS
g146		LFFGNKVIMY	AVCFAFTRRR	ARRMRHGNQA	QTMVCQQPRH	QRGFARAGSG	RNDKDVAFSIS
		130	140	150	160	170	180
		190	200	210			
m146.pep		GHIFYLYIFQ	PIVSQWTPSFL	FADAHILPLLF	X		
g146		GHIFYLYIFQ	PIVSQRTPYF	IFADAHILPLLF	X		
		190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 581>:

```

al46.seq
1  ATGGCGCAAA TCCTCCTCCG CCCGCGCCAA GTCATCATTG ACCACGACAA
51  AATCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCCGACT GTC CGTCCGTTGA GACGCGCAGC
151 AAGCATCTCG AAAGACGGCG GCAGGATAAA GATGCCGAGC GCTTCCGGGA
201 GCGCATCTCG AACCTGAGCC GCGCCCTGAA CGTCGATTTT CAAATACACG
251 TCATAACCTG CGCGCGCCAA CGCATTCACA CCCTCGCGCG TTGTGCGGTA
301 ATAGTTGCCG AACACGTCCG CGTATTCCAA AAAAGCCTCC TGC GCGATAA
351 GCGACTCAAA CTTCTCTTTG GAAACAAGAT GATAATGTAC GCGCTTTGCT
401 TCGCCTTCAC GCGCGGGACG CGTGTGTGTC GACACGGAAA CCGCGAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTG CCGGTGCGCG
501 AAGCGCGCGA AATGATAAAG ATGTTGCSTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAACGGAC ACCCGGTTTC
601 CTATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 582; ORF 146.a>:

```
a146.pap
1  MAQILLRPRQ  VIIDHKIEQ  YGLDFMPCL  RQPLDNFPT  VRPASVETRS
51  KHIERRQDK  DADGFGQIS  NLSRALNVDF  QNHVITCRQ  RIHTLRACAV
101 IVAEHVRVFQ  KSLLRDKRLK  LFFGNKVIMY  AVCFAFTRRT  RVRRHGNAQT
151 VMVCCQPRHQ  RGFAAGSGR  NDKDVAFFSIS  GHIFYLYIFQ  PIVSQRTGFG
201 LFADAHLLPL  LF*
```

m146/a146 90.6% identity in 212 aa overlap

	10	20	30	40	50	60
m146.pep	MAQILLRSRQVV	IDHDKVKYGLLD	FMPCLRQPPLD	NFTVRPASVEA	RGYKVERRRQ	DK
a146	MAQILLRPRQVI	IDHDKIEQYGLF	DMPCLRQPPLD	NFTVRPASVET	RSKHIERRRQ	DK
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m146.pep  DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK
          |||||::|| |||||::|| |||||::|| |||||::|| |||||::|| |||||::||
a146      DADGFGQRI SNLSRALNVDFQNHVITCRRQRIHTLRACAVIVAEHVRVVFQKSLLRDKRLK
          70          80          90          100         110         120

          130         140         150         160         170         180
m146.pep  LFFGNKVIMYAVCFATRRARRVRHGNATVMVCQQPRHQRFARAGSGRNDKDVAFSIS
          |||||::|| |||||::|| |||||::|| |||||::|| |||||::|| |||||::||
a146      LFFGNKVIMYAVCFATRRARRVRHGNATVMVCQQPRHQRFARAGSGRNDKDVAFSIS
          130         140         150         160         170         180

          190         200         210
m146.pep  GHIFYLYIFQPIVSQWTPSFLFADAHILPLLFX
          |||||::|| |||||::|| |||||::|| |||||::|| |||||::||
a146      GHIFYLYIFQPIVSQRTPGFLFADAHILPLLFX
          190         200         210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 583>:

```

g147.seq (partial)
1  ..ATGCGACGAG AAGCCAAAAT GGCACAAATC ACACTCAAAC CCATTGTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CGCCCAAGCG CATGAAACTG
101 AGCAATCGGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCGACTT CGGGGCTGCT GCACACTTCG ACCGCCTCCG ACAAATCAT
201 CTCCGGCGAT ACTTTGCGCC AAAAAGCCGT CAACTTGGGC GACGCTTTGG
251 ACGGCGTACC GGCATCCAC GCTTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC GGGCAGACGG ATTAAAGTAT TGAACCATCA
351 CGGCGAAACG GGCATATGG CGGACTTTTC TCCGATCAC GCCATTATGG
401 TAGATACCGC CTGTGCGCAA CAGGTTGAAA TCCTGCGCGG GCCGTTACG
451 CTCTTGTA CA GCTCGGgcaa tgtggccgGG GCTGGtcaat gttgccgatg
501 gAAAAAtccc ccaaaaATatg cc..

```

This corresponds to the amino acid sequence <SEQ ID 584; ORF 147.ng>:

```

g147.pep (partial)
1  ..MRREAKMAQI TLKPIVLSIL LINTPLLAQA HETEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFSPDH AIMVDTALSQ QVEILRGPVT
151 LLYSSGNVAG AGQCCRWKNP PKNA..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 585>:

```

m147.seq (partial)
1  ..CCGCATAAAA CTGAGCAATC GGTGGATTG GAAACGGTCA GCGTCGTCGG
51  CAAAAGCCGT CCGCGCGCCA CGTCGGGGCT GTTGCACTACT TCGACCGCCT
101 CCGACAAAAT CATCTCCGGC GATACCTTGC GCCAAAAGC CGTCAACTTG
151 GCGGACGCTT TAGACGGCGT ACCGGGCATC CACGCTTCGC AATACGGCGG
201 CGGCGGCTCT GCTCCCGTCA TTCGCGGTCA AACAGGCAGG CGGATTAAG
251 TGTGTAACCA TCACGGCGAA ACAGGCGATA TGGCGGATT TTCGCCCGAT
301 CACGCCATTA TGGTAGATAC CGCCTTGTCG CAACAGGTCG AAATCCTGCG
351 CGGGCCGGTT ACGCTCTTGT ACAGCTCGGG CAATGTGGCG GGGCTGGTCG
401 ATGTTGCCGA TGGCAAAATC CCCGAAAAA TGCCTGAAAA CGGCGTATCG
451 GGCGAACTCG GATTGCGTTT GAGCAGCGGC AATCTGGA AAATCACGTC
501 CGGCGGCATC AATATCGGTT TGGGCAAAAA CTTTGATTG CACACGGAAG
551 GGCTGTACCG CAAATCGGGG GATTACGCCG TACCGCGTTA CCGCAATCTG
601 AAACGCCTGC CCGACAGCCA CGCCGATTCT CAAACGGGCA GCATCGGGCT
651 GTCTTGGGTT GGCGAAAAAG GTTTTATCGG CGTAGCGTAC AGCGACCGTC
701 GCGACCAATA TGGTCTGCCT GCCACAGCC ACGAATACGA TGATTGCCAC
751 GCCGACATCA TCTGGCAAAA GAGCTTGATT AACAAACGCT ATTTACAGCT
801 TTATCCGCAC CTGTTGACCG AAGAAGACAT CGATTACGAC AATCCGGGCT
851 TGAGCTGCGG CTTCACGAC GACGATAATG CACACGCACA CACCACAGC
901 GGCAGACCGT GGATAGACCT GCGCAACAAA CGCTACGAAC TCCGTGCCGA
951 ATGGAAGCAA CCGTTCCCGG GTTTTGAAGC CCTGCGCGTA CACCTGAACC
1001 GCAACGACTA CCGCCACGAC GAAAAAGCAG GCGATGCAGT CGAAAACTTT
1051 TTAAACAACC AAACGCAAAA CGCCCGCATC GAGTTGCGCC ACCAACCCAT

```

```

1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACAAACCGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCCGACC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTACAGC CACAACACAA ACTCAGCCTG ACCGCCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAAGAGCG
1551 TTCCAACAAT ATCGAATCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCCTTCG GTAACATAC TTAGCCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGCGCG CGACTTCTAC GGCGCGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCCGTCT GAAAAACCTG CTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGCTGACC
1951 GACCGTATCG ATGCCAATTG GGACTACTAC CGCGTGTTCG CCAAAACAA
2001 ACTCGCCCGC TACGAAACGC GCACGCCGGG ACACCATATG CTCAACCTCG
2051 GCGCAAACCTA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACA GCAGCTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGCGCGC GTGAACGTGA
2201 AGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1  ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STADKIIISG DTLRQKAVNL
51  GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLGKNFVL HTEGLYRKSG DYAVPRYRNL
201 KRLPDSHADS QTGSIGLSWV GEKGFIVGAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWQKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTS
301 GRPWIDLRNK RYELRAEWKQ PFPGFALRV HLNRRNDYRD EKAGDAVENF
351 FNNQTQNARI ELRHQPIGRL KGSWGVQYLQ QKSSALSAIS EAVKQPMLLD
401 NKVQHYSFFG VEQANWDNFT LEGGVRVEKQ KASIQYDKAL IDRENYNHP
451 LPDLGAHRQT ARSFALSGNW YFTPOHKLSL TASHQERLPS TQELYAHGKH
501 VATNTFEVGN KHLNERSNN IELALGYEGD RWQYNLALYR NRFGNYIYAQ
551 TLNDGRGPKS IEDDSEMCLV RYNQSGADFY GAEGEYFKP TPRYRIGVSG
601 DYVRGRLLNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

m147.pep                                10      20      30
                                PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
g147                                10      20      30      40      50      60
MRREAKMAQITLKPVL SILLINTPLLAQAHETE QSVGLETVSVVGKSR PRATSGLLHTS

m147.pep                                40      50      60      70      80      90
TASDKIIISGDTLRQKAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
g147                                40      50      60      70      80      90
TASDKIIISGDTLRQKAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET

m147.pep                                100     110     120     130     140     150
GDMADFS PDHAIMVDTALS QQVEILRGPV TLLYSSGNVAGLVDVADGKI PEKMPENGVS
g147                                100     110     120     130     140     150
GDMADFS PDHAIMVDTALS QQVEILRGPV TLLYSSGNVAGAGQCCRWNPPKNA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

```
a147.seq
1  ATGCGACGAG AAGCCAAAAT GGCACAAACT ACACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCTCCT CTCCAAGCG CATGGAAGTG
101 AGCAATCAGT GGGCTTGGA ACGGTCAGCG TCGTCGGCAA AAGCCGTCGG
151 CGCGCCACTT CGGGGCTGCT GCACACTTCT ACCGCTCCG ACAAATCAT
201 CAGCGGCGAC ACCTTGCGAC AAAAAGCCGT CAACTTGGGT GATGCTTTAG
251 ACGGCGTACC GGGCATTCAT GCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAGTGT TGAACCATCA
351 CGGCGAAACG GCGGACATGG CGGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTCGCAA CAGGTCGAAA TCCTGCGCGG TCCGGTTACG
451 CTCTTGTA CA GCTCGGGCAA TGTGGCGGGG CTGGTCGATG TTGGCGATGG
501 CAAAATCCCC GAAAAAATGC CTGAAACGG CGTATCGGGC GAACTCGGAT
551 TGCGTTGAG CAGCGGCAAT CTGAAAAAC TCACGTCGGG CGGCATCAAT
601 ATCGGTTTGG GCAAAACTT TGTATTGCAC ACGGAAGGGC TGTACGCCAA
651 ATCGGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTGCGAA ACGGGCAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATAACAGC GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGG
1001 TAGACCTGCG CAACAAACGC TACGAACTCC GCGCCGAATG GAAGCAACCG
1051 TTCCCGGTTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAACCTTTTT AACAACCAAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCGATGCT GCTTGACAAT AAAGTCAAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTTACGCTT
1351 GAAGCGGCG TACGCGTGGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGAAA ACTACTACAA CCATCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAACCGGCC CGCTCATTG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAAACT CAGCCTGACC GCCTCCATC AGGAACGCCT
1551 GCCGTCAACG CAAGAGCTGT ACGCACACGG CAAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGCTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAAACGACG
1751 GACGCGGCCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGCGC
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACGACA CCGCGCTACC GCATCGGCGT TTCCGCGGAC TATGTACGAG
1901 GCCGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACCGCCAC TCATTGCCCA AGCCGACCAA AACGCCCTC GCGTTCGGG
2001 TGCGCGCCTC GCGTCCACC TGAAAGCCTC GCTGACCGAC CGCATCGATG
2051 CCAATTGGA CTACTACCGC GTGTTGCGCC AAAACAAACT CGCCCGCTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGGAATTG GTACGTCAA GCCGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CGGCGCGTG AACGTGAAGT TTAA
```

This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

```
a147.pep
1  MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRQGTGRR IKVLNHHGET GDMADFSPDH AIMVDSALSQ QVEILRGVPT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVSF ELGLRLSSGN LEKLTSGGIN
201 IGLGKNFVLH TEGLYRKSGD YAVPYRNLK RLPDSHADSQ TGSIGLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEDIDIDYN PGLSCGFHDD DDAHAHAHNG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTQNAIE LRHQPIGRK
401 GSWGVOYLQ KSSALSATSE AVKQPMLLDN KVQHYFFGV EQANWONFTL
451 EGGVRVEKQK ASIRYDKALI DRENNYHPL PDLGAHRQTA RSFALSGNWI
501 FTPQHKLSLT ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR
```

601 YNQSGADFYG AEGEIYFKPT PRYRIGVSGD YVRGRLKNLP SLPGREDAYG  
651 NRPLIAQADQ NAPRVPAARL GVHLKASLTD RIDANLDYYR VFAQNKLARY  
701 ETRTPGHHML NLGANYRRNT RYGEWNWYVK ADNLLNQSVY AHSSFLSDTP  
751 QMGRSFTGGV NVKF\*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DLETVS	VVVGKSRPRATSGLLHTS
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQA	HGTEQSV	GLETVS	VVVGKSRPRATSGLLHTS		
	10	20	30	40	50	60
m147.pep		40	50	60	70	80
		TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET			
a147	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
	70	80	90	100	110	120
m147.pep		100	110	120	130	140
		GDMADFS	PDHAIMVDTALSQQVEILRGPVTLLYSSGNVAGLVDVADGKIPEKMPENGVS			
a147	GDMADFS	PDHAIMVDSALSQQVEILRGPVTLLYSSGNVAGLVDVADGKIPEKMPENGVS				
	130	140	150	160	170	180
m147.pep		160	170	180	190	200
		ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNLKRLPDSHAD				
a147	ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNLKRLPDSHAD					
	190	200	210	220	230	240
m147.pep		220	230	240	250	260
		TGSIGLSWVGEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHL		
a147	TGSIGLSWVGEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHL			
	250	260	270	280	290	300
m147.pep		280	290	300	310	320
		LTEEDIDYDNPGLS	CGFHDDNAHAH	THSGRPWIDLANKRYELRAEWKQFFPGFEALRVH		
a147	LTEEDIDYDNPGLS	CGFHDDDAHAH	AHNGKRPWIDLANKRYELRAEWKQFFPGFEALRVH			
	310	320	330	340	350	360
m147.pep		340	350	360	370	380
		LNRNDYRHDEKAGDAVENFFNNQ	TQNARIELRHQPIGRLKGSWGVQYLGQKSSALSATSE			
a147	LNRNDYRHDEKAGDAVENFFNNQ	TQNARIELRHQPIGRLKGSWGVQYLGQKSSALSATSE				
	370	380	390	400	410	420
m147.pep		400	410	420	430	440
		AVKQPMLLDNKVQHYSFFGVEQANW	NFTLEGGV	RVKQKASIQYDKALIDRENYNHP		
a147	AVKQPMLLDNKVQHYSFFGVEQANW	NFTLEGGV	RVKQKASIRYDKALIDRENYNHP			
	430	440	450	460	470	480
m147.pep		460	470	480	490	500
		PDLGAHRQTAR	SFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK			
a147	PDLGAHRQTAR	SFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
	490	500	510	520	530	540
m147.pep		520	530	540	550	560
		HLNKERSNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM				
a147	HLNKERSNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM					
	520	530	540	550	560	570

	550	560	570	580	590	600
m147.pep	580	590	600	610	620	630
	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFFIAQDDQ					
a147	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPPLIAQADQ					
	610	620	630	640	650	660
m147.pep	640	650	660	670	680	690
	NAPRVPAARLGFHLKASLTDRIANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
a147	NAPRVPAARLGVHLKASLTDRIANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
	670	680	690	700	710	720
m147.pep	700	710	720	730		
	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGctgg  ttcaTCCCCG
51  AgctATgagt  gtcggcgCGC  TTGccgAcaa  AATCCGCAAA  AtcgaAAact
101 gGCCGCAAAA  AGgcaTCTTA  TTCCACGACA  TCACGCCCGT  CCTGCAAAAGT
151 GCGGAATACT  TCCGCCTTTT  GGTTCGATTG  CTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGCTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAg  CTCaACgtcg  gctTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCGTATCG  CAAAGCTAcg  cgcTCGAATA
351 CGGGGAAGCT  GCGGTGGAAA  TCCACACCGa  tgccgTCAAA  CCCGGTTCGC
401 GCGTCTGCT  GGTTCGATGAT  TTGGTTGCCA  CGGGCGGCAC  AATGCTTGCC
451 GGGCTGGAAC  TGATCCGCAA  ACTCGGCGGG  GAAATTGTCT  AAgccgcccG
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGCGCAAGTG
551 GCGCGCCCTT  ATTTACCCCTG  CTTCAAAACG  AAGGCTGCAT  GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK
101 KGKLPFETVS  QSYALEYGEA  AVEIHTDAVK  PGSRVLLVDD  LVATGGTMLA
151 GLELIRKLGG  EIVEAAAILE  FTDLQGGKNI  RASGAPLFTL  LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGCTGG  TTCATCCCCG
51  AGCTATGAGT  GTCGGCGCGC  TTGCCGACAA  AATCCGCAAA  ATCGAAAAC
101 GGCCGCAAAA  AGGCATCTTA  TTCCACGACA  TCACGCCCGT  CCTTCAAAGC
151 GCGGAATACT  TCCGCCTTTT  GGTTCGATTG  TTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGTTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAg  CTCACGTCG  GTTTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCGTATCG  CAAAGCTACG  CGCTCGAATA
351 CGGGGAAGCT  GCGGTGGAAA  TCCACACCGA  TGCGGTCAAA  CTCGGTTCGC
401 GCGTCTGCT  GGTTCGATGAT  TTGATTGCCA  CGGGCGGCAC  GATGCTTGCC
451 GGACTGGAAC  TGATCCGCAA  ACTCGGCGGA  GAAATTGTCT  AAGCCGCCGC
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGTGAAGCG
551 GCGCGCCCTT  ATTTACCCCTG  CTTCAAAACG  AAGGCTGTAT  GAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK

```



101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LIATGGTMLA  
 151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m148 / g148 99.0% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
g148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m148.pep	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
g148	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m148.pep	AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
g148	AVEIHTDAVKPGSRVLLVDDLATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
	130	140	150	160	170	180
	190	200				
m148.pep	RASGAPLFTLLQNEGCMKGX					
g148	RASGAPLFTLLQNEGCMKGX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 593>:

a148.seq  
 1 ATGGCGTTAA AAACATCAAA CTGGAACAC GCAATGCTGG TTCATCCCGA  
 51 AGCTATGAGT GTCGGTGCGC TTGCCGACAA AATCCGCAAA ATCGAAACT  
 101 GGCCGCAAAA AGGCATCTTA TTCCACGACA TCACGCCCGT CCTGCAAAGC  
 151 GCGGAATACT TCCGACTTTT GGTGATTTA TTGGTTTACC GCTATATGGA  
 201 TCAGAAAATC GACATCGTTG CCGGTTTGA CGCGCGCGG TTCATTATCG  
 251 GCGCGGCACT CGCCTACCAG CTCAACGTCG GTTTCGTCCC CATCCGCAAA  
 301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTACG CGCTCGAATA  
 351 CGGGGAAGCT GCGGTGGAAA TCCACACCGA TGCCGTCAAA CTCGGTTCCG  
 401 GCGTGCTGCT GGTGATGAT TTGGTTGCCA CGGGCGGCAC GATGCTTGCC  
 451 GGAATGGAGC TGATCCGCAA ACTCGGCGGG GAAATTGTGC AAGCCGCCGC  
 501 CATTTTGGAA TTTACCGACC TTCAAGGCGG CAAGAATATC CGTGCAAGCG  
 551 GCGCGCCCTT ATTTACCCTG CTTCAAACG AAGGCTGTAT GAAGGGCTGA

This corresponds to the amino acid sequence <SEQ ID 594; ORF 148.a>:

a148.pep  
 1 MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKIL FHDITPVLQS  
 51 AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPIRK  
 101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LVATGGTMLA  
 151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG\*

m148/a148 99.5% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
a148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m148.pep  LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYLEYGEA
a148       LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYLEYGEA
           70      80      90      100     110     120

           130     140     150     160     170     180
m148.pep  AVEIHTDAVKLGSRVLLVDDLATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
a148       AVEIHTDAVKLGSRVLLVDDLATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
           130     140     150     160     170     180

           190     200
m148.pep  RASGAPLFTLLQNEGCMKGX
a148       RASGAPLFTLLQNEGCMKGX
           190     200

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 595>:

```

g149.seq
1  ATGTTGATTG ACAACAATGT CCGCCATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAATTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATCCGTAC GACAAAGCAT TGATTGATCG AGAAACTAC
151 TACAACCAGC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCCTC
201 GTTCGCACTT TCGGGCAACT GGTATTTTAC GCCACACCAC AAACCTAGCC
251 TGACCGCCTC CCATCAGGAA cgCCTGCCGT CAACGCaagA actGtACgca
301 cacggcAAGC ACgtcgccac CAACACCTTT GAagtctggca acaaACACCT
351 CAACAAAGaG CgttccaacA atatcgaACT CGCGCTGGgc tAcaaaggcg
401 accGCTGGCA ATACAATCTG GCAGCCTACC GCAACCGAtT CGGCAACTAC
451 ATTTACGCCC AAACCTTAaa cgacggacgC GGCCCCAAAT CCATCgaaga
501 cgacagcgaa ATGaagcTCG TCGCTACAA CCAATCCGGT GCCGACTTCT
551 ACGgcgcgga aggcgaaatc tACTTcaaaC CGAcACCGCG CTACCGCATC
601 GGTGTTTCCG GCGACTatgt acgaggccgT CTGAAAAACC TGCCGTCCTT
651 ACCCGGCAGG gaagatccCT AcggcAAACG TCccttcaTC GCACAAGCCG
701 ACCAAAACGC CCCCCTGATT ccggctGCGC GCCTCGGCTT CCACCTGAAA
751 ACCTCGCTAA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801 CGCCCAAAAC AAACCTCGCCC GCTACGAAAC GCGTACGCCC GGACACCATA
851 TGCTCAACCT CCGTGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGctc aACcaatCcg tTTACGCCCa
951 cAGCAGCTTC CTCTCTGATA CGCCGCAAAat gGGCCGCAGC TTtgccgGCg
1001 gcgtaAACGT GaAGTTtaa

```

This corresponds to the amino acid sequence <SEQ ID 596; ORF 149.ng>:

```

g149.pep
1  MLIDNNVRHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51  YNQPLPDLGA HRQTARSFAL SGNWYFTPHH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YKGDWQYNL AAYRNRFGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVS GDYVVRGR LKNLPSLPGR EDPYGRPFPI AQADQNAPRI PAARLGFHLK
251 TSLTDRIDAN LDYYRVFAQN KLARYETRTP GHMLNLNLAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FAGGVNVKF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 597>:

```

m149.seq
1  ATGCTGCTTG ACAACAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAATTCA CGCTTGAAGG AGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATTCACTAC GACAAAGCAT TGATTGATCG GGAAACTAC
151 TACAACCACC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAACCTAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGGCAAAC ACgtcgccac CAACACCTTT GAAGTCGGCA ACAAACACCT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGTAACCTAC

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451	ATTTACGCC	AAACCTTAAA	CGACGGACGC	GGCCCCAAAT	CCATCGAAGA
501	CGACAGCGAA	ATGAAGCTCG	TGCGCTACAA	CCAATCCGGC	GCCGACTTCT
551	ACGGCGCGGA	AGGCGAAATC	TACTTCAAAC	CGACACCGCG	CTACCGCATC
601	GGCGTTTCCG	GCGACTATGT	ACGAGGCCGT	CTGAAAAACC	TGCTTTCCTT
651	ACCCGCGCAG	GAAGATGCTT	ACGGCAACCG	TCCTTTTCATC	GCACAGGAGC
701	ACCAAAATGC	CCCCGTGTGT	CGCGTCTGCG	GCGTCGGTTC	CCACTTGAAA
751	GCCTCGCTGA	CCGACCGTAT	CGATGCCAAT	TTGGACTACT	ACCGCGTGTT
801	CGCCCCAAAC	AAACTCGCCC	GCTACGAAAC	GCGCACGCCC	GGACACCATA
851	TGCTCAACCT	CGGCGCAAAC	TACCGCCGCA	ATACGCGCTA	TGGCGAGTGG
901	AATTTGGTAC	TCAAAGCCGA	CAACCTGCTC	AACCAATCCG	TTTACGCCCA
951	CAGCAGCTTT	CTCTCTGATA	CGCCGCAAAAT	GGGCCGCGAG	TTTACCGGCG
1001	GCGTGAACGT	GAAAGTTTAA			

This corresponds to the amino acid sequence <SEQ ID 598; ORF 149>:

m149.pep

1	MLLDNKVQHI	SFFGVEQANW	DNFTLEGGVR	VEKQKASIQY	DKALIDRENY
51	YHHPPLDPLG	HRQTARSLAF	SGNWYETTPQH	KLSTLASHQE	RLPSTQBELY
101	HGHKVATNTF	EVGNKSHLNKE	RSNNIYELAG	YEGDRWQYNL	ALYRNRFELGY
151	IYAQTLNDGR	GPKSIEDDSE	MKLVRYNQSG	ADFGAEGEII	YFKPTPRYRI
201	GVSGDYYVRG	LKNLPSLPGR	EDAYGNRPFI	AQDDONAPRV	PAARLGFLHK
251	ASLTDRIDAN	LDYYRVFAQN	KLARYETRTP	GHHMLNLGAN	YRRNTRYGEW
301	NWYVKDANLL	NOSVYAHSSF	LSDTPMOMRS	FTGGVNVKE*	

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N.gonorrhoeae*

ORF 149 shows 95.9% identity over a 339 aa overlap with a predicted ORF (ORF 149.ng) from *N. gonorrhoeae*:

m149/q149

	10	20	30	40	50	60
m149.pep	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIQYDKALIDREYNNHPLPDLGA					
g149	MLIDNNVRHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDREYNNQPLPDLGA					
	10	20	30	40	50	60
m149.pep	HRQTARSPALSGNWFYTPQHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
g149	HRQTARSPALSGNWFYTPPHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	RSNNIELALGYEGDRWQYNLALYRNRFGNYIIYAQTLNDGRGPKSIEDDSEMKLVRYNQSG					
g149	RSNNIELALGYKGRWQYNLAAYRNRFGNYIIYAQTLNDGRGPKSIEDDSEMKLVRYNQSG					
	130	140	150	160	170	180
m149.pep	ADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFFIAQDDQNAPRV					
g149	ADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDPYGKRPFIAQADQNAPRI					
	190	200	210	220	230	240
m149.pep	PAARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEW					
g149	PAARLGFHLKTSLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEW					
	250	260	270	280	290	300
m149.pep	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
g149	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	310	320	330	340		

420

g149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFAGGVNVKFX  
 310 320 330 340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 599>:

a149.seq  
 1 ATGCTGCTTG ACAATAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA  
 51 GGCAAACTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC  
 101 AAAAAGCCTC CATCCGCTAC GACAAAGCAT TGATTGATCG GGAAAACTAC  
 151 TACAACCATC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC  
 201 ATTCGCACTT TCGGGCAACT GGTATTTCAC GCCACAACAC AAACCTCAGCC  
 251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA  
 301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT  
 351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG  
 401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACGCTT CGGCAACTAC  
 451 ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA  
 501 CGACAGCGAA ATGAAGCTCG TCGCTACAA CCAATCCGGT GCGGACTTCT  
 551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC  
 601 GGCGTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT  
 651 ACCCGGCAGG GAAGACGCCT ACGGCAACCG CCCACTCATT GCCCAAGCCG  
 701 ACCAAAACGC CCCTCGCGTT CCGGCTGCGC GCCTCGGCGT CCACCTGAAA  
 751 GCCTCGCTGA CCGACCGCAT CGATGCCAAT TTGGACTACT ACCGCGTGTT  
 801 CGCCCCAAAC AAACTCGCCC GCTACGAAAC GCGCACGCCC GGACACCATA  
 851 TGCTCAACCT CGGCGCAAAC TACCGCGCA ATACGCGCTA TGGCGAGTGG  
 901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCA  
 951 CAGCAGCTTC CTCTCTGATA CGCCGCAAAT GGGCCGCAGC TTTACCGGCG  
 1001 GCGTGAACGT GAAGTTTTAA

This corresponds to the amino acid sequence <SEQ ID 600; ORF 149.a>:

a149.pep  
 1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY  
 51 YNHPLPDLGA HRQTARSFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA  
 101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFGNY  
 151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI  
 201 GVSGDYVRGR LKNLPSLPGR EDAYGNRPLI AQADQNAPRV PAARLGVHLK  
 251 ASLTDRIDAN LDYYRVFAQN KLARYETRTP GHMMLNLGAN YRRNTRYGEW  
 301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF\*

m149/a149 98.8% identity in 339 aa overlap

	10	20	30	40	50	60
m149.pep	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIQYDKALIDRENYNHPLPDLGA					
a149	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPLPDLGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m149.pep	HRQTARSFALSGNWYFTPQHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
a149	HRQTARSFALSGNWYFTPQHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m149.pep	RSNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
a149	RSNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m149.pep	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRKLNPLPGREDAYGNRPFIAQDDQNAPRV					
a149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRKLNPLPGREDAYGNRPLIAQADQNAPRV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m149.pep	PAARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHMMLNLGANYYRRNTRYGEW					

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a149      |||||  |||||ASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEW
          250    260    270    280    290    300

              310    320    330    340
m149.pep  NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
          |||||  |||||
a149      NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
          310    320    330    340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 601>:

**g149-1.seq**

1	ATGGCACAAA	TCACACTCAA	ACCCATTGTT	TTATCAATTC	TTTTAATCAA
51	CACACCCCTC	CTCGCCCAAG	CGCATGAAAC	TGAGCAATCG	GTGGGCTTGG
101	AAACCGGTAC	GTCGTCCGCG	AAAGCCGCTC	CGCGCGCGAC	TCGGGGCTGT
151	CTGCACACTT	CGACCCGCTC	CGCAAAAATC	ATCTCCGGCG	ATACTTTGCG
201	CCAAAAAGCC	GTCAACTTGG	GGCAGCGTTT	GGACGGCGTA	CCGGGCATCC
251	ACGCTTCGCA	ATACGGCGCG	GGCGCATCCG	CTCCCGTTAT	TCGCGGTGAA
301	ACGGGCAGAC	GGATTAAAGT	ATTGAACCAT	CACGGCGAAA	CCGGCGATAT
351	GGCGGACGTT	TCTCCCGATC	ACGCCATTAT	GGTAGATACC	GCCTTGTCGC
401	AACAGGTTGA	AATCTCTGCG	GGGCGGGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GCGTGGTCGA	TGTTGCCGAT	GGAAAAATCC	CGCAAAAAAT
501	GCCTGAAAAC	GGCGTATCGG	GCGAagccgG	ATTGCGTTTG	AGCAGCGGCA
551	ATTTAGAAAA	ACTGACATCC	CGAGGCGATCA	ATATCGGACT	GGGCAAAAAAC
601	TTCTGCTGTC	ATACCGAAGG	CTTGTACCGC	AAATCGGGCG	ATTACCCGCT
651	ACCGCGTTAC	CGCAATCTGA	AACGCCTGCC	CGACAGCCAT	CCCGATTTCG
701	AAACGGGGAG	CATCGGGCTG	TCTTGGGTGG	GCGAAAAAGG	CTTTATCGGC
751	CGACATACAC	GCGACCGCTG	CGACCGCTAC	GGCCTCGCTG	CCCCACAGCCA
801	CGAATACGAT	GATTGCCACG	CGACATCATC	CTGGCAAAAAG	AGGTTTGATCA
851	ACAAACGCTA	TTTGCGAGCTT	TATCCGCACT	TGTTGACCGA	AGAAGACATC
901	GATTACGACA	ATCCGGGCTT	GAGCTCGCGC	TTCACCGACG	GCGACGGGTG
951	ACACGCACAC	ACCCACAACG	CGAAACCGTG	GATAGACCTG	CGCAACAACAC
1001	GCTACGAACT	CCGCGCCGAA	TGGAAGCAGC	CATTCCCCGG	TTTTGAAGCC
1051	CTCGCGGTAC	ATCTGAACCG	CAATGACTAC	CACCACGACG	AAAAAGCAGG
1101	CGATGCAGTA	GAAAACTTCT	CAAGACAACA	AACACACAAC	GCCCGTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGGCAGCTG	GGGCGTGCAA
1201	TATTTGGGAC	AAAAATCCAG	CGCGCTTTCG	GCCATTCCCG	AAACCGTCCA
1251	ACAAACGATG	TTGATTGACA	ACAATCTCCG	CCATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAATTGGGAC	AACTTCACGC	TTGAAGCGCG	CTGTACGGCTG
1351	GAaaaaCAAA	AAGCCTCCAT	CCGGTAGCAG	AAAGCATTTA	TTGATCGAGA
1401	AAACTACTAC	AACACGCCCC	TGCCCGACCT	CGGCGCGCAC	CGCCAAACCG
1451	CCCGCTCGTT	CGCACTTTCG	GGCAACTGGT	ATTTCAGCCG	ACACCAACAA
1501	CTCAGCCTGA	CCGCTTCCCA	TCAGGAACGC	CTGCGCTGAA	CGCAAGAACT
1551	GTACGCACAC	GCGAAGCAGC	TCGCCACCAA	CACCTTTGAA	CTCGGGCAACA
1601	AACACCTCAA	CAAGAGCGGT	TCCAACAATA	TGCAACTTCG	GCTGGGGTCA
1651	GAAGCGCACC	GCTGGCAATA	CAATCTGGCA	GCCTACCGCA	ACCGATTTCG
1701	CAACTACATT	TACGCGCCAA	ACCTTAAACG	CGGACGCGCG	CCCAAAATCCA
1751	TCCAAGACGA	CAGCGAAATG	AAGTCTGTGC	GCTACAACCA	ATCCGGTGCC
1801	GACTTCTACG	GCGCGGAAGG	CGAAATCTAC	TTCAAACCGA	CACCGCGCTA
1851	CCGCACTCGT	GTTTCTGGCG	ACTATGTACG	AGGCCGTCTG	AAAAACCTGC
1901	CGTCCCTATC	CGGCAGGGAA	GATCCCTACG	GCAACCGTCC	CTTCAATCGCA
1951	CAAGCCGACC	AAAACGCCCC	CCGCAATTCC	GCTGGCGGCC	TCGGGTTCCA
2001	CCTGAAAAAC	TCGCTAACCG	ACCGTATCGA	TGCAAAATTG	GACTACTTACC
2051	GCGTGTTCGC	CCAAACACAA	CTCGCCCGCT	ACGAAATTCG	TACGCGCCGGA
2101	CCGCATATGC	TCAACCTCGG	TGCAAACTAC	GCGCCCAATA	CGCGCTATGG
2151	CGAGTGGAAAT	TGCTACGTCA	AAGCGACACAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCGCACG	CAGCTTCTCT	TCTGATACGC	GCGAAATGGG	CCCGACGTTT
2251	ACCGCGCGCG	TAAACGTGAA	GTTTTTAA		

This corresponds to the amino acid sequence <SEQ ID 602; ORF 149-1.ng>:

**g149-1.pap**

1	MAQITLKPIV	LSILLINTPL	LAQAHETEQS	VGLETVSUVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDVG	PGIHASQYGG	GASAPVILRYG
101	TGRIKVLVNH	HGETGDMADF	SPDHAIMVDV	ALSQOQVEILR	GPVTVLLYSSG
151	NVAGLVVDVAD	GKIEPKMPEN	GSFGEAGLRL	SSNGLEKITS	AGINTGLGKN
201	FVLHTEGLYLR	KSGDYAVPEY	RNLKRLPQSH	ADSQGYSIGL	SWVGKEGFTDI
251	AAYSDDRDRY	GLPAHSVEYD	DCHADIIWSH	SILINKRYQL	YPHLLTEETI
301	DYDNPGLSCG	FHDGDGAHAH	THNGKPWDL	RNKRYELRAE	WKQPFPGFEA

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351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVQ
401 YLGQKSSALS AIPETVQQPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA AYRNRFNGYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSPGPRE DPGKRPFFIA
651 QADQNAIPRI AARLGFHLKT SLTDRI DANL DYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.seq

```

1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAAATC ATCTCCGGCG ATACCTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCTG CTCCCGTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAAGT GTTGAACCAT CACGCGGAAA CAGGCGATAT
351 GGCGGATTTT TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTGCGCAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAA GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGAAAAA ACTCACGTCC GCGGCGATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTAC CGCAATCTGA AAGCGCTGCC CGACAGCCAC CCGGATTTCG
701 AAACGGGCGC CATCGGGCTG TCTTGGGTTG GCGAAAAAGG TTTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCGTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAACCGCTA TTTACAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCAGACCG GCAGACCGTG GATAGACCTG CGCAACAAC
1001 GCTACGAACT CCGTGCCGAA TGGAAGCAAC CGTTCGCCGG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCGATC GAAAACTTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCGCCA CCAACCCATA GGTCGTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAC AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTAA
1251 ACAACCGATG CTGCTTGACA ACAAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AACTGGGAC AACTTCACGC TTGAAGGAGG CGTACCGGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AACTACTAC AACCACCCCG TGCCCGACCT CGCGCGCAC CGCCAAACCG
1451 CCGCTCAAT CGCACTTTCG GGCAACTGGT ATTTCAGCC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAACACG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAACTACATT TACGCCCAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GTACAACCA ATCCGGCGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTCCGGCG ACTATGTACG AGGCCGTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGAGAA GATGCCATCG GCAACCGTCC TTTTCATCGCA
1951 CAGGACGACC AAAATGCCCC CCGTGTTCGG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAGGCC TCGCTGACCG ACCGTATCGA TGCCAATTTG GACTACTACC
2051 GCGTGTTCGC CAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACCTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAA TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCTCT TCTGATACGC CGCAAATGGG CCGCAGCTTT
2251 ACCGCGCGCG TGAACGTGAA GTTTTAA

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This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pep

```

1 MAQTTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQQVEILR GPVTLLYSSG
151 NVAGLVVDVAD GKIPEKMPEN GVSSELGLRL SSGNLEKLTS GGINIGLGRN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 VAYSRRRDQY GLPAHSHEYD DCHADIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPGLSGC FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQPPFGFEA
351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVQ
401 YLQKSSALS AISEAVKQPM LLDNKVQHYH FFGVEQANWD NFTLEGGVRV
451 EKQKASIQYD KALIDRENY NHPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

```

551 EGDRAWQYNLA LYRNRFGNYI YAQTINDGRG PKSIEDDSEM KLVRYNQSGA  
601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSPGRE DAYGNRPFIA  
651 QDDQNAPRVP AARLGFLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG  
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF  
751 TGGVNVKF\*

m149-1/g149-1 96.2% identity in 758 aa overlap

	10	20	30	40	50	60
m149-1.pep	MAQTTLKPIVLSILLINTPLLAQAHETEQSV	DLETVSVVGKSRPRATSGLLHTSTASDKI				
g149-1	MAQITLKPIVLSILLINTPLLAQAHETEQSV	GLETVSVVGKSRPRATSGLLHTSTASDKI				
	10	20	30	40	50	60
	70	80	90	100	110	120
m149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGG	SAPVIRGQTGRRIKVLNHHGETGDMADF				
g149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGG	SAPVIRGQTGRRIKVLNHHGETGDMADF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m149-1.pep	SPDHAIMVDTALSQQVEILRGPVTL	LYSSGNVAGLVDVADGKIPEKMPENGVS	GELGLRL			
g149-1	SPDHAIMVDTALSQQVEILRGPVTL	LYSSGNVAGLVDVADGKIPEKMPENGVS	GEAGLRL			
	130	140	150	160	170	180
	190	200	210	220	230	240
m149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYR	KSGDYAVPRYRNLRKLPD	SHADSQTGSIGL			
g149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYR	KSGDYAVPRYRNLRKLPD	SHADSQTGSIGL			
	190	200	210	220	230	240
	250	260	270	280	290	300
m149-1.pep	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDD	CHADIIWQKSLINKRYLQLYPHLLTEEDI				
g149-1	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDD	CHADIIWQKSLINKRYLQLYPHLLTEEDI				
	250	260	270	280	290	300
	310	320	330	340	350	360
m149-1.pep	DYDNPGLSCGFHDDNAHAHTHSGRPWIDLR	NKRYELRAEWKQFPFGFEALRVHLNRNDY				
g149-1	DYDNPGLSCGFHDDNAHAHTHSGRPWIDLR	NKRYELRAEWKQFPFGFEALRVHLNRNDY				
	310	320	330	340	350	360
	370	380	390	400	410	420
m149-1.pep	RHDEKAGDAVENFFNNQTNARIELRHQPIGR	LKSGWGVQYLQKSSALSASEAVKQPM				
g149-1	HHDEKAGDAVENFFNNKTHNARIELRHQPIGR	LKSGWGVQYLQKSSALSAPETVQQPM				
	370	380	390	400	410	420
	430	440	450	460	470	480
m149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVR	VEKQKASIQYDKALIDRENYYNHPLD	LGAH			
g149-1	LIDNNVRHYSFFGVEQANWDNFTLEGGVR	VEKQKASIRYDKALIDRENYYNQPLD	LGAH			
	430	440	450	460	470	480
	490	500	510	520	530	540
m149-1.pep	RQTARSFALSGNWFYTPQHKLSLTASHQER	LPSTQELYAHGKHVATNTFEVGNKHLN	KER			
g149-1	RQTARSFALSGNWFYTPHKKLSLTASHQER	LPSTQELYAHGKHVATNTFEVGNKHLN	KER			
	490	500	510	520	530	540
	550	560	570	580	590	600
m149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYI	YAQTINDGRGPKSIEDDSEM	KLVRYNQSGA			
g149-1	SNNIELALGYEGDRWQYNLAAYRNRFGNYI	YAQTINDGRGPKSIEDDSEM	KLVRYNQSGA			
	550	560	570	580	590	600
	610	620	630	640	650	660
m149-1.pep	DFYGAEGEIIYFKPTPRYRIGVSGDYVRG	RKKNLPSPGREDAYGNRPFIAQDDQNAPR	VP			
g149-1	DFYGAEGEIIYFKPTPRYRIGVSGDYVRG	RKKNLPSPGREDPYGRPFIAQADQNAPR	IP			
	610	620	630	640	650	660

	670	680	690	700	710	720
m149-1.pep	AARLGFLHKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN					
	:	:	:	:	:	:
g149-1	AARLGFLKTSLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN					
	670	680	690	700	710	720
	730	740	750	759		
m149-1.pep	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
g149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 605>:

a149-1.seq

1	ATGGCCACAAA	CTACACTCAA	ACCATTGTGT	TTATCAATTC	TTTTAATCAA
51	CACACCCCTC	CTCTCCCAAG	CGCATGGAAC	TGAGCAATCA	TGGGGCTTGG
101	AAACGGTCAG	CGTCGTCGGC	AAAAGCCGTC	CGCGCGCCAC	TTCGGGGCTG
151	CTGCACACTT	CTACCGCCTC	CGACAAATAC	ATCAGCGGCG	ACACCTTTGC
201	ACAAAAGGCC	GTCAACTTGG	GTGATGCTTT	AGACGGCGTA	CCGGGCATCC
251	ATGCCTCGCA	ATACGGCGGC	GGCGCATCCG	CTCCCGTTAT	TCGCGGTCAA
301	ACAGGCGAGC	GGATTTAAGT	GTTGAACCAT	CAGGGCGAAA	CGGGCGACAT
351	GGCGGACTTC	TTCTCCAGAC	ATGCAATCAT	GCTGGACAGC	GCCTTGTCTG
401	AACAGGTCGA	AATCCTGCGC	GGTCCGGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GGCTGGTCTG	TGTTGCCGAT	GGCAAAATTC	CCGAAAAAAT
501	GCGTGA AAAA	GCGTATCTCG	GCGAACTCGG	ATTGCGTTTC	AGGCAAGCGGA
551	ATCTGGA AAAA	ACTCATCGTC	GGCGGCATCA	ATATCGGTTT	GGGCAAAAAAC
601	TTTGATTATGC	ACACGGAAGG	GCTGTACCGC	AAATCGGGGG	ATTACGCCGT
651	ACCGCGTTAC	CGCAATCTGA	AACGCTCTGC	CGACAGCCAC	CCCGATTCTGC
701	AAACGGGCGAG	CTACGGGCTG	TCTTGGGTTG	CGGAAAAAAG	CTTTATCGGC
751	CGAGCATACA	GGCAGCGTCG	CGACCAATAT	GGTCTGCCTG	CCCACAGCCA
801	CGAATACGAT	GATTGGCCAC	CTCAGCATCAT	CTGGCAAAAG	AGATTTGATTA
851	ACAAAACGCTA	TTTGCAGCTT	TATCGCGACC	TGTTGACCGA	AGAGGACATC
901	GATTACGACA	ATCCGGGCTT	GAGCTGCGGC	TTTCACGACG	ACGATGATGC
951	ACACGCCCAT	CGCCACAACG	CGAAACCTTG	GATAGACCTG	CGCAACAACAC
1001	GCTACGAAC	CGCGGCCGAA	TGGAAGCAAC	CGTTCGCCGC	TTTTGAAGCC
1051	CTGCGCGTAC	ACCTGAACCG	CAACGACTAC	CGCCACGACG	AAAAAGCAGG
1101	CGATGCGAGTA	GAAAACCTTTT	TTAAACRACCA	AACGCAAAAC	CGCCGATATCG
1151	AGTTGCGCCA	CAACACCATTA	GGCGCTCTGA	AAGGCAAGCTG	GGGCGTGCAA
1201	TATTTGGGAC	AAAAATCCAG	TGCTTTATCT	GCCACATCCG	AAGCGGTCAA
1251	ACAACCGATG	CTGCTTGACA	ATAAAGTGCA	ACATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAACTGGGAC	AACTTCACGC	TTGAAGCGCG	CTTACGCGTG
1351	GAAAAACAAA	AAGCCTCCAT	CCGCTACGAC	AAAGCATTGA	TTGATCGGGA
1401	AAACTACTAC	AACCATTTCC	TCCCGCAAGT	CGCGCGGCAC	CGCCAAACCG
1451	CCCGCTCAT	CGCATTTTTG	GGCAACTGTT	ATTTCAACGC	ACCAACAAA
1501	CTCAGCCTGA	CCGCTCCCA	TCAGGAACGC	CTGCCGTCAA	CGCAAGAGCT
1551	GTACGCGAC	GGGAAACAGC	TGCCCACCATA	CACCTTTGAA	GTGGGCAACA
1601	AACACTCAA	CAAGAGCGT	TTCAACRACCA	TCGAACTCGC	CTCGGGCTAC
1651	GAAGGCGACC	GCTGGCAATA	CAATCTGGCA	CTCTACCGCA	ACCGCTTCGG
1701	CAACTACAT	TACGCCCAAA	CCTTAAACGA	CGGACGCGGC	CCCAAAATCCA
1751	TCGAAGACGA	CAGCGAATG	AAGCTCGTGC	GTACAACCA	ATCCGGTTCG
1801	GACTTCTACG	CGCGGGAAGG	CGAAATCTAC	TTCAAACCGA	CACCGCGCTA
1851	CCGCACTCGC	GTTTCGGGCG	ACTATGTACG	AGGCCGTCTG	AAAAACCTGC
1901	CTTCCCTACC	CGGACGGGAA	GACGCCTACG	GCAACCGCCC	ACTCATTTCC
1951	CAAGCGGACC	AAACGCGCCC	TCCGGTTCCG	GCTGCGGCGC	TCGGCGATCA
2001	CCTGAAAGCG	TCGCTGACCG	ACCGCATCGA	TGCCAATTTG	GACTACTACC
2051	GCGTGTTCGC	CCAAAACAAA	CTGCCCCGCT	ACGAAACCGC	CAGCCGCCGA
2101	CACCATATGC	TCAACTCGG	CGCAAACTAC	CGCCGCAATA	CGCGCTATTG
2151	CGAGTGAAT	TGGTAGCTCA	AAGCCGACAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCACAG	CAGCTTCTCT	TCTGTATACG	CGCAAATGGG	CCGCAAGTTT
2251	ACGGCGGGCG	TGAACGTGAA	GTTTTTAA		

This corresponds to the amino acid sequence <SEQ ID 606; ORF 149-1.a>:

a149-1 pep

1	MAQTTLKPIV	LSILLINTPL	LSQAHGTEQS	VGLETVSVVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDGV	PGIHASQYGG	GASAPVIRGO
101	TGRRIKVLNV	HGETGDMADF	SPDHAIMVDS	ALSOQVEILR	GPVTLLYSSG
151	NVAGLVDDVD	GKPEKPMEN	GVSGELGLRL	SSNGNLEKLS	GGINIGLGNK
201	FVLHTEGLYR	KSGDYAVPRY	RNLKRLPDSh	ADSQTSGTGL	SWGGEKGFIG
251	AYASDRDRQD	GLPHASHHEYD	DCHADITWQK	SLINKRYLYL	YPHLLTEEDI
301	DYDNPGLSG	FHDHDDAAHA	AHNKGPIWLD	RNKRYELRAE	WKOPFPGEFA



351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVO  
 401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV  
 451 EKQKASIRYD KALIDRENY NHPLPDLGAH RQTARSFALS GNWYFTPOHK  
 501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY  
 551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA  
 601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DAYGNRPLIA  
 651 QADQNAPRVP AARLGVHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG  
 701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF  
 751 TGGVNVKF\*

a149-1/m149-1 98.0% identity in 758 aa overlap

	10	20	30	40	50	60
a149-1.pep	MAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLET	VS	VVGKSRPRATSGLLHTSTASDKI			
m149-1	MAQTTLKPIVLSILLINTPLLAQAHETEQSV	DLET	VS	VVGKSRPRATSGLLHTSTASDKI		
	10	20	30	40	50	60
a149-1.pep	70	80	90	100	110	120
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
m149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
a149-1.pep	130	140	150	160	170	180
a149-1.pep	SPDHAIMVDSALSQQVEILRGPTLLYSSGNVAGLVVDVADGKIPEKMPENGVSSELGLRL					
m149-1	SPDHAIMVDTALSQQVEILRGPTLLYSSGNVAGLVVDVADGKIPEKMPENGVSSELGLRL					
	130	140	150	160	170	180
a149-1.pep	190	200	210	220	230	240
a149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSTGSGIGL					
m149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSTGSGIGL					
	190	200	210	220	230	240
a149-1.pep	250	260	270	280	290	300
a149-1.pep	SWVGEKGFIGAAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
m149-1	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
a149-1.pep	310	320	330	340	350	360
a149-1.pep	DYDNPGLSGCGFHDDDAHAHNGKPWDLRNKRKYELRAEWKQPFPGFEALRVHLNRNDY					
m149-1	DYDNPGLSGCGFHDDDAHAHNGKPWDLRNKRKYELRAEWKQPFPGFEALRVHLNRNDY					
	310	320	330	340	350	360
a149-1.pep	370	380	390	400	410	420
a149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQYLGQKSSALSATSEAVKQPM					
m149-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQYLGQKSSALSATSEAVKQPM					
	370	380	390	400	410	420
a149-1.pep	430	440	450	460	470	480
a149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPLPDLGAH					
m149-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPLPDLGAH					
	430	440	450	460	470	480
a149-1.pep	490	500	510	520	530	540
a149-1.pep	RQTARSFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
m149-1	RQTARSFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
	490	500	510	520	530	540
a149-1.pep	550	560	570	580	590	600
a149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
m149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
	550	560	570	580	590	600
	610	620	630	640	650	660

a149-1.pep	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPFLIAQADQNAPRVP
m149-1	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPFLIAQDDQNAPRVP
	610 620 630 640 650 660
a149-1.pep	670 680 690 700 710 720
	AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGANYRRNTRYGEWN
m149-1	AARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGANYRRNTRYGEWN
	670 680 690 700 710 720
a149-1.pep	730 740 750 759
	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
m149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
	730 740 750

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

g150.seq (partial)

1	..TACTGCAAGG	CAGACCCCTT	TCCC GCCGCC	CTGCTGGCCA	ATCAGAAAAT
51	CACCGCCCGC	CAATCCGATA	AAGACGTGCG	CCACATCGAA	ATCGATTGTA
101	GCGGTTTCGA	TTTGCACTAC	CTCCCGGGCG	ACGCGCTCGG	CGTTTGGTTT
151	GACAACGATC	CGGCACTGGT	CGGGGAAATC	CTAGACCTGC	TGGGCATCAA
201	TCCGGCAACG	GAAATACAGG	CGGGCGGAAA	AACCTTGCCG	GTTGCCTCCG
251	CACTGTATAT	CCATTTTCGA	CTCACGAAA	ACACCCCGCG	CTTTGTCAAA
301	GGCTATGCCA	CGTTCGCCGA	TAATGACGAA	CTCGACCGTA	TTGCTGCCGA
351	CAACGCCGTT	TTGCAAGGCT	TTGTGCAAG	CACGCCGATT	GCCGGTGTGC
401	TGCACCGCTT	CCCGGCAAAA	CTGACGGCGG	AACAATTCGC	CGGCCTGCTG
451	CGCCCGCTTG	CGCCGCGCCT	GTATTCGATT	TCCTCGTCGC	AGGCGGAAGC
501	GGGGGACGAA	GTGCACCTGA	CCGTGCGCGC	AGTGCGTTTC	GAACACGAAG
551	GGCGCGCCAG	GGCGGGCGGC	GCATCGGGTT	TCTTTGCCGA	CCGGCTGGAA
601	GAGGACGGCA	CGGTGCGCGT	GTTTGCGGAA	CGCAACGACG	GCTTCAGGCT
651	GCCCGAAGAC	AGCCGCAAGC	CGATTGTGAT	GATCGGCTCC	GGTACCGGCG
701	TCGCACCGTT	CCGCGCCTTC	GTCCAACAAC	GTGCCGCAGA	AAATGCGGAA
751	GGCAGAAACT	GGCTGATTTT	CGGCAATCCG	CATTTTGCCG	CCGACTTCCT
801	CTATCAGACC	GAATGGCAGC	AGTTTGCCAA	AGACGGCTTC	CTGCACAGAT
851	ATGACTTCGC	CTGGTCGCGC	GATCAGGAAG	AAAAAATCTA	TGTGCAGGAC
901	AAAATCCGCG	AACAGGCGGA	AGGACTTTGG	CAATGGCTGC	AGGAAGGCGC
951	GCATATCTAT	GTGTGCGGCG	ATGCGGCAAA	AATGGCAAAA	GAAGTGAAG
1001	CCGCCTTGCT	GGATGTGATT	ATCGGGCAG	GGCATTGCGA	CGAAGACGGC
1051	GCAGAAGGAT	ATTTGGATAT	GCTGCGCGAA	GAAAAACGCT	ATCAGCGTGA
1101	TGTTTATTGA				

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

g150.pep (partial)

1	..YCKADFPFAA	LLANQKITAR	QSDKDVRHIE	IDLSGSDLHY	LPGDALGVWF
51	DNDPALVGEI	LDLLGINPAT	EIQAGGKTLF	VASALLSHFE	LTQNTPAFVK
101	GYATFADNDE	LDRIAADNAV	LQGFVQSTPI	AGVLHRFPK	LTAEQFAGLL
151	RPLAPRLYSI	SSSQAEAGDE	VHLTVGAVRF	EHEGRARAGG	ASGFFADRLE
201	EDGTVRVFAE	RNDGFRLPED	SRKPIVMIGS	GTGVAPFRAF	VQQRAAENAE
251	GRNWLI FGNP	HFAADFLYQT	EWQQFAKDF	LHRYDFAWSR	DQEEKIYVQD
301	KIREQAEGW	QWLQEGAHY	VCGDAAKMAK	EVEAALLDVI	IGAGHSDEDEG
351	AEGYLDMLRE	EKRYQRDVY*			

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

m150.seq

1	ATGCAGAACA	CAAATCCGCC	ATTACCGCCT	CTGCCGCCCG	AAATCACGCA
51	GCTCCTGTCG	GGGCTGGACG	CGGCACAATG	GGCGTGGCTG	TCCGGCTACG
101	CTTGCGGCAA	AGCAGGAAAC	GGGGCATCTG	CAGGACTGCC	CGCGCTTCAG
151	ACGGCATTGC	CGGCGGCGA	ACCTTTTTC	GTAACCGTCC	TTTCCGCCTC
201	GCAAACCGGC	AATGCGAAAT	CCGTTGCCGA	CAAAGCGGCG	GACAGCCTGG
251	AAGCCGCCCG	CATCCAAGTC	AGTCGCGCCG	AACTGAAAGA	CTATAAGGCG
301	AAAAACATCG	CCGGCGAACG	CGCCTGCTG	CTGGTTACCT	CCACCCAAGG
351	CGAAGGCGAA	CCGCCGAAAG	AAGCCGTCGT	GCTGCACAAA	CTGCTGAACG
401	GCAAAAAAGC	CCCGAAATTG	GACAACTCC	AATTTGCCGT	ACTGGGTTTG

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451 GCGGACAGTT CCTATCCGAA TTTCTGTCAG GCAGGTAAAG ATTTGACCG
501 GCGTTTTGAA GAATTGGGCG CAAAACGGCT GCTCGAACGC GTTGATGCGG
551 ATTTGGACTT TACCGCCTCC GCAAACGCCT GGACAGATAA TATCGCCGCA
601 CTCTTAAAG AAGAGCCGC AAAAAACCGG GCAACGCCCG CGCCGAGAC
651 AACGCCCCC GCCGGCCTTC AGACGGCACC GGATGGCAGG TACTGCAAGG
701 CAGCCCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT CACCGCCCGC
751 CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGGA GCGGTTTCGGA
801 TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT GACAACGATC
851 CGGCACTGGT CAGGGAAATC CTAGACCTGC TCGGCATCGA TCCGGCAACG
901 GAAATACAGG CGGGCGGAAA GATGATGCCG GTTGC GCGCG CACTTTCATC
951 TCATTTTCGAA CTCACGCAAA AACTCCGGC TTTCTGCAAA GGCTATGCCG
1001 CGTTCGCCCCA TTATGAAGAA CTCGATAAAA TCATTGCCGA TAACGCCGTT
1051 TTGCAGGATT TCGTGCAAAA CACGCCTATT GTCGATGTGC TGCACCGCTT
1101 CCCGGCAAGC CTGACGGCAG AACAATTCAT CCGTTTACTG CGTCCGCTTG
1151 CACCCCGTTT GTATTTCGATT TCTTCAGCAC AGGCGGAAGT GGGCGATGAA
1201 GTGCATTTAA CTGTCGGCGT GGTTTCGTTT GAACACGAAG GCCGCGCCAG
1251 AACGGGCGGC GCATCGGGTT TCCTTGCCGA CCGGCTGGAA GAGGACGGCA
1301 CGGTGCGCGT GTTTGTGGAA CGCAACGACG GCTTCAGGCT GCCCGAAGAC
1351 AGCCGCAAGC CGATTGTGAT GATCGGCTCG GGCACCGCGC TCGCACCGTT
1401 CCGCGCTTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA GGCAAAAATC
1451 GGCTGATTTT CGGCAATCCG CATTTTGCCC GTGATTTTCT CTATCAAACC
1501 GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGGT ACGATTTCGC
1551 CTGGTCCCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC AAAATCCGCG
1601 AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC GCATATCTAT
1651 GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GACGTGGAAG CCGCCTTGCT
1701 GGATGTGATT ATCGGGGCAG GACATTTGGA CGAAGAGGGC GCAGAAGAAT
1751 ATTTGGATAT GCTGCGCGAA GAAAACGCT ATCAGCGTGA TGTTTATTGA

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This corresponds to the amino acid sequence <SEQ ID 610; ORF 150>:

m150.pep

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1  MQNTNPPLPP LPPETIQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
51  TALPAAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
101 KNIAGERLL LVTSTQGEGE PPKEAVVLHK LLNGKKAPKL DKLQFAVLGL
151 GDSSYPNFCQ AGKDFDRRFE ELGAKRLLER VDADLDFTAS ANAWTDNIAA
201 LLKEEAAKNR ATPAPQTTTP AGLQTAPDGR YCKAAPFPAA LLANQKITAR
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDPAT
301 EIQAGGKMP VARALSSHFE LTQNTPAFVK GYAAFAHYEE LDKIIADNAV
351 LQDFVQNTPI VDLHRFPAS LTAEQFIRLL RPLAPRLYSI SSAQAEVGDE
401 VHLTVGVVRF EHEGRARTGG ASGFLADRL EEDGTVRVFVE RNDGFRLPED
451 SRKPIVMIGS GTGVAPFRAF VQQRAAENAE GKNWLI FGNP HFARDFLYQT
501 EWQQFAKDF LHYRDFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHY
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 150 shows 91.3% identity over a 369 aa overlap with a predicted ORF (ORF 150.ng) from *N. gonorrhoeae*:

m150/g150

	210	220	230	240	250	260
m150.pep	LLKEEAAKNRATPAPQTTTPAGLQTAPDGRYCKAAPFPAA LLANQKITARQSDKDVRHIE					
g150	YCKADFPFAALLANQKITARQSDKDVRHIE					
				10	20	30
	270	280	290	300	310	320
m150.pep	IDLSGSDLHYLPGDALGVWFDNDPALVREILDLLGIDPAT EIQAGGKMPVARALSSHFE					
g150	:					
	40	50	60	70	80	90
	330	340	350	360	370	380
m150.pep	LTQNTPAFVKGYAAFAHYEELDKIIADNAV LQDFVQNTPIVDLHRFPASLTAEQFIRLL					

	:     :
g150	LTQNTPAFVKGYATFADNDELDRIAADNAVLQGFGVQSTPIAGVLHRFPKLTAEQFAGLL
	100 110 120 130 140 150
	390 400 410 420 430 440
m150.pep	RPLAPRLYSISSAQAEVGDEVHLLTVGVVRFEHEGRARTGGASGFLADRLEEDGTVRVFVE
	:     :     :
g150	RPLAPRLYSISSSQAEAGDEVHLLTVGAVRFEHEGRARAGGASGFADLRLEEDGTVRVFAE
	160 170 180 190 200 210
	450 460 470 480 490 500
m150.pep	RNDGFRLPEDSRKPIMIGSGTGVAPFRAFVQQRAAENAEGKNWLIFGNPHFADFPLYQT
g150	RNDGFRLPEDSRKPIMIGSGTGVAPFRAFVQQRAAENAEGRNWLI FGNPHFAADFLYQT
	220 230 240 250 260 270
	510 520 530 540 550 560
m150.pep	EWQQFAKDGLFHLRYDFAWSRDQEEKIYVQDKIREQAEGLWQWLQEGAHIYVCGDAAKMAK
g150	EWQQFAKDGLFHLRYDFAWSRDQEEKIYVQDKIREQAEGLWQWLQEGAHIYVCGDAAKMAK
	280 290 300 310 320 330
	570 580 590 600
m150.pep	DVEAALLDVII GAGHLDEEGAE EYL DMLREEKRYQRDVYX
	:
g150	EVEAALLDVII GAGHSDEDGAEGYLDMLREEKRYQRDVYX
	340 350 360 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 611>:

```

a150.seq
1    ATGCAGAACA CAAATCCGCC ATTACGCCT ATGCCGCCCG AAATCACGCA
51   GCTCTGTGTC GGGCTGGACG CGGCACAATG GGCCTGGCTG TCCGGCTACG
101  CTTCCGGCAA AGGCAGAAAG AGGCGCATCT GAGCATGTCC CGCGCTTACG
151  ACGGCATTGC  CGACGGCAGA ACCTTTTTCG GTAACCGTCC TTTCCGCCTC
201  GCAAACCGGC  AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251  AAGCCGCGCG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301  AAAAAACATCG CCGCGCAAGC CCGCTGTGCT CTGGTTACCT CCACCCAAGG
351  CGAAGGCGAA  CGCGCGGAAG AAGCCGTCTG CTGTCACAAA CTGCTGAACG
401  GCAAAAAAGC  CCCGAAATTG GACAAACTCC AATTTGCCGT ACTGGGTTTG
451  GGCACAGACT  CCTATCCGAA TTTCTGCCGG GCGGGCAAAG ATTTTCGACAA
501  ACGTTTTGAA  GAATTTGGCG CAAAACGCCT GCTCGAACGC GTTGATGCGG
551  ATTTGGACTT  TGCCGCGCCG GCAGACGGAT GGACAGATAA TATCGCCGCA
601  CTCTTAAAG  AAGAAGCCGC AAAAAACCGG GCAACGCCCC CGCCGCAGAC
651  AACGCCCCCC  GCCGGCCTTC AGACGCCACC GGATGGCAGG TACTGCAAGG
701  CAGACCCTTT  TCCCGCCGCG CTGCTGGCCA ATCAGAAAT  CACCGCCCGC
751  CAATCCGATA  AAGAGTGGC  CCACATCGAA ATCGATTTGA GCGGTTCCGA
801  TTTGCACTAC  CTCCCGGGCG ACGCGTCTGG CTGTTGGTTT GACAACGATC
851  CGGCACTGGT  CAGGGAAATC CTAGACCTGC TCGGCATCGA TCAGGCAACG
901  GAAATACAGG  CGGGCGGAAA AACCCTGCCG GTTGCTTCCG CACTGTTATC
951  CGATTTTGA  CTACGCAAAA ACACCCCCCG CTTTGTCAAA GGCTATGCCC
1001 CATTTCGCCG  TGATGACGAA CTGACCCGTA TTGCTGCCGA CAACCGCGTT
1051 TTGCAAGGCT  TTGTGCAAAG CACGCCGATT GCCGATGTGC TGCACCCTT
1101 CCCGGCAAAA  CTGACAGCGG AACAATTGCG CGGCCTACTG CGCCCGCTTG
1151 CGCCCGCCTT  GTATTGCAAT TCCTCGTTCG AGGCGGAAGT GGGGACGCAA
1201 GTGCAGCTGA  CCGTCGCGCG GGTGCGTTTC GAACACGAAG GCGCGCCGAG
1251 GCGGGGCGGC  GCATCGGGTT TCCTTGCCGA CCGGCTGGAA GAGGACGGCA
1301 CGGTGCGCGT  GTTTGTGGAA CGCAACGACG GCTTCAGGCT GCCCGAAGAC
1351 AGCCGCAAGC  CGATTGTGAT GATCGGCTCG GGCACCGGCG TCGCACCGTT
1401 CCGCGCTTTC  GTCCAACAAC GTCCGCGAAG AAATCGCGAA GGCAAAACT
1451 GGCTGTTTTT  CGGCAATCCG CATTTTGCCC GTGATTTTCT CTATCAAAC
1501 GAATGGCAGC  AGTTTGCCAA AGACGGCTTC CTGCACAGAT ACGATTTGCG
1551 CTGCTGCGCG  GATCAGGAAG AAAAAATCTA TGTGCAGGAC AAAATCCGCG
1601 AACAGCGCGA  AGGACTTTGG CAATGGCTGC AGGAAGGCGC GCATATCTAT
1651 GTGTGGCGCG  ATCGCGCAAA ATGGCAAAA  GACGTGGAAG CGCCCTTGCT

```

1701 GGATGTGATT ATCGGGGCAG GACATTGGA CGAAGAGGC GCAGAAGAAT  
1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTTTATTGA

This corresponds to the amino acid sequence <SEQ ID 612; ORF 150.a>:

a150.pep  
1 MQNTNPPLPP MPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ  
51 TALPTAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA  
101 KNIAGERRLL LVTSTQGEGE PPEEAVVLHK LLNGKKAPKL DKLQFAVLGL  
151 GDSSYPNFCR AGKDFDKRFE ELGAKRLLER VDADLDFAAA ADGWTDNIAA  
201 LLKEEAAKNR ATPAPQTPP AGLQTAPDGR YCKADFPFAA LLANQKITAR  
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDQAT  
301 EIQAGGKTLF VASALLSHFE LTQNTPAFVK GYAPFADDDE LDRIAADNAV  
351 LQGFVQSTPI ADVLHRFPK LTAEQFAGLL RPLAPRLYSI SSSQAEVGDE  
401 VHLTVGAVRF EHEGRARAGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED  
451 SRKPIVMIGS GTGVAFPPRA VQRAAENAE GKNWLFFGNP HFARDFLYQT  
501 EWQQFAKDG LHRDYFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHY  
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY\*

m150/a150 94.8% identity in 599 aa overlap

m150.pep	10	20	30	40	50	60
	MQNTNPPLPPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQ	TALPTAEPFS				
a150	10	20	30	40	50	60
	MQNTNPPLPPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQ	TALPTAEPFS				
m150.pep	70	80	90	100	110	120
	VTVLSASQTGNAKSVADKAAADSLEAAGIQVSRAELKDYKAKNIAGERRLL	VTVLSASQTGNAKSVADKAAADSLEAAGIQVSRAELKDYKAKNIAGERRLL				
a150	70	80	90	100	110	120
	VTVLSASQTGNAKSVADKAAADSLEAAGIQVSRAELKDYKAKNIAGERRLL	VTVLSASQTGNAKSVADKAAADSLEAAGIQVSRAELKDYKAKNIAGERRLL				
m150.pep	130	140	150	160	170	180
	PPKEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCQAGKDFDRREEL	PPKEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCQAGKDFDRREEL				
a150	130	140	150	160	170	180
	PPKEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCQAGKDFDRREEL	PPKEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCQAGKDFDRREEL				
m150.pep	190	200	210	220	230	240
	VDADLDFASANAWTDNIAALLKEEAAKNRATPAPQTPPAGLQTAPDGRYCKA	VDADLDFASANAWTDNIAALLKEEAAKNRATPAPQTPPAGLQTAPDGRYCKA				
a150	190	200	210	220	230	240
	VDADLDFASANAWTDNIAALLKEEAAKNRATPAPQTPPAGLQTAPDGRYCKA	VDADLDFASANAWTDNIAALLKEEAAKNRATPAPQTPPAGLQTAPDGRYCKA				
m150.pep	250	260	270	280	290	300
	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI				
a150	250	260	270	280	290	300
	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI				
m150.pep	310	320	330	340	350	360
	EIQAGGKMPVARALSSHFELTQNTPAFVKGYAAFAHYEELDKIADNAVLQ	EIQAGGKMPVARALSSHFELTQNTPAFVKGYAAFAHYEELDKIADNAVLQ				
a150	310	320	330	340	350	360
	EIQAGGKMPVARALSSHFELTQNTPAFVKGYAAFAHYEELDKIADNAVLQ	EIQAGGKMPVARALSSHFELTQNTPAFVKGYAAFAHYEELDKIADNAVLQ				
m150.pep	370	380	390	400	410	420
	VDVLRFPASLTAEQFIRLLRPLAPRLYISSAQAEVGDEVHVTGVRFEHEGR	VDVLRFPASLTAEQFIRLLRPLAPRLYISSAQAEVGDEVHVTGVRFEHEGR				
a150	370	380	390	400	410	420
	VDVLRFPASLTAEQFIRLLRPLAPRLYISSAQAEVGDEVHVTGVRFEHEGR	VDVLRFPASLTAEQFIRLLRPLAPRLYISSAQAEVGDEVHVTGVRFEHEGR				
m150.pep	430	440	450	460	470	480
	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAVQ	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAVQ				
a150	430	440	450	460	470	480
	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAVQ	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAVQ				
m150.pep	490	500	510	520	530	540
	GKNWLIFGNPHFARDFLYQTEWQQFAKDGFLHRYDFAWSRDQEEKIYVQD	GKNWLIFGNPHFARDFLYQTEWQQFAKDGFLHRYDFAWSRDQEEKIYVQD				
a150	490	500	510	520	530	540
	GKNWLIFGNPHFARDFLYQTEWQQFAKDGFLHRYDFAWSRDQEEKIYVQD	GKNWLIFGNPHFARDFLYQTEWQQFAKDGFLHRYDFAWSRDQEEKIYVQD				

```

a150      GKNWLF FGNPHF ARDFLY QT EWQQ FAKD GFLHRY DFAWSR DQEEKI YVQDKI REQA EGLW
           490      500      510      520      530      540

           550      560      570      580      590      600
m150.pep  QWLQEGAH IYVCGDAAKMAKDVEAALLDVII GAGHLDEEGAE EYLDML REEKRYQRDVYX
           |||||
a150      QWLQEGAH IYVCGDAAKMAKDVEAALLDVII GAGHLDEEGAE EYLDML REEKRYQRDVYX
           550      560      570      580      590      600

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 613>:

g151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCACACGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGA AAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT AC GAAGGCTG
201 CCACATCAAT ATCGTCGACA CGCGGGGACA CGCCGACTTC GCGGGCGAAG
251 TGGAGCGCGT TTGGGGGATG GTGGATTGCG TCGTCTTGTT GGTGGACGCA
301 CAGGAAGGTC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGCG
351 TTGGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAACCGTCCG
401 CCCGTCCGAG CTGGGTTATC GACCAGACTT TCGAGTTGTT CGACA ACTTG
451 GGTGCGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTACG CTTCAGGTTT
501 GAGCGGCTTT GCCAAGCTGG AAGAAAccga CGAGAGCAGC GATATGCGCC
551 CGCtggttcgA CACCATCCTA AAATACAcgc ctgCACCGAG CGGCAGCGCG
601 GACGAGCCGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTGATGAAC CACGAGCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGCTTGGA CCGTGCCGC TTGAAGAAGC
801 CGAAGCCGCG GACATTGTGA TTATTTCCGG TATCGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCA AAGGCCTGCC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTAAACA CCAGCCCGCT
951 CGCAGGTACA GAAGGCAAT TCGTGACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTTGCCC TGCGCGTGGA AGACACCGCC
1051 GatgCCGACG TGTTCCGCGT ATCcgGGCGC GGCGAACTGC ACCTGACGAT
1101 TTTGCTGGAA AATATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAGC
1151 CGCGCGTCGT GTACCGAGAC ATCGACGGTC AAAATGCGA ACCTTATGAA
1201 AACCTGACTG TGACGTACc cgacgacAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACCAA TATGGAAAGC GACGGCAACG
1301 GacgCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGGCGAAT TCATGACCCT GACGCGCGGC GTCGGGCTGA TGAgccacGT
1401 GTTcgacgac tacgcgcccg tcaAACCCGA TATGCCCGGC CGCCACAACG
1451 GCGTactggt GtcccaAGAG CAGGGCGAGG CGGTTGCTTA CGCCTTGTTG
1501 AATCTTGAAG ACCGCGGCCG TATGTTGTA TCGCCCAACG ACAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGCCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTCACCAATA TCCGTGCCAG CGGTACCGAC
1651 GAAGCGGTGC GCCTGACCAC GCCGATCAAA CTGAcgcTGG AAGGCGCGGT
1701 CGAGTTTATC GACGATGACG AGCTGGTGGA AATCAGCCG CAAtccatcc
1751 gcctgcgcat gcgttacctG AGCGaattgg aacgccgccg tcaTTTTAA
1801 AagctgGATT AA

```

This corresponds to the amino acid sequence <SEQ ID 614; ORF 151.ng>:

g151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGCHIN IVDTPGHADF GGEVERVLGM VDCVLLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESS DMRPLFDTL KYTPAPSGSA
201 DEPLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HEQQIAQGRI
251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDPDDN QGAVMEELGR RRGELTNMES DGNRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVFD D YAPVKPDM PG RHNGVLVSQE QGEAVAYALW

```

501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD  
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMYL SELERRRHF  
 601 KLD\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 615>:

m151.seq  
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTCG ACCACGGCAA  
 51 AACACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA  
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA  
 151 CGCGGCATCA CCATCCTCGC CAAAACACC GCCATCGATT ACGAAGGCTA  
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG  
 251 TAGAGCGCGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG  
 301 CAGGAAGGCC CGATGCCGCA AACCCTTTC GTGACCAAAA AAGCCTTGGC  
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAGCCGTCCG  
 401 CTCGTCCGAG CTGGGTATC GACCAAACCT TCGAGCTGTT CGACAACTTG  
 451 GGCGCGACCG ACGAGCAGTT GGATTTCCTG ATTGTTTACG CTTCAGGGTT  
 501 GAGCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC  
 551 CGCTGTTTCA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG  
 601 GACGAAACGC TGCAACTGCA AATTTCCTCA CTCGACTACG ACAACTACAC  
 651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC  
 701 AAACCGTTGC CGTCATGAAC CACGATCAGC AAATCGCCCA AGGCCGCATC  
 751 AACAGCTTT TGGGTTTCAA AGGTTTGGA CGCGTGCCGC TTGAAGAAGC  
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATCGAAGAC ATCGGTATCG  
 851 GCGTAACCAT CACCGACAAA GACAAATCCA AAGGCCTACC GATGTTGAGC  
 901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGCT  
 951 GGCGGGTACG GAAGGCAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC  
 1001 TGCAAAAAGA ATTGCTGACC AACGTGCGCC TGCGCGTGGA AGATACCGCC  
 1051 GATGCCGACG TGTTCGCGT ATCCGGGCGC GCGGAGCTGC ACCTGACCAT  
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAC  
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAAATGCGA ACCGTATGAA  
 1201 AACCTGACCG TGGATGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA  
 1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAGC GACGGCAACG  
 1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC  
 1351 CAAGGCGAAT TTATGACCTT GACGCGCGG GTCGGGCTGA TGAGCCACGT  
 1401 GTTCCAGCAT TACGCGCCCG TCAAACCCGA TATGCCCGGC CGCCACAACG  
 1451 GCGTGCTGGT GTCCCAAGAG CAGGCGGAGG CAGTCGCTTA CGCCTTGTTG  
 1501 AATCTGGAAG ACCGCGGCCG TATGTTGTA TCGCCCAACG ACAAATCTA  
 1551 CGAAGGCATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA  
 1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC  
 1651 GAAGCCGTTT GCCTGACCAC GCCAATCAAG CTGACGCTGG AAGGTGCGGT  
 1701 TGAGTTTATC GACGATGACG AACTCGTTGA AATCAGCCCG CAATCCATCC  
 1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCGCCCG CCACTTTAAA  
 1801 AAGCTGGATT GA

This corresponds to the amino acid sequence <SEQ ID 616; ORF 151>:

m151.pep  
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE  
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLLVDA  
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL  
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDLIL KYTPAPSGSA  
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HDQQIAQGRI  
 251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IIGIVTITDK DNPKGLPMLS  
 301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDLRLQKELLT NVALRVEDTA  
 351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE  
 401 NLTVDPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF  
 451 QGEFMTLTRG VGLMSHVDDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW  
 501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD  
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHF  
 601 KLD\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

m151.pep	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT					
g151	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT					
m151.pep	70	80	90	100	110	120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
g151	70	80	90	100	110	120
	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
m151.pep	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFLFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN					
g151	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFLFDNLGATDEQLDFPIVYASGLSGFAKLEETDESS					
m151.pep	190	200	210	220	230	240
	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
g151	190	200	210	220	230	240
	DMRPLFDITILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
m151.pep	250	260	270	280	290	300
	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
g151	250	260	270	280	290	300
	HEQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
m151.pep	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
g151	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
m151.pep	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQAVMEELGR					
g151	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQAVMEELGR					
m151.pep	430	440	450	460	470	480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
g151	430	440	450	460	470	480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
m151.pep	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
g151	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
m151.pep	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					



m151.pep      KLDX  
                  ||||  
 g151            KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

```
a151.seq
1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGA AAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
301 CAGGAAGGCC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGGC
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAAATCGAC AAACCGTCCG
401 CCCGTCGAG CTGGGTCATC GACCAAACTT TCGAGCTGTT CGACAACTTG
451 GGCGCGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTATG CTTCCGGTCT
501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
551 CGCTGTTCGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
601 GACGAAACGC TGCAACTGCA AATTTCCTCA CTGACTACG ACAACTACAC
651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC
701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGATC
751 AACCAGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATTGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGTT
951 GGCAGGTACG GAAGGCAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGGA AGATACCGCC
1051 GATGCCGACG TGTTCGCGT ATCCGGGCGC GGCGAGCTGC ACCTGACCAT
1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAGC GACGGCAACG
1301 GACGCACCGC CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGCTTC
1351 CAAGGCGAAT TTATGACCCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCTGGC CGCCACAACG
1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTGG
1501 AATCTGGAAG ACCGCGGCCG TATGTTTCGTA TCGCCCAACG ACAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
1651 GAAGCCGTTT GCCTGACCAC GCCGATTAAG CTGACGCTGG AAGGTGCGGT
1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCACGCCG CAATCCATCC
1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCATTTCAAA
1801 AAGCTAGATT GA
```

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

```
a151.pep
1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDLIL KYTPAPSGSA
201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQIAQGRI
251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGPLMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVFDY YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD
551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK
601 KLD*
```

m151/a151 99.8% identity in 603 aa overlap

10 20 30 40 50 60

m151.pep	MKQIRNIAIIAHVDHGKTTLV	DQLLRQSGTFRANQQVDERV	MSNDLEKERGITILAKNT
a151	MKQIRNIAIIAHVDHGKTTLV	DQLLRQSGTFRANQQVDERV	MSNDLEKERGITILAKNT
	10 20 30 40 50 60		
m151.pep	AIDYEGYHINIVDTPGHADFG	GEVERVLGMVDCVLLVDAQ	EGPMPQTRFVTKKALALGL
a151	AIDYEGYHINIVDTPGHADFG	GEVERVLGMVDCVLLVDAQ	EGPMPQTRFVTKKALALGL
	70 80 90 100 110 120		
m151.pep	KPIVVINKIDKPSARPSWVIDQ	TFFELFDNLGATDEQLDFPI	VYASGLSGFAKLEETDES
a151	KPIVVINKIDKPSARPSWVIDQ	TFFELFDNLGATDEQLDFPI	VYASGLSGFAKLEETDES
	130 140 150 160 170 180		
m151.pep	DMRPLFDITILKYTPAPSGSA	DETLQLQISOLDYDNYTGRL	GIGRILNGRIKPGQTVAVMN
a151	DMRPLFDITILKYTPAPSGSA	DETLQLQISOLDYDNYTGRL	GIGRILNGRIKPGQTVAVMN
	190 200 210 220 230 240		
m151.pep	HDQQIAQGRINQLLGFKGLER	VPLEEAEAGDIVIISGIEDI	GIGVTITDKDNPKGLPMLS
a151	HDQQIAQGRINQLLGFKGLER	VPLEEAEAGDIVIISGIEDI	GIGVTITDKDNPKGLPMLS
	250 260 270 280 290 300		
m151.pep	VDEPTLTMDFMVNTSPLAGTE	GKFVTSRQIRDLQKELLTN	VALRVEDTADADVFRVSGR
a151	VDEPTLTMDFMVNTSPLAGTE	GKFVTSRQIRDLQKELLTN	VALRVEDTADADVFRVSGR
	310 320 330 340 350 360		
m151.pep	GELHLTILLENMRREGYELAV	GKPRVYRDI	DGQKCEPYENLTVDVPDDN
a151	GELHLTILLENMRREGYELAV	GKPRVYRDI	DGQKCEPYENLTVDVPDDN
	370 380 390 400 410 420		
m151.pep	RRGELTNMESDGNRTRLEYHI	PARGLIGFQGEFMTLTRGV	GLMSHVFDYAPVKPDMPG
a151	RRGELTNMESDGNRTRLEYHI	PARGLIGFQGEFMTLTRGV	GLMSHVFDYAPVKPDMPG
	430 440 450 460 470 480		
m151.pep	RHNGVLVSQEQGEAVAYALW	NLEDGRMFVSPNDKIYEGMI	IIGIHSRDNDLVNPLKGKK
a151	RHNGVLVSQEQGEAVAYALW	NLEDGRMFVSPNDKIYEGMI	IIGIHSRDNDLVNPLKGKK
	490 500 510 520 530 540		
m151.pep	LTNIRASGTDEAVRLTTPIKL	TLEGAVEFIDDELVEITPQS	IRLKRKRYLSELERRRHFK
a151	LTNIRASGTDEAVRLTTPIKL	TLEGAVEFIDDELVEITPQS	IRLKRKRYLSELERRRHFK
	550 560 570 580 590 600		
m151.pep	KLDX		
a151	KLDX		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAAaca aaACCaaagt ctgGGacttc cCacccgcc ttTCCactG
51  GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGGTCG GGCTGCTCGT CCTTTTCCTG

```

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```

151 CTCGTATTCC GCCTCTGCTG GGGCATTGG GGCagcgATA CCGCCCGTTT
201 CTCccgTtTC GTCCGAGGTT GGGCAGGTAT ACGCGGCTAT CTGAAAAAcg
251 gCATTCCCGA ACAtatcCAG CCCGGACACA ACCCCTTGGG CGCACTgatg
301 gtcGTTGCGC TTTTGgcccgc cgteTCATTT CAagtcggcA CGGGGCTTTT
351 Tgccgccaat gaaaacacct tcagcaCCAA cggctacctc aaccatttgg
401 tttccgaaca tacgGGCAGC CTTATACGGA AAATCCACCT CAACTTTTTC
451 AAGTGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCATATTC AAAAAGAAAA ACCTCGTCCG CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 620; ORF 152.ng>:

g152.pep

```

1 MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KAGGDMQWH TRVGLLVFLF
51 LVFRLCWGIW GSDTARFSRF VRGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAN ENTFTNGYL NHLVSEHTGS LIRKIHLNFF
151 KLLAVFSAVH IAAVAAYRIF KKKNLVRPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 621>:

m152.seq

```

1 ATGAAAAACA AAACCAAGT CTGGGACCTC CCCACCCGCC TTTTCCACTG
51 GCTGCTTGCC GCGTCCCTGC CCTTTATGTG GTATAGCGCG AAAGCCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTCGT CCTTTTCTTG
151 CTCGTATTTC GCCTCTGCTG GGGCATTGG GGCAGCGATA CCGCCCGTTT
201 TTCCCGTTTC GTCCAAGGCT GGGCAGGCAT ACGCGGCTAT CTGAAAAACG
251 GTATTCCCGA ACACATCCAG CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGCCCGC CGTGTCCTTC CAAGTCGGCA CCGGGCTTTT
351 TGCCGCCGAT GAAAACACCT TCAGCACCAA CGGCTACCTC AACCATTGCG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCACCT CAACTTTTTC
451 AAGTGCTCG CCGTTTTTTC TGCAATCCAC ATCGCCGCCG TCGCCGCATA
501 CCGGTATTC AAAAAGAAAA ACCTCATCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCAGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CTCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 622; ORF 152>:

m152.pep

```

1 MKNKTKVWDL PTRLFHWLLA ASLPFMWYSA KAGGDMQWH TRVGLFVLFL
51 LVFRLCWGIW GSDTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD ENTFTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAIH IAAVAAYRVF KKKNLILPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVASLA AAAILLLS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/g152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTTRLFWLLAASLPFMWYSAKAGGDMQWHTRVGLFVLFLLVFRLCWGIW					
	:     :     :     :     :					
g152	MKNKTKVWDFPTTRLFWLLAASLPFMWYSAKAGGDMQWHTRVGLLVFLFLVRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:     :     :     :     :					
g152	GSDTARFSRFVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAIHIAAAYAAYRVFKKNLILPMI					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFSAVHIAAAYAAYRIFKKNLVRPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

a152.seq

1	ATGAAAAACA	AAACCAAGT	CTGGGACTTC	CCCACCCGCC	TTTTCCACTG
51	GCTGCTTGCC	GCATCCCTAC	CCTTTATGTG	GTATAGCGCG	AAAACCGGCG
101	GCGATATGCT	GCAATGGCAC	ACGCGCGTCG	GGCTGTTTAT	CCTTTTCCTG
151	CTCGTATTCC	GCCTCTGCTG	GGGCATTTGG	GGCAGCGATA	CCGCCCGTTT
201	CTCCCGTTTC	GTCCGCGGAT	GGTCGGGTAT	CAGAGAGTAT	ATGAAAAACG
251	GTATTCCCGA	ACACGTCCAA	CCCGGACACA	ACCCCTTGGG	CGCACTGATG
301	GTCGTTGCGC	TTTTGGCCGC	CGTGTGCTTC	CAAGTCGGCA	CAGGGCTTTT
351	TGCCGCCGAT	GTAAACACCT	TCAGCACCAA	CGGCTACCTC	AACCATTGCG
401	TTTCCGAACA	TACGGGCAGC	CTTATGCGGA	AAATCCATCT	CAACTTTTTC
451	AAACTGCTCG	CCGTTTTTTC	CGCAGTCCAC	ATCGCCGNCG	TCGCCGCATA
501	CCGCGTGTTT	AAAAAGAAAA	ACCTCGTCCT	CCCGATGATA	ACCGGCTTCA
551	AATACATCGA	AGGCAAAACC	TCAATCCGCT	TTGCCGGCAA	AGCCGCGCTT
601	GCCGCCGCAT	TATCGGTTGC	CGCGCTTGCC	GCAGCCGCCA	TCCTGCTCCT
651	GTCCTGA				

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

a152.pep

1	MKNKTKVWDF	PTRLFHWLLA	ASLPFMWYSA	KTGGDMLQWH	TRVGLFILFL
51	LVFRLCWGIW	GSDTARFSRF	VRGWSGIREY	MKNGIPEHVQ	PGHNPLGALM
101	VVALLAAVSF	QVGTGLFAAD	VNTFSTNGYL	NHLVSEHTGS	LMRKIHLNFF
151	KLLAVFSAVH	IAXVAAYRVF	KKKNLVLPMI	TGFKYIEGKT	SIRFAGKAAL
201	AAALSVAALA	AAAILLS*			

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFHWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVFLFLLVFRLCWGIW					
a152	MKNKTKVWDFPTRLFHWLLAASLPFMWYSAKTGGDMLQWHTRVGLFILFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNIGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAIHIAAAYAAYRVFKKNLILPMI					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAVHIAAXVAAYRVFKKNLVLPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```
g153.seq
1  atgggggtttg cttacAgtat gacgtatatc gaggtCGGga taccggagge
51  ggcattccgtc ctttCgctGC CCGAGATgat ggcctgatG GTGTTtCagg
101 attATGGTTT TttggeCGAA GTGATGTTTG TGtgaCTTT cGGCGcgcCG
151 GTTCTGTtTc TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCTACTCT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AAAGGTTTCG TTCGGGCCCG CGTTTTATCT
351 GATGTTTCGCG CTGTCTGGTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTCCTAA ATCGGGCGGC TGACGGGGAA TAATGCGGTT
451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTTCcg
501 cgacAGTgcc gaatccCCCT GCGGGGTGTg cgCGGcgga CTgtacggcg
551 gacggcgcaa aagtCTGAGt atttCgtCGG CGTTTCtgac ggcggcggtt
601 GTTTTGTATT TCCctgCcaa TATCctgccc attatGAttt cgtccAATCc
651 tgccgccacg GAGGcCAACA CCATCTTAG CCGCATCGCT TATATGTGGG
701 ACGagggcgA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CCGCGGCACG
801 GTTCGCTTTG CCGGCGGGCG CAAAGAAATT GTCGCACCTC tacCGCATCA
851 CCGAAGCGGT CCGCGCTGCG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCcaca TTATGCCGCG CGCGTCATT CCGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTTT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAACGAAA CGGAAAAATA TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```
g153.pep
1  MGFAYSMTYI EVGIPEAAVS LSLPEMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY
101 IKLSSVAKVR FGPAPYLMFA LSVMLIRTSV SVPQHVVYFQ IGRLTGNNAV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYGGRPKSL S ISSAFLTA AV
201 VLYFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIAAARFAL PAGAKLSHL YRTEAVGRV SMIDIFVII
301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL L WDKRASDGIA
351 FNETEKYD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```
m153.seq
1  ATGGCGTTTG CTTACGGTAT GACGTATATC GAGGTCGGGA TACCGGGTGC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CCGCGCGCCG
151 GTTCTGTtTc TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCTACTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTTCG TTCGGGCCCG CGTTTTATCT
351 GATGTTTCGCG CTGTCTAGTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATGCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCGG
501 CGACAGTGCC GAATCCCTCT GCGGCGTGTG CGGTGCGGAA CTGTACCGCC
551 GACGGCCGAA AAGTCTGAGT ATTTCTGTCG CGTTTCTGAC GCGGCGGTT
601 ATTTTGTATT TCCCTGCCAA TATCTGCCG ATTATGATT CGTCCAATCC
651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CCGCATCGCT TATATGTGGG
701 ACGAGGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCG
801 CTTTCGCTTT CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA
851 CCGAAGCGGT CCGCGCTGCG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCACAC TTATGCCGCG CGCGTCATT CCGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```
m153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY
```

```

101 IKLSSVAEVR FGPAFYLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNAV
151 QTASEGKTC SRCLYFRDSD ESPCVTCGAE LYRRRPSKLS IAASFALTA
201 ILYFPANLTC IMISSNPAPT ENVNTILGIA YMWDEGRDL IAVVFASLSL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIT
301 LMCSFTHYA RVIPGSAAVY FCLVVILTML SAYYFDPRL LWDRASDGLA
351 FNETKTHD*

```

m153 / g153 96.1% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLLCLYV					
	: : :					
g153	MGFAYSMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLLCLYV					
	10	20	30	40	50	60
m153.pep	70	80	90	100	110	120
	YAALIRKQAYPALRLATRVMMVRLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
	: : :					
g153	YAALIRKQAYPALRLATRVMMVRLRQAMMVDVFFVSTLVAYIKLSSVAKVRFGPAFYLMFA					
	70	80	90	100	110	120
m153.pep	130	140	150	160	170	180
	LSVMLIRTSVSVPHQHWYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSEAESPCGVCGBAE					
	: : :					
g153	LSVMLIRTSVSVPHQHWYFQIGRLTGNNNAVQTASEGKTCCSRCLYFRDSEAESPCGVCGBAE					
	130	140	150	160	170	180
m153.pep	190	200	210	220	230	240
	LYRRRPKSLSSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
	: : :					
g153	LYGGRPKSLSSISSAFLTAAVVLYFPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI					
	190	200	210	220	230	240
m153.pep	250	260	270	280	290	300
	AAVIFSASILVPVLKIAAMSVLIAARFALPTGAKKLSHLYRITEAVGRWSMIDIFVII					
	: : :					
g153	AAVIFSASILVPVLKIAAMSVLIAARFALPAGAKKLSHLYRITEAVGRWSMIDIFVII					
	250	260	270	280	290	300
m153.pep	310	320	330	340	350	359
	LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLLDWDKRASDGIAPNETEKHDX					
	: : :					
g153	LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLLDWDKRASDGIAPNETEKYDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 629>:

```

a153.seq
1  ATGGCGTTTG  CTTACGGTAT  GACGTATATC  GAGGTCGGGA  TACCGGGTGC
51  GGCATCCGTC  CTTTCGCTGT  CCGAGATGAT  GCGCCTGATG  GTGTTTCAGG
101 ATTATGGTTT  TTTTGCCGAA  CGTGATGTTT  TGCTGACCTT  CGGC CGCGCG
151 GTTCTGTTTC  TGCTGCTGTG  CCTGTATATC  TATGCGCGCG  GTATACGGAA
201 ACAGGCGTAT  CCTGCGCTGC  GTTTGGCAAC  GCGTGTGATG  GTGCGCTTGA
251 GACAGCGCAT  GATGCTGGAT  GTGTTTTTTT  TTTCCACTTT  GGTGGCGTAT
301 ATCAAGCTCT  CGTCTGTGGC  AGAGGTTTCG  TTCGGATCGG  CGTTTTATCT
351 GATGTTCCGG  CTGTCCGTTA  TGCTGATTCC  GACTTCGTGA  TCGTTTCCCC
401 AGCATTGGGT  GTATTTTCAA  ATCGGGCGGC  TGACGGGGGA  TAATGCGGTT
451 CAGACGGCAT  CGGAAGGTAA  AACCTGTTGC  AGCCGCTGCC  TGTATTTCCG
501 CGACAGTGCC  GAATCCCCCT  CGGGCGTGTG  CGGTGCGGAA  CTGTACCGCC
551 GACGCCCGAA  AAGTCTGAGT  ATTTGCTCGG  GCTTTCGTAC  GCGCGCGGTT
601 ATTTTGTATT  TCCCTGCCAA  TATCCTGCCG  ATTATGATTT  GCGCCAATCC
651 TGCCGCCACG  GAGGTCAATA  CCATCCTTAA  CGGCATCGCT  TATATGTGGG
701 ACGAGGGCGA  CAGGCTGATT  GCGCGGGTTA  TTTTCAGCGC  GAGTATTTTG
751 GTGCCGGTAC  TGAAGATTGC  GGC AATGTCG  GTTTTGATTG  CGTCCGCCCC
801 CTTCGCTTTG  CCAACGGGTG  CAAAGAAATT  GTCGCACTCT  TACCGCATC

```

```

851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLELLLCLYV YAALIRKQAY PALRLATRV MRLRQAMMVD VFFVSTLVAY
101 IKLSSVAEVR FGSAFYLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL S ISSAFLTA
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDR LI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL WDKRASDGIA
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVQDYGFLAEVMFVLTFGAPVFLLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVQDYGFLAEVMFVLTFGAPVFLLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDASPCGVCGAE					
a153	LSVMLIRTSVSVQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDASPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDR LI					
a153	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDR LI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHTYAA RVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
a153	LMCSFHTYAA RVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCTCAAG CACGCGTCCG
51  CAAAAACAAC accttctctCT CCGCCGCTCTG GCTGTCCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCAATTAAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CAAAAAGGC GTGGAAGTTA CTGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtaa CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

```

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401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCTA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGcg GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGAcccG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTGAGGCG CGATTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCCT GTcgaATACA AAGGGctgaA
951 TGTcggCATG GTTTCCGATG TCCCTTATT TGACCGCAAT gacagCCTGC
1001 ACCTgtTTGA aaacggctgg aTTcccGtac gCATCCGCAT cgagccTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAAACAACA
1101 ATTCCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCGGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GCGGTTTTGG ATGACTTGCA GGTCAAATTG GCGGATTTGC
1301 TGGACaaatT CAACAATCTG CCATTggata aaACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaaTCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACTCTG AAAGAGTTGC GCATAACCCT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGagacgta caAAATAcgc tgCaAAGTTT
1551 GGACAAAACC TTAAAgacg TtcaACCCGT CATTAACACT TTGAAGAAA
1601 aacCCaaCgc actGATTtC aacaACAGCA GCAAAGAccc tATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

g154.pep

```

1   MTDNSPPFNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGLTL SGSYIAFTPG KSGEAKDVFQ
151 VQDIPPVTAI QSGGLRLNLI GKNDRIILNVN SPVLYENFMV QQIESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIPIEPS
351 RLEINADEQS KEHWKQOFQ ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATRG GGLDDLQVKL ADLLDKFNNL PLDKTVAELN
451 GSLAELKSAL KSANAALSSI DKLVGNPQTQ NIPNELNQLT KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSSKDPIPK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

m154.seq

```

1   ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGCTCG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTATCAAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGAGC AGGCAAAAGA CGTGTTCCTA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTGCGGCG CGATTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTGCGCC GTGAGTACA AAGGGCTGAA
951 TGTGCGGCTG GTTTCCGACG TTCCTTATT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTTTCAGAC GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

```



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1201 TCACCTAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GGCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTTCG
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCTG AAAGAGTTGC GCACAACCTC GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAACTT TAAAGACG TTCAACCGT GATTAATACT TTGAAAGAAA
1601 AACCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

```

m154.pep
1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVPFQ
151 VQDIPPVTAI GQSGRLRLNI GKNDRIILNV SPVLYENFMV QGVESAHPDQ
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAPFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFPQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVABL
451 GSLAEKSTL KSANAALSSI DKLVGKPTQ NIPNELNQL KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKFNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
g154	MTDNSPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
	10	20	30	40	50	60
m154.pep	70	80	90	100	110	120
	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
g154	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	130	140	150	160	170	180
	SGVTGLGTLT SGSYIAFTPG KSDEAKDVPFQ VQDIPPVTAI GQSGRLRLNIGKNDRIILNV					
g154	SGVTGLGTLT SGSYIAFTPG KSDEAKDVPFQ VQDIPPVTAI GQSGRLRLNIGKNDRIILNV					
	130	140	150	160	170	180
m154.pep	190	200	210	220	230	240
	SPVLYENFMV GQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
g154	SPVLYENFMV GQIESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
	190	200	210	220	230	240
m154.pep	250	260	270	280	290	300
	KLSAPLPALL LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAPFFKQ					
g154	KLSAPLPALL LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAPFFKQ					
	250	260	270	280	290	300
m154.pep	310	320	330	340	350	360
	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
g154	SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
	310	320	330	340	350	360
m154.pep	370	380	390	400	410	420
	KEHWKQFPQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG					
g154	KEHWKQFPQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATRG					

442

	370	380	390	400	410	420
	430	440	450	460	470	480
m154.pep	GGLDDLQVKLADLLDKFDKLPDKTVAEIENGSLAEKSTLKSANAALSSIDKLVGKPQTQ					
	:     :     :     :     :					
g154	GGLDDLQVKLADLLDKFNNPLDKTVAEIENGSLAEKSAKLSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154.pep	NIPNELNQTLELRITTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	:     :     :     :     :					
g154	NIPNELNQTLELRITTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154.pep	NSSSKDPIPKGSRX					
	:					
g154	NNSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCATCAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGC GCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTTCG
401 ACATCGCCTT TACACCCGCG AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCCT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTGACCCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTGAT TCCGCCAGCC GTTCTGGCTT GGAAGCGGCG ATCAATATCG
701 AAACCACAGG CAGCGGCATC AACTCAATT CCGCCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTTCA TTGATTCGCC AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACGCGGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTTGCGCT GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTCCGATG TTCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCCTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGAAT TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTTAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCTTGG CCGAGCTCAA ATCCCACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAAACTGG TCGGCAAAAC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCTCAAT CGCTATCTA CGGCGACGTA CAAATACGC TGCAAAGTTT
1551 GGACAAAACC TTTAAAGACG TTCAACCCGT CATTAACACT TTGAAAGAAA
1601 AACCCACGCG GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCAGAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154.pep
1  MTDNSPPFNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLL SGSYIAFTPG KSDEAKDVFG

```

151 VQDIPPVTAI QSGSLRLNLI GKNDRIILNVN SPVLYENFMV QGVESAHFDP  
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL  
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ  
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS  
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA  
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN  
451 GSLAELKSTL KSANAALSSI DKLVGKPTQ NIPNELNQT LKELRTTLQGV  
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDEIPK  
551 GSR\*

## m154/a154 100.0% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPN	GHAQARVR	KNNTFLSA	VWLVLPLI	ALIAGGWL	VWKEIRNR
a154	MTDNSPPPN	GHAQARVR	KNNTFLSA	VWLVLPLI	ALIAGGWL	VWKEIRNR
	10	20	30	40	50	60
m154.pep	70	80	90	100	110	120
	GIEVNNTVI	KVLSIDVG	RVTRIKLR	DDQKGVEV	TAQLNADV	SGLIRSDT
a154	GIEVNNTVI	KVLSIDVG	RVTRIKLR	DDQKGVEV	TAQLNADV	SGLIRSDT
	70	80	90	100	110	120
m154.pep	130	140	150	160	170	180
	SGVTGLGTL	LSGSYIAF	TPGKSDEA	KDVQVQDI	PPVTAIGQ	SGLRLNL
a154	SGVTGLGTL	LSGSYIAF	TPGKSDEA	KDVQVQDI	PPVTAIGQ	SGLRLNL
	130	140	150	160	170	180
m154.pep	190	200	210	220	230	240
	SPVLYENFM	VGVQVESA	HFDPDQSV	HYTIFIQSP	NDKLIHSA	SASFLES
a154	SPVLYENFM	VGVQVESA	HFDPDQSV	HYTIFIQSP	NDKLIHSA	SASFLES
	190	200	210	220	230	240
m154.pep	250	260	270	280	290	300
	KLNSAPLPA	LLSGAISF	DSFKTKNS	KNVKSSED	SFTLYDSR	SEVANLP
a154	KLNSAPLPA	LLSGAISF	DSFKTKNS	KNVKSSED	SFTLYDSR	SEVANLP
	250	260	270	280	290	300
m154.pep	310	320	330	340	350	360
	SVRGLTVGS	PVEYKGLN	VGVVSDVP	YFDRNDSL	HLFENGWI	PVRIRIEP
a154	SVRGLTVGS	PVEYKGLN	VGVVSDVP	YFDRNDSL	HLFENGWI	PVRIRIEP
	310	320	330	340	350	360
m154.pep	370	380	390	400	410	420
	KEHWKQFQT	ALNKGLTA	TISSNNLL	TGSKMIEL	NDQPSASP	KLRPHTV
a154	KEHWKQFQT	ALNKGLTA	TISSNNLL	TGSKMIEL	NDQPSASP	KLRPHTV
	370	380	390	400	410	420
m154.pep	430	440	450	460	470	480
	GGLDDLQVK	LADLLDKF	DKLPLDKT	VAELNGSL	AELKSTLK	SANAALSS
a154	GGLDDLQVK	LADLLDKF	DKLPLDKT	VAELNGSL	AELKSTLK	SANAALSS
	430	440	450	460	470	480
m154.pep	490	500	510	520	530	540
	NIPNELNQT	LKELRTTL	QGVSPQSP	PIYGDVQN	TLQSLDKT	LKDVQPV
a154	NIPNELNQT	LKELRTTL	QGVSPQSP	PIYGDVQN	TLQSLDKT	LKDVQPV
	490	500	510	520	530	540

```

                    550
m154.pep      NSSSKDPIPKGSRX
              |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1  atGAAaatcg GtaccCCACG CGAGTCAtta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gCCACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAGgt TTGGCGGCAA GTTTggaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCCC
201 TTTAATTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CTTGCGCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCTCCG ATTTCCCGCG CTCAGGCCTT GGACGCTTGT TCTTCAATGG
401 CAAACATCAG CGGTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCTGCGCA
501 GGTTTTGGTG ATTGGCGCCG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTGGAAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GCGGCGACG GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTGT CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACGCG CGCCATTCCG GGCAAACCCG CTCCCAAGCT
801 GATTACAAA GAAATGGTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAACCG GCAACGGCGT GAAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgaAATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTTCCCGCCT CGcgcgaTTc aggtTTCgc cggccgCAG CAAAcgcgt
1151 ctgaAAAagc cgcGCCTGCC GCCAagcccg AgccGaaacc tgttCCcctg
1201 tggaAAAaac tcgCGCCGCG CGCcatcgCC GCCGTATTGG tgctgtgGgt
1251 cggCgcggtc gcaccgcgag CATTCCTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCCTGCGT CATCGGCTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGAtgtcggt aaccaaCgcc atctccGGCA tcatggtcgt
1401 cggCGCGCTG CTGCAAATCG GTCAGGGcaa cggttcgtT TCgctGCTGT
1451 CGTTTGTGTC CATCCTGATT GCCGGCATCA ATATCTTCGG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDVPR ISRAQALDAL SSANISGYR AVIEAANAAG
151 RFFTGTITAA GKVPQAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFLQES GSGDGYAKV MSDEFIAAEM KLFQAEQAEV
251 DIIITTAaip GKPAKLITK EMVESMKSGS VIVDLAATGG NCELTRPDEL
301 SVTGNVVKII GYTDMANRLA GQSSQLYATN LVNLTLLSP NKDGEITLDF
351 EDVIRNMTV TRDGEITFPF PPIQVSARPO QTPSEKAAPA AKPEPKPVL
401 WKKLAPAAIA AVLVLWVGAV APAFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAL LQIGQNGFV SLLSFVAILI AGINIFGGFA
501 VTRRLNMFK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1  ATGAAATCG GTATCCACG CGAGTCATTA TCCGCGGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGTGCAGGT TTGGCGGCAA GTTTGACGCA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAACG CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

```

```

301 TTGGTCGAAG CCTTGC GCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCGC ATTTCGCGC CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCGCGCA
501 GGTTTGTGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GCGGCGAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCT
801 GATTACCAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GGGCAGGGC GGCAACTGCG AACTCACCCG CCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGGAAA AACTCGCGCC CGCGTCAATC GCCGCCGTCT TGGTACTGTG
1251 GGTCGGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGTGATGTC GGTAAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCGCGA TCAACATCTT CGGCGGCTTT
1501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTQGITA AAGKVPQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRELV
201 AEQIESMGKK FLKLDPPQES GSGDGYAKV MSDEFIAAEM KLFQAEQKEV
251 DIIITTAAP GKPAKPLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTGNVSKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QPTPSEKAVP AAKPEPKPVP
401 LWKKLAPAVI AAVLVLVWGA VAPAAFLNHF IVFVLACVIG YVWVNVSHS
451 LHTPLMSVTN AISGIIVVGA LLQIQGNGF VLLSFAVAIL IAGINIFGGF
501 AVTRRLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
          10      20      30      40      50      60
m155.pep  MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
          |||
g155      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
          10      20      30      40      50      60

          70      80      90      100     110     120
m155.pep  AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR
          |||:|||||
g155      AAVWACPLIYKVNAPSEGEPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR
          70      80      90      100     110     120

          130     140     150     160     170     180
m155.pep  ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPQVLVIGAGVAGLAA
          |||
g155      ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPQVLVIGAGVAGLAA

```

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	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155						
	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
m155.pep	250	260	270	280	290	300
	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155						
	250	260	270	280	290	
	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155						
	310	320	330	340	350	
	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
m155.pep	370	380	390	400	410	420
	VTHDGEITFPPPIQVSAQPQQTPEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVWVGA					
g155	:     :     :     :     :					
	360	370	380	390	400	410
	VTRDGEITFPPPIQVSAQPQQTPEKAAPAKPEPKPVPLWKKLAPAAIAAVLVLVWVGA					
m155.pep	430	440	450	460	470	480
	VAPAAFLNHFIVFVLACVIGYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
g155						
	420	430	440	450	460	470
	VAPAAFLNHFIVFVLACVIGYHVVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
m155.pep	490	500	510			
	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
g155						
	480	490	500	510		
	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAAATCG GTATCCCACG TGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCG GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGGCATACCC
201 TTTAATTAT AAGGTTAACG CGCGTCCGA AGACGAGCTG CCGTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGCAGCG CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGNTTGT TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTGTGTG ATTTGTCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGCGCAGTG GTACGCGTGT TCGATACCCG CCTG.AAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GCGGCAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTGT CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGACGGGC GGCAACTGCG AACTACCAA ACAGGGCGAA
901 TTGTTTCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGACAGT CTTGCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGCGGAAAT CACGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCCAAGC CCGAACCGAA ACCCGTTCCC

```

```

1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTCCGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTGGAAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCGG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
  1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51 QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDXL SXMANISGYR AVIEAANAFG
151 RXFTGQITAA GKVPAPQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDLPQES GSGDGYAKV MSDEFIAAEM KLFQAEQAKEV
251 DIIITTAAP GKPAKXXXK EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LFVTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLVVGA VAPAAFLNHF IVFVLACVIG YYVWVNVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQNGF VSLLSFVAIL IASINIFGGF
501 FVTRRLNMF RKG*

```

m155/a155 95.3% identity in 513 aa overlap

	10	20	30	40	50	60
m155.pep	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK					
a155	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m155.pep	AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
a155	AAVWAYPLIYKVNAPSEDELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m155.pep	ISRAQALDALSSMANISGYRAVIEAANAFGRFFTGTGQITAAGKVPPAQVLVIGAGVAGLAA					
a155	ISRAQALDXLSXMANISGYRAVIEAANAFGRXFTGTGQITAAGKVPPAQVLVIGAGVAGLAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m155.pep	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGSGDGYAKVMSDEFIAAEM					
a155	IGTANSLGAVVRVFDTRLXVAEQLESMGGKFLKLDLPQESGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m155.pep	KLFQAEQAKEVDIIITTAAPGKPAKPLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
a155	KLFQAEQAKEVDIIITTAAPGKPAKXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m155.pep	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
a155	LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	310	320	330	340	350	360
	370	380	390	400	410	420
m155.pep	VTHDGEITFPPIQVSAQPQQTPEKAVPAKPEPKVPLWKKLAPAVIAAVLVLVVGA					
a155	VTRDGEITFPPIQVSAQPQQTPEKAAPAAKPEPKVPLWKKLAPAXIAAVLVLVVGA					
	370	380	390	400	410	420



```

              430      440      450      460      470      480
m155.pep    VAPAAFLNHFI FVLACVIGYYVVWNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF
              |||||
a155        VAPAAFLNHFI FVLACVIGYYVVWNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF
              430      440      450      460      470      480

              490      500      510
m155.pep    VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX
              |||||:|||||
a155        VSLLSFVAILIASINIFGGFFVTRRMLNMFRRKGX
              490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

g156.seq

```
1  ATGACTTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCGC TATGCCAAAA AAGCGGGCGG ATTCGGGTTT AAAGACAACC
101 ACAATCCTCG CTGGTTTCTG GCACATACCG AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTCGACCGT TTGCCGCGCC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG ATTGTTTCAT CTGTTCCGCC TCGCGTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT CGGCTCGTG ATGTGGCGCG GCGGATTTCG
351 CTGCACCGTC GGACTGTTTG TCGCGGCTGC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

g156.pep  
1 MTFAYWCILI ACLLLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAARA  
51 HAAQQNGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LFRLAFIWCY  
101 IADKAALRSL MWAGGFACTV GLFVAAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```
m156.seq
1  ATGACTTTTCG  CCTATTGGTG  TATTCTGATT  GCCTGCCTAT  TGCCGCTTTT
51  TTGTGCGGCG  TATGCCAAAA  AAGCGGGCGG  ATTCCGGTTT  AAAGACAACC
101 ACAATCCGCG  CGGTTTCTTA  GCGCACACGC  AAGGCGCAGC  CGCCCCGTCC
151 CACGCCGCAC  AGCAAAACGG  TTTTGAAGCC  TTTCACCGCT  TTGCCGCGCG
201 CGTTTTGACG  GCACACGCAA  CCGGCAATGC  GGCGCAATCG  ACCATCAACA
251 CGCTTGCTGC  CCGTTTCATC  CTGTTCCGCC  TCGCCTTTAT  CTGGTGCTAT
301 ATCGCCGACA  AAGCCGCTAT  CGCGTCACTG  ATGTGGGCGC  GCGGATTTCG
351 CTGCACCGTC  GGGCTGTTTG  TCGCGGCTGC  TTGA
```

This corresponds to the amino acid sequence <SEO ID 646; ORF 156>:

```
m156.pep
1  MTFAYWCILI ACLLLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAAQs TINTLACLFt LFRLAFIWCY
101 IADKAAMRSL MWAGGFACTV GLFVAAA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**m156 / g156** 96.1% identity in 127 aa overlap

	10	20	30	40	50	60
m156.pep	MTFAYWCILIA CLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA					
g156	MTFAYWCILIA CLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m156.pep	FAPFAAVLTAHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFAC TV					
	:::  :					



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```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWAGGFAC TV
              70          80          90          100          110          120

m156.pep  GLFVAAAX
            |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
  1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
 51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGTTT AAAGACAACC
101  ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151  CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201  CGTTTGTACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251  CGCTTGCCGG CCTGTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301  ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTGTG
351  CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
  1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAARA
 51  HAAQONGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LFRFAFIWCY
101  IADKAALRSL MWVGGFVCTV GLFVVAAX*

```

m156/a156 90.6% identity in 127 aa overlap

```

              10          20          30          40          50          60
m156.pep  MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
            |||||
a156      MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAAQONGFEA
              10          20          30          40          50          60

              70          80          90          100          110          120
m156.pep  FAPFAAAVLTAHATGNAAQSTINTLACLFI LFRFAFIWCYIADKAAMRSLMWAGGFAC TV
            |||||
a156      FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWVGGFVCTV
              70          80          90          100          110          120

m156.pep  GLFVAAAX
            |||||
a156      GLFVVAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
  1  atgaggaacg aggAAAAACg cgcctgcgc cgcgaattgC gCgGgcggcg
 51  ttcgcAAATg GGgcgagacg tGCGggCGGC GGCGgCgata Aaaatcaacc
101  gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151  cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201  ACGCgCGCA AAactctatc tgccttATAT CGAACCGCAC ACGCGCGGA
251  TGTGTTTAC GCCGTATCCT GAACGCGGAA TGAACCGGA ACGCAAGCGC
301  GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351  GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGSCATA GACCGCGAAG
401  GCTACCGTTT GGGGCGAGCA GCGGCTATT ACGATGCGAC GCTTTCGGCG
451  ATGAAATACC GTTTGCAGGC GAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501  GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551  TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
1  MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLLKRYI KRGRKIGVYW
51  PMGKELRLGG FVRAAQKRGK KLYLPYIEPH TRRMWFPTYP ERGMERERKR
101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGFACQLVD RLPREAHDLF LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
1  ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGCG
51  TTCGCAAATG GGGCGGGACG TGCGGGCGGC GGCAACGGTA AAAATCAACC
101 ACCTGCTCAA ACGTTATATT AAAAAAGGCG GGAATACGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGTTTAC GCCGTATCCT CCCGATGGAG TAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCGGA AAAAGCGTGT
351 GCATGATTTC AACCTCCTGC TTGTGCCAGT GGTCCGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GGCGGCTATT ACGATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTTCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTGCCCG TCGAGGCGCA CGACCGGTCT TTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
1  MRNEEKRALR RELRGRRSQM GRDVRAAATV KINHLLKRYI KKGRKIGVYW
51  PMGKELRLDG FVRAAQKRGK ELYLPYIEPR SRRMWFPTYP ADGVKQERKR
101 GRAKLHVPQF AGRKIRVHDL NLLVPVVG M DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALR	RELGRRSQM	GRDVRAAATV	KINHLLKRYI	KKGRKIGVYW	PMGKELRLDG
g157	MRNEEKRALR	RELGRRSQM	GRDVRAAAAI	KINRLLKRYI	KRGRKIGVYW	PMGKELRLGG
	10	20	30	40	50	60
	70	80	90	100	110	120
m157.pep	FVRAAQKRGK	AEYLPYIEPR	SRRMWFPTYP	PADGVKQERK	GRAKLHVPQF	AGRKKRVHDL
g157	FVRAAQKRGK	AEYLPYIEPH	TRRMWFPTYP	PERGMERERK	GRAKLHVPQF	AGRKKRVHGL
	70	80	90	100	110	120
	130	140	150	160	170	180
m157.pep	NLLLVVVGMD	RDLGYRLGQ	AGGYDATLSA	MKYRLQAKTV	GVGFACQLVD	RLPVEAHDRS
	:::					
g157	SVLLVPLVGI	DREGYRLGQ	AGGYDATLSA	MKYRLQAKTV	GVGFACQLVD	RLPREAHDLP
	130	140	150	160	170	180
	190					
m157.pep	LDGFVSEAGI	LCFX				
g157	LDGFVSEAGI	LCFX				
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
1  ATGAGGAACG AGGAAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCG
51  CGCGCAGATG GGCATCAAG GCGGTTGGC GCGGGGCAA ACGATTAACC
```

451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGAACGCGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCCGCATA GACCGGAGG
401 GCTACCGCTT AGGACAGGCA GGCGGCTATT ACGATGCGAC GCTTGGCGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCGTG GGCGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACCGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

**a157.pap**

```

1 MRNEEKHALR RELRRARAQM GHQGRLAAGQ TINRLLKRYI KRGRKIGVYW
51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWTFYPY ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFAQCFVD RLPREPHDLL LDGFVSEAGI LCF*

```

**m157/a157** 82.4% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pap	MRNEEKRALRRELRRSOMGRDVR	RAAATVKINHLLKRYIKKGRKIGVYW	PMGKELRLDG			
a157	MRNEEKHALRRELRRARAQM	GHQGRLAAGQTINRLLKRYIKRGRKIGVYW	PMGKELRLDG			
	10	20	30	40	50	60
m157.pap	FVRAAQKRGAE	LYLPYIEPRSRMWTFYPADGVKQERKGR	AKLHVPQFAGRKRVHDL			
a157	FVRAAQKRGAKLYLPYIEPRSRMWTFYP	ESGMERERIRGRAKLNVPQFAGRKIRVHGL				
	70	80	90	100	110	120
m157.pap	NLLLVFVVGMDRLGYRLGQAGGYDATLS	AMKYRLQAKTVGVGFACQLVDR	LPEAHDRS			
a157	SVLLVPLVGIDREGYRLGQAGGYDATLA	AMKYRLQAKTVGVGFACQFVDR	LPREPHDLL			
	130	140	150	160	170	180
m157.pap	LDGFVSEAGILCFX					
a157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

**g158.seq**

```

1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
51 CCGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAAcCTGctc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTCGCGCT GGATTCGCGC
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCcgac TTTCGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCGCG AGAATTGGAC
451 GATTCCGGGC TGCGTGACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG  
 851 TATTTTGGGA TTTTATTAGTG AAGGAACTGG GAAAAAATAT GAATAGAACG  
 901 AATACCAAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep

1 MKTNSEELTV FVQVVEGSGF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL  
 51 NRTTRQLNLT EEGAQYFERR QRILQEMAAA ETEMLAVHEV PQGVLRVDSA  
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD  
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN  
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE  
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNLL RLRVFLDFLV KELGKNMNR  
 301 NTK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq

1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG  
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG  
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC  
 151 AACC GCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT  
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA  
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTGAGCGT GGATTCCGCG  
 301 ATGCCGATGG TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA  
 351 ACGCTATCCG CATATCCGAC TTTCGCTCGT TTCTTCGAA GGCTATATCA  
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGG AGAATTGGAC  
 451 GATTCCGGGC TCGCTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT  
 501 CGCCAGTCCT GAATACCTGG CAAACACGG CACGCCGCAA TCTACAGAAG  
 551 AGCTTGCCCG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT  
 601 ACATGGGCGG TTTTAGATGC GCAGGGAAAT CCCTATAAGA TTTCACCGCA  
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT  
 701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGTGAA  
 751 GGAAAGTTAA TTCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC  
 801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG  
 851 TATTTTGGGA TTTTATTAGTG GAGGAACTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep

1 MKTNSEELTV FVQVVEGSGF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL  
 51 NRTTRQLSLT EEGAQYFERR QRILQEMAAA ETEMLAVHEI PQGVLSVDSA  
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD  
 151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN  
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE  
 251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNLL RLRVFLDFLV EELGNNLCG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSGFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
g158	MKTNSEELTVFVQVVEGSGFSRAAEQLEMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m158.pep	EEGAQYFERRAQRILQEMAAEETEMLAHVHEIPQGVLSVDSAMPVHLHLLAPLAAKFNERYP					
g158	EEGAQYFERRAQRILQEMAAEETEMLAHVHEVPQGVLRVDSAMPVHLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

m158.pep	130	140	150	160	170	180
	HIRLSLV	SEGYIN	LIERKVD	IALRAGEL	DDSGLRAR	HLFDSRFR
g158	130	140	150	160	170	180
	HIRLSLV	SEGYIN	LIERKVD	IALRAGEL	DDSGLRAR	HLFDSHFRV
m158.pep	190	200	210	220	230	240
	STEELAG	HQCLGF	TEPGSLN	TWAVLDA	QGNPYK	ISPHTASS
g158	190	200	210	220	230	240
	SAEDLAN	HQCLGF	TEPGSLN	TWAVLDA	QGNPYK	ISPHTASS
m158.pep	250	260	270	280	290	300
	DFLVDND	IAEGKLI	PLLAEQ	TSKTHP	NAVYYS	DKAVNL
g158	250	260	270	280	290	300
	DFLVDND	ITEGKLI	PLFAEQ	TSNKT	HPNAVY	YSDKAVN
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAAACCA	ATTCAGAAGA	ACTGACCGTA	TTTGTTC AAG	TGGTGGA AAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCGCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGCACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTATGATGC	GCAGGGAAT	CCCTATAAGA	TTTACCCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTGGAA	TTTTTTAGTG	GAGGAACCTG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVEGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRRR	QRILQEMAAA	ETEMLAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQC	LGFTTEPGSLN
201	TWAVLDAQGN	PYKISPHTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYYSKAVNL	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

m158.pep	10	20	30	40	50	60
	MKTNSEELTV	FVQVVEGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL	NRTTRQLSLT
a158	10	20	30	40	50	60
	MKTNSEELTV	FVQVVEGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL	NRTTRQLSLT
m158.pep	70	80	90	100	110	120
	EEGAQYFRRR	QRILQEMAAA	ETEMLAVHEI	PQGVLRVDS	SAMPVLHLL	APLAAKFNERYP
a158	70	80	90	100	110	120
	EEGAQYFRRR	QRILQEMAAA	ETEMLAVHEI	PQGVLRVDS	SAMPVLHLL	APLAAKFNERYP

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	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151 GCGGAAACTT  CCCCgcGTCC  GGTcGGCACG  GGCgATATTG  TATTTTCCCT
201 GCGCGGCTTG  GGTcATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATAcGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCggc
301 AACGGGCTGG  ATATGAGCCT  GTTTTGCGCC  CGTTTCCGCT  ACGACACCCA
351 CGCCGATTG  ATGAACGGGC  TGCCGGAAAC  CGTTTTCTG  AACATTGCCC
401 ATCCAAGTTT  GCAGTATGTG  GTTCAATGC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTcCTGCT
501 GGTGCTTATC  CTGCGGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAACTCT
551 CGGGCGTATT  GAAAGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601 AAGGTGATAG  ACAAACCGGA  AGACGAATGG  AATATTGACA  AAATGGTTGC
651 CGCCGCCAAT  ATGTCGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGCACGCC  TTTGTGAACC  ATATCCGCCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAAC  CCCGATTTCG  GTTTTGGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAAA  CGCATTTCGG  CAAGGCCTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGGCAA  TACCGGAAAG  AAGCGGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHEH  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151 PLTGTFSVVN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAEAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKTPDS  VLEVALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTcGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGCAG  CGGCTATCTC
151 TGCATCGACG  GCGAAACTTC  CCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGCggCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTCCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTGTCGTC

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455

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501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCTT TTGTGAACCA TATCCGCTTG
751 CAAAAGGCGG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTTGTGCGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AggCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
  51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
 101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
 151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
 201 LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS PHAFVNHRL
 251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
 301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      MDILDKLV DLAQLTGSADVQ CLLGGQW---HETLQREGLV HIVTAGSGYL CIDGETSPRP
          10      20      30      40      50

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      VGTGDIVFFP RGLGHVLSHD GKYGESLQPD IRQNGTFMVK QCGNGLDMSL FCARFRYDTH
          60      70      80      90      100     110

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTVS MVNALSSVLL VLILRAYLEQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SEKPLTGTVS VVNALPSVLL VLILRAYLEQ
          120     130     140     150     160     170

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSQVGLS
          180     190     200     210     220     230

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      PHAFVNHIRL QKGALLLKKTPDSVLEVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          240     250     260     270     280     290

m160.pep KX
          ||
g160      KX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
  1 ATGGACATTC TGGACAAACT GGTGATTTC GCCCAATTGA CGGGCAGTGT
 51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

```
101 TGCAACGCGA AGGATTGGTA CACATTGTTA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTCCCG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCGGCA ACGGACAGGA TATGAGCCTG TTTTGCGCCG GTTCCGCTA
351 CGACACCCAC GCCGATTGTA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCTGCTG GTGCTTATCC TGCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTGGC AGGACAAACG TTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTGCG TTTTGTGCGT
801 CGCACTGTG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGTCAAT ACCGAAAAGA AGGCGGGCAA
901 AAATAA
```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```
a160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*
```

m160/a160 100.0% identity in 301 aa overlap

```
          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||||
a160      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||||
a160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          70      80      90      100     110     120

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTV SMVNALSSVLL VLILRAYLEQ
          |||||
a160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTV SMVNALSSVLL VLILRAYLEQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||||
a160      DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKNP DSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||||
a160      PHAFVNHIRL QKGALLLKNP DSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          250     260     270     280     290     300

m160.pep KX
          ||
a160      KX
```



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GCGGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCG TTTACACGCA GCGGTGCTG CTCCTTGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTCAGGAA
451 CCGCGGCAC TCGCCGGGCT GCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTACCT TTCCGCAACC GCGGTGGCGA TGTCGTcgg ttgggagacg
601 Ctgaccggct ggCACaccT GTCCTTcca tcggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgCgtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCCCTCGC tttcctaTat gaccgtcGTC
751 TTTCCGCCCT TGTCTGCCG ATTTTCTGg ggcaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAA CAGCGGCTGC AAGCCCTCTT CCGCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVTLGAAAVL RRDFTERTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPFSRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GCGGGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCG TTTACACGCA GCGGTGCTG CTCCTTGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCGTcgg TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCG ATTTTCTGg GGCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAA CAGCGGCTGC AATCCCTGTT CCGCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVALGAAAVL RDXFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPFSRSGQE

```

151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT  
 201 LTGWHTLSEF SAVYLSICIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV  
 251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR  
 301 \*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	:     :     :     :     :					
g161	MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLSTVTLGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSIFLAVFSFLILKE					
	:     :     :     :     :					
g161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLTTGVTLSYTSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFAGVVLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELAGEPG					
	:     :     :     :     :					
g161	RISVYTQAVLLLGFAGVVLLNPSFRSGQEPALAGLAGGAMSGWAYLKVRELAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
	:     :     :     :     :					
g161	WRVVFYLSATGVAMSSVWATLTGWHTLSFSAVYLSIGIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	:     :     :     :     :					
g161	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
	250	260	270	280	290	300
m161.pep	X					
g161	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

a161.seq

1	ATGGATACCG	CAAAAAAGA	CATTTTAGGA	TCGGGCTGGA	TGCTGGTGGC
51	GGCGGCCTGC	TTTACCATTA	TGAACGTATT	GATTAAAGAG	GCATCGGCAA
101	AATTTGCCCT	CGGCAGCGGC	GAATTGGTCT	TTTGGCGCAT	GCTGTTTTCA
151	ACCGTTGCGC	TCGGGGCTGC	CGCCGTATTG	CGTCGGGACA	CCTTCCGCAC
201	GCCCCATTGG	AAAAACCACT	TAAACCGCAG	TATGGTCGGG	ACGGGGGCGA
251	TGCTGCTGCT	GTTTACGCG	GTAACGCATC	TGCCTTTGGC	CACCGGCCTT
301	ACCCTGAGTT	ACACCTCGTC	GATTTTTTTG	GCGGTATTTT	CCTTCTGAT
351	TTTGAAAGAA	CGGATTTCCT	TTTACACGCA	GGCGGTGCTG	CTCCTTGGTT
401	TTGCCGGCGT	GGTATTGCTG	CTTAATCCCT	CGTCCGCAG	CGGTACAGAA
451	ACGGCGGCAC	TCGCCGGGCT	GGCGGGCGGC	GCGATGTCCG	GCTGGGCGTA
501	TTTGAAAGTG	CGCGAACTGT	CTTTGGCGGG	CGAACCCGGC	TGGCGCGTCG
551	TGTTTTACCT	TTCCGTGACA	GGTGTGGCGA	TGTCATCGGT	TTGGGCGACG
601	CTGACCGGCT	GGCACACCCT	GTCCTTTCCA	TCGCGAGTTT	ATCTGTCGTG
651	CATCGGCGTG	TCCGCGCTGA	TTGCCCAACT	GTCGATGACG	CGCGCCTACA
701	AAGTCGGCGA	CAAATTCACG	GTTGCCTCGC	TTTCTATAT	GACCGTCGTT
751	TTTTCCGCTC	TGTCTGCCGC	ATTTTTCTG	GCCGAAGAGC	TTTTCTGGCA
801	GGAAATACTC	GGTATGTGCA	TCATCATCCT	CAGCGGTATT	TTGAGCAGCA

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA  
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep  
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMIFS  
51 TVALGAAAVL RRDTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV  
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE  
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT  
201 LTGWHITLSEF SAVYLSICIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV  
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR  
301 \*

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMIFSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMIFSTVALGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLLGFAGVVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLLGFAGVVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHITLSEFSVAVYLSICIGVSALIAQLSMT RAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHITLSEFSVAVYLSICIGVSALIAQLSMT RAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq  
1 ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT  
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAAGAAG  
101 TCATTTTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTTTt  
151 ctgGGTTTtc tgctGATACT CTCGGTCAGC GGTTTGGGAA ACATcagGCT  
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA  
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGCC TGATGTTTTT CGGCGTGGCA  
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGGAACA  
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG  
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC

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451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTGTAGCGA GTTGAACCTG
751 GGCCTTGCCT TTTTGCTGCT GTTTTTGTG TTGGCGGCGG ACCCCTACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGGAATC
851 TGGTGCCTCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTGAAT CTTGGACGGT GCTTTATTGG GCGTGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTGTGTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCGGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCTC TCCGGAACG CTGCTTTTAA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAACCTCT GCCGACTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGCGGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCTGA TTGTTTCCCT
1401 GCGGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTGCGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAAC TG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

g163.pep

```

1  MVILTTLEFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51  LGFLLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSGVQV LIIAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLEFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLEFFVTS ADSGIYVLNN ITSRDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

m163.seq

```

1  ATGTTATTTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCATTGG GCGTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTT
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCCTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTGTGTT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGGAAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTGTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGAAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTATTGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGCGTG CTGATGCTG CCGTGGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGCC CTGCTGATG TGATAATGTG TTTGAGCCTG TGGAAAGGCT
1451 TGAGTGCAGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTG
1501 TTTTGGACGG GCGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAAGAG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGCT
1651 CGGTCGATA AAATGTTTCA TCGGACGAG CCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFISIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSEK TYAYERHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPLGFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELOR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

	10	20	30	40	50	60
m163.pep	MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFISIFLGFLLILSVS					
g163	MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFISIFLGFLLILSVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m163.pep	SLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ					
	:					
g163	GLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ					
	70	80	90	100	110	120
	130	140	150	160	170	180

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPLALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPLALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWAENSFSVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKQTASPMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKHTASPMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

a163.seq	1	ATGGTTATTT	TGACGACTTT	GTTTTTGTG	TGTGTTTGG	TGGTATTGGT
	51	TTTAACCGTG	CCGGATCAGG	TGCAGATGTG	GCTCGATCGG	GCAAAAGAAG
	101	TCATTTTAC	CGAGTTCAGC	TGGTTTATG	TTTAAACGTT	TTCCATTTT
	151	CTGGGTTTCC	TGCTGATACT	CTCGTCAGC	AGTTTGGGAA	ACATCAGGCT

```

201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCGGGGATG GCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACAG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTTT
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGGCATC ATCACCACAT TGGGGTTTCGG GGCTTCGCAA
601 CTGGGCGCGG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAAGTT TTGATTATCG CCGCCGTCAT GTCCTTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGCCT TTTTGTGCT GTTTTTTGT TTTGGCGGCG GTCCCACTGT
801 TTACCTGTTG TCGGCATTGC GCGACAACAT AGGGAACCTAC CTCGGAATC
851 TGGTGCGCCT CAGTTTTTAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGCG
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACTTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGGC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGAT
1451 TGAGTGCAGA TAAGAAATAT TTTGAGACCC GGGTTAACC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCAGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 TACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFISIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIOW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSEK TYAYERHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLEKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMVGW LMSAVAVLLM
451 RSGGLNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQGEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFISIF LGFLLILSVS
          |||||
a163       MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFISIF LGFLLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA EPLMHYFSDI TAGTPEHRQQ

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|||||
a163      SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
           70      80      90      100     110     120

           130     140     150     160     170     180
m163.pep  QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
           |||||
a163      QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
           130     140     150     160     170     180

           190     200     210     220     230     240
m163.pep  MALLATFFGIITTLGFGASQLGAGLQEMGWIENSFSVQVLIIAAVMSLAVVSAISGVGK
           |||||:|||||
a163      MALLATFFGIITTLGFGASQLGAGLQEIIGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
           190     200     210     220     230     240

           250     260     270     280     290     300
m163.pep  GVKVLSSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
           |||||
a163      GVKVLSSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
           250     260     270     280     290     300

           310     320     330     340     350     360
m163.pep  WFESWTVLYAWWCWAPFVGLFIARISKGRITREFVFGVLLIPGLFGLVWFTVFGNTAI
           |||||
a163      WFESWTVLYAWWCWAPFVGLFIARISKGRITREFVFGVLLIPGLFGLVWFTVFGNTAI
           310     320     330     340     350     360

           370     380     390     400     410     420
m163.pep  WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
           |||||:|||||
a163      WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
           370     380     390     400     410     420

           430     440     450     460     470     480
m163.pep  ITS RDKGLSAPRWQAVMWGVLMSAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
           |||||
a163      ITS RDKGLSAPRWQAVMWGVLMSAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
           430     440     450     460     470     480

           490     500     510     520     530     540
m163.pep  WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQE QDILKFLKQTAS PAMHELQR
           |||||
a163      WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQE QDILKFLKHTAS PAMHELQR
           490     500     510     520     530     540

           550     560     570     580     590     600
m163.pep  ELSEEYGLSVRVDMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
           |||||:|||||
a163      ELSEEYGLSVRVDMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
           550     560     570     580     590     600

           610     620     630     640     650     660
m163.pep  HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLM LDDVGQELMAHEQVELAE
           |||||
a163      HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLM LDDVGQELMAHEQVELAE
           610     620     630     640     650     660

m163.pep  X
           |
a163      X
```



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGCGC TTCCTGTTTC CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCG GTCGAAAAAA TCATTTGGAC GGACAAAAGC
151 CGGCCGCGCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCCG ACTTGGGCGG CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTcctg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAATc cgttttCCcC ttttccaacG TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTCAGATG GTTCAACCGC
601 ATCCGCTGTG TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCCTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751 GCCCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGCGCA AGTGGGCGAA CTGATCGTCA
851 GGGCGGTTTC GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAAACG GGCgATTTCG TTACCATAGA
951 CGAGGACGCG TTTATCTTTA TCGTCGACCG CAAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GGCGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTTGG
1151 GCGAGGACGA aatccgccgc caccTGCGTA CCGTGCTGGC AAATTTCAAA
1201 ATCCCAAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPDLGRQPR INDLAHIIYT SGTGHPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MULLPIYMAC
151 SILLVKSVEP FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKDD LIISKGQNVY PREIEEIIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACGGA AACGGCACGG CAGTGTTCTG CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGCGGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCAC
201 AGAATTTATT ACCGCTATT TCGCCATCTC CGCCATCGGC GCGGTGCGCG
251 TACCGATGAA CACATTTTGT AAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGCGCTGT CAAAAGAATT
351 GCGGGGCTTG AAGGCGCAA CGCCGTCGA AAAATCATT TGGACGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAA ACCCGACTTG GGCCGCCAAC CCCGATAAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTTG
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGCGT TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATTCG CCTGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA

```

```

951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGCCAAAGCC
1051 GTCGATGAAG AATTGGTCGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTGAT
1251 TATTTCCAA GGTCAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1 MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51 IGVKFGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQTLKRA TV FLGVPAIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVGELIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDEGFIFV DRKKDLISK GQNVYPREIE EEIYKLDAVE AAAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
501 TGKVLKRVLK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

m164.pep	60	70	80	90	100	110
	GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARLFASAGLSK					
g164						
				10	20	30
m164.pep	120	130	140	150	160	170
	ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT					
g164						
	40	50	60	70	80	90
m164.pep	180	190	200	210	220	230
	SGTTGHPKGALISYANL FANLNGIERIFKISKRDRFIVFLPMFHSFTLTAMVLLPIYMAC					
g164						
	100	110	120	130	140	150
m164.pep	240	250	260	270	280	290
	SIILVKSVFPFSNVLKQTLKRA TV FLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAP					
g164						
	160	170	180	190	200	210
m164.pep	300	310	320	330	340	350
	LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNT PERQKARSVG IPLPGLEAKAVDEEL					
g164						
	220	230	240	250	260	270
	360	370	380	390	400	410

467

```

m164.pep  VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
           |||
g164       VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
           280      290      300      310      320      330

           420      430      440      450      460      470
m164.pep  LIISKQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
           |||
g164       LIISKQNVYPREIEEEIHKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
           340      350      360      370      380      390

           480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
           |||
g164       HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
           400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCTTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTGT AAAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GCGGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCGGCT TCCCGCAAAA ACCCGACTTG GGCCGCCAAC CCGGATAAAA
501 TGATTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TCCCCTTTTC CAACGTTTGT
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATGCG TGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGG AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTG AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGTGA TCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTATCGTC GACCGCAAAA AAGATTGTAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPDL GRQPRINDLA HIIYTSCTTG HPGKALISYA NLFANLNGIE
201 RIFKISKRRD FIVFLPMFHS FTLTAMVLLP IYMACSIIIV KSVFPFSNVL
251 KQALLKRATV FLGVPPIYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGEIVRGG SVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDEGFIFIV DRKKDLISK QNVYPREIE EEIYKLDAVE AAAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRTV LANFKIPKQI HFKDGLPRNA

```

501 TGKVLKRVLK EQFDGNK\*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKN	NGTAVFDGKEKTAYRAL	KQEA	EAVAA	YLQNI	GVKFGDTVA
a164	MNRTYANFYEMLAACRKN	NGTAVFDGKEKTAYRAL	KQEA	EAVAA	YLQNI	GVKFGDTVA
	10	20	30	40	50	60
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISA	IGAVAVPMNTFLKNSEY	AYI	LN	DKARFL	FASAGLSKELAGL
a164	LAVSNSTEFITAYFAISA	IGAVAVPMNTFLKNSEY	AYI	LN	DKARFL	FASAGLSKELAGL
	70	80	90	100	110	120
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPT	GETAEGDAFFEDVRRF	PEKPD	LGRQPR	INDLAH	IITYSGTTG
a164	KAQTPVEKIIWTDKSRPT	GETAEGDAFFEDVRRF	PEKPD	LGRQPR	INDLAH	IITYSGTTG
	130	140	150	160	170	180
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNG	IERIFKISK	RDRFIV	FLPMFHS	FTLTAM	VLLPIYMACSIILV
a164	HPKGALISYANLFANLNG	IERIFKISK	RDRFIV	FLPMFHS	FTLTAM	VLLPIYMACSIILV
	190	200	210	220	230	240
m164.pep	250	260	270	280	290	300
	KSVFFFSNVLKQTLKRA	TVFLGVP	AIYTAM	SKAKIP	PWYFRW	FNRI
a164	KSVFFFSNVLKQTLKRA	TVFLGVP	AIYTAM	SKAKIP	PWYFRW	FNRI
	250	260	270	280	290	300
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGY	GLSEASPV	VAVNT	PERQKAR	SVGIPL	PGLEAKAVDEELVEVPR
a164	ILDFKAKFPRAKLLEGY	GLSEASPV	VAVNT	PERQKAR	SVGIPL	PGLEAKAVDEELVEVPR
	310	320	330	340	350	360
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGY	LNMPAAT	DETIVNG	WLKTG	DFVTI	DE
a164	GEVGELIVRGGSVMRGY	LNMPAAT	DETIVNG	WLKTG	DFVTI	DE
	370	380	390	400	410	420
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLD	AVEAAV	IGVKDR	YADEE	IVAFV	QLKEGMDLGENEIRRH
a164	GQNVYPREIEEEIYKLD	AVEAAV	IGVKDR	YADEE	IVAFV	QLKEGMDLGENEIRRH
	430	440	450	460	470	480
m164.pep	490	500	510			
	LANFKIPKQIHFKDGL	PRNATG	KVLKRV	LKEQ	FDGNKX	
a164	LANFKIPKQIHFKDGL	PRNATG	KVLKRV	LKEQ	FDGNKX	
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq

1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GGCGGCGGCA TTATGAGCGC

```

51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCCCTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgcGTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCGGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CcTGCTGGgC gAATTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

g165.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTQKLFEN MEFSTDNRKI
151 SDWAPLIMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GLPVSGLFRR NSNPETAEOH NAKVYQASV GAPMMSVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSFM DLPLSIHMDN LYPLMRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

m165.seq (partial)

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCCTCAT CAATGCCGTG CCGCATATGT CTTTGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGATTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCG TGTCGGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

m165.pep (partial)

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD AFKTQKLFEN MEFSTDNRKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGVKTEF

```

201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK  
 251 SGIPEGKGYG GFPVSGLFFR NSNPETAQEH NAKVYQASV GAPPMSVPHL  
 301 DTRNVDGKRH LMFGPYAGFR SNFLKQGLSL DLPLSIHMDN LYPMLCAGWA  
 351 NMPLTK...

Computer analysis of this amino acid sequence gave the following results:  
 Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

m165.pep	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC
g165	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED
g165	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMRGRDENQPVAANYSAEGTDVDF
g165	HCRYLQKRYDVFKTQKLFENMEFSTDNRKISDWAPLMRGRDENQPVAANYSAEGTDVDF
m165.pep	GRLTRQMVKYLGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDGQLTLRTRFLFLGA
g165	GRLTRQMVKYLGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDWQLTLRTRFLFLGA
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQEHNAKVYQASVGAPPMSVPHL
g165	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAQEHNAKVYQASVGAPPMSVPHL
m165.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGLSLDLPLSIHMDNLYPMLCAGWANMPLTK
g165	DTRNVDGKRHLMFGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
g165	ELRX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

a165.seq

1	ATGGCTGAAG	CGACAGACGT	TGTCTTGGTG	GGCGGCGGCA	TTATGAGCGC
51	GACTTTGGGC	GTTTTGCTCA	AAGAACTCGA	ACCGTCTTGG	GAAATCACCC
101	TGATTGAACG	CTTGAAGAT	GTGGCGTTGG	AATCGTCAAA	CGCGTGGAAC
151	AACGCCGCGCA	CGGGGCATTC	CGCGCTGTGC	GAATTGAACT	ATGCGCCGTT
201	GGGTGCAAAT	GGGATTATCG	ATCCGGCGCG	CGCCCTCAAT	ATTGCCGAAC
251	AGTTTCATGT	CAGCCGCCAG	TTTTGGGCGA	CGTTGGTCCG	GGAAGGCAAG
301	TTGGAAGACA	ATTCTTCAT	CAATGCCGTG	CGCATATGT	CTTTGGTGAT
351	GAATGAAGAC	CATTGTTCTT	ATCTTCAAAA	ACGTTATGAC	GCGTTTAAAA
401	CCCAAAACT	TTTTGAAAAT	ATGGAATTTT	CCACCGATCG	GAACAAAATT
451	TCCGATTGGG	CTCCGCTGAT	GATGCGCGGC	CGGGACGAAA	ACCAACCCGT
501	CGCCGCCAAC	TACTCCGCCG	AAGGCACGGA	TGTCGATTTC	GGACGGCTGA
551	CGCGCCAAAT	GGTGAAATAT	TTGCAGGGCA	AGGGCGTAAA	AACCGATTTC

```
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACGCG CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACTTATG GATTGCGCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATAA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGCACACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGAT TGCTGGGCGC GTCGCCGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGT ACGGCATCAA
1401 GTTGAACGAA AACCCGAAA GGC CGGATGA AATTATCGC TATACCGCGA
1451 AAGTGTGGA TATTAA
```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```
a165.pep
 1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLEYYPEA NPDDWELITA QQRVQIIKID
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*
```

m165/a165 99.7% identity in 356 aa overlap

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
a165	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
	10	20	30	40	50	60
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
a165	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
a165	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	130	140	150	160	170	180
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF					
a165	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
m165.pep	GRLTRQMVKYLQKGKVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA					
a165	GRLTRQMVKYLQKGKVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA					
	190	200	210	220	230	240
m165.pep	GRLTRQMVKYLQKGKVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA					
a165	GRLTRQMVKYLQKGKVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA					
	250	260	270	280	290	300
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSPVPHL					
a165	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSPVPHL					
	250	260	270	280	290	300

	310	320	330	340	350
m165.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK				
a165	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG				
	310	320	330	340	350
	360				
a165	ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS				
	370	380	390	400	410
	420				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT AtgcgccGCT
201 GGGtgccgac ggcgtcatCA ATCCGGCGCG cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctggTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAACGAAGAC CACTGCCGTT ACCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgcCTGAT TATGCGCGGC GGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TATTCGCCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAACCCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCGCCACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACCAAC AAGCCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTGCCCGC
1001 TGTCATCCCA TATGGACAAC CTCTATCCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATAA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTt gCCTCCCTGC TGgaatacta cccGaggcag acccGACGAc
1151 tggtaactcat caccgagcnc acCGCTcata tcattanata tgactCGaaa
1201 ctgcgcgtgc tgcagttgta cgagattgtg ccaCGGacg ctcgctcgcg
1251 cattctggag cgtcgcgcg catcacgctn tgcgctgata tccgctgatg
1301 acactgtccc gaGCGcgccc gtcttggaat gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSAIC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLMIRG BDENPVAAN YSAEGTDVDF GRLTRQMVKY LQSGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SRIPEGKYGG GLPVSGLFFR NSNPETAEOH NAKVYGQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPQR TRRLVLITQX TRHIIYDSK
401 LRVLQLEYIV PRDARSRIE RRGASRXALI SADDTAPSAP VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

m165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCCCGGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATGTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCGCTGAT GATGCGCGCG GGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACCAAC AAGCCCAAAG

```



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851 TGTACGGGCA GGCCTCCGTC GCGCGCCGCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACTTCC TCAAGCAAGG CTCGCTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAAT CATACCGCA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGAT TGCTGGGCGC GTCGCCGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

m165-1.pep

```

1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDNRKI
151 SDWAPLMRGR RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQGGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFFVSGLFFR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSMD LPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIHKD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165-1/g165-1 89.7% identity in 428 aa overlap

	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
g165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGIIDPARALN	IAEQFHVSQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
g165-1	ELNYAPLGADGVINPARALN	IAEQFHVSQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
	70	80	90	100	110	120
	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFSTDNRKISDWAPLMRGR	DENQPVAANYSAEGTDVDF			
g165-1	HCRYLQKRYDVFKTQKLFEN	MEFSTDNRKISDWAPLMRGR	DENQPVAANYSAEGTDVDF			
	130	140	150	160	170	180
	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKYLQGGKGVKTEF	NRHVEDIKRES	DGAWVLKTADTRNPDGQLT	LRTRFLFLGA		
g165-1	GRLTRQMVKYLQGGKGVKTEF	NRHVEDIKRES	DGAWVLKTADTRNPDGQLT	LRTRFLFLGA		
	190	200	210	220	230	240
	250	260	270	280	290	300
m165-1.pep	GGGALTLLQKSGIPEGKGYGG	FVSGLFFRNSNPETAQH	NAKVYQASVGAPPMSVPHL			
g165-1	GGGALTLLQKSGIPEGKGYGG	LPVSGLFFRNSNPETAQH	NAKVYQASVGAPPMSVPHL			
	250	260	270	280	290	300
	310	320	330	340	350	360
m165-1.pep	DTRNVDGKRHLMFGPYAGFR	SNFLKQGSMDLPLSIHMDN	LYPMLCAGWANMPLTKYLLG			
g165-1	DTRNVDGKRHLMFGPYAGFR	SNFLKQGSMDLPLSIHMDN	LYPMLCAGWANMPLTKYLLG			
	310	320	330	340	350	360
	370	380	390	400	410	420
m165-1.pep	ELRKTKEERFASLLEYYPEAN	PDDWELITAGQRVQIHKD	SEKGGVLQFGTEIVAHADGS			
g165-1	ELRKTKEERFASLLEYYPEAN	PDDWELITAGQRVQIHKD	SEKGGVLQFGTEIVAHADGS			
	370	380	390	400	410	420
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNNPERADEIIA  
:  
111  
g165-1 ILERRGASRXALISADDTAPSAPVLESVX  
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq  
1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCGCA TTATGAGCGC  
51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTTGG GAAATCACCC  
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC  
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT  
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATGCGCGAAC  
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG  
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT  
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA  
401 CCCAAAAACT TTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT  
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCTG  
501 CGCGCCCAAC TACTCCGCCG AAGGCACGGA TGTGATTTC GGACGGCTGA  
551 CGCGCCCAAT GGTGAAATAT TTGCAAGGCA AGGGCGTAAA AACCGAGTTC  
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT  
651 CAAAACCGCC GATACCCGCA ACCCGACGCG GCAGCTCACC CTCCGTACCC  
701 GCTTCCTCTT CCTCGGCGCG GCGCGCGGCG CGCTGACCCT GCTGCAAAAA  
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT  
801 GTTCTTCGCG AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG  
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC  
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC  
951 AGGCTTCCGT TCCAATTCC TCAAGCAAGG CTCACTTATG GATTTGCCGC  
1001 TGTCATCCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG  
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA  
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACT CCCCAGGGA AACCCGACG  
1151 ACTGGGAAGT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC  
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC  
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCGGGGC GCATCGACCG  
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC  
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA  
1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA  
1451 AAGTGTGGA TATTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep  
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN  
51 NAGTGHSAALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK  
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI  
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQGGKGVKTEF  
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK  
251 SGIPPEGKGYG GFPVSGLFRR NSNPETAQH NAKVYQASV GAPPMSVPHL  
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA  
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKKD  
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT  
451 PSWEGRLKEL VPGYGIKLNE NPERADEIIA YTAKVLDI\*

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSAALC					
m165-1	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSAALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165-1	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF					
m165-1	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240

```

a165-1.pep  GRLTRQMVKYLGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
m165-1       GRLTRQMVKYLGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL
m165-1       GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
m165-1       DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
m165-1       ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
m165-1       LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
m165-1       YTAKVLDIX

```

**a165-1/p33940**

sp|P33940|YOJH\_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION  
>gi|1736851|gnl|PID|d1016718 (D90850) ORF\_ID:o372#5; similar to [SwissProt Accession Number P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical to 490 residues of YOJH\_ECOLI SW: P33940 (492 aa) but contains 56 additional N-term aa; 100 pct identical to GB: ECOHU49\_33  
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548  
Score = 458 bits (1167), Expect = e-128  
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```

Query: 3  EATDVVLVGGGIMSATLGVLKLEPSWEITLIERLEDVALESSNAWNNAGTGHSA LCEL 62
      + TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSA L EL
Sbjct: 30 QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSA LMEL 89

Query: 63 NYAPL GANGIIDPARALNIAEQFHVS RQFWATLVAEGKLED-NSFINAVPHMSLV MNEDH 121
      NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90 NYTPQNADGSISIEKAVAINAEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

Query: 122 CSYLQKRYDAFKTKL FENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDFG 181
      ++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150 VNFLRARYAALQQSSLFRGMRYSEDHAQIKEWAPLVMEGRDPQQKVAATRTEIGTDVNYG 209

Query: 182 RLTRQMVKYLGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
      +TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210 EITRQLIASLQKKS N FSLQLSSEVRALKRNDNTWTVTVADLKNGT AQ-NIRAKFVFIGA 268

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL 300
      Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVNVNHLAKVYGKASVGAPPMSVPHI 328

Query: 301 DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
      DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329 DTRVLDGKRVLFGFPATFSTKFLKNGSLWDLMSSTTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
      ++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGLV+ GTE+v
Sbjct: 389 QVMLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDAEKGGLVRLGT EVVSDQQGT 448

Query: 421 XXXXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478

```

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +  
 Sbjct: 449 IAALLGASPGASTAAPIMLNLLKRVFGDRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508  
 Query: 479 IAYTAKVLDI 488  
 + YT++VL +  
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq  
 1 atggcggcgg cggaaataaa acgccccctc gctgtcgatt tccagcacat  
 51 agcgtccggt ctgcacggcg gcatagccgc ttttgcctgc ctgatagggg  
 101 tgcagggcgg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc  
 151 ggcgatattg cccaccagtt tggcaacaa ggatggcac acgccgtttt  
 201 ccgcccagcc cgaaggcggc tcctttccgt cggtttccat acatttgccg  
 251 acgacggcct ccaagtcggt gggatgcttt ccggtcagcc ggacggcgtt  
 301 ttgttccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt  
 351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta  
 401 ttgtcgatgt atttgacttt gaaaaccggg ttcggcggcg tttgtgccgc  
 451 attttgcccgc tgttccggcg tattttcgga tttgccgcag gcggcaagca  
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc  
 551 tgatggtttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg  
 601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcac  
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgct ttttgcgcgc  
 701 ctgcctgcaa aatctcttcg atttgcaag gattagaggt caatgcgttg  
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep  
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF  
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQVV GMLSGQPDGV  
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDFD ENRFRRALCR  
 151 ILRLFRRIFG FAAGGKQQA AOHGKRYFQH SALLMVSKCR LKCRLLKRRR  
 201 RFGRHVYFN GRMPTASRTL SNNSRASLRA FCAPACKISS ICEGLEVNAL  
 251 \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq  
 1 ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTGCGATT TCCAGCACAT  
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCTGC CTGATAGGGT  
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC  
 151 GGCATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT  
 201 CTGCCCAACC TGCCGGACTG TCCTTATCAT CGGTTTCCAT ACATTGCGG  
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT  
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT  
 351 TGGTTTGGCC TTCGCTGCTT TGTCCCAAT CCAAACCGGC AATCGCCGTA  
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC  
 451 GTTTTGGCGC TGTACCGCCG TATTWCGGA TTTGCCGCaC GGCaArGCAG  
 501 CAGGCAGCCG CCAATACGG CAAAaAwGT wTTCAGCATT CCACaYTCCT  
 551 GATGGTTTCA AAATGCCGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC  
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATcGT ACTTGTCCTA  
 651 ATAATTCGCG TGCTTCTTTA CGCGCTTTCG CCGCGCCTGC CTGCAAAATC  
 701 TCTTCGATT GCGAAGGGTC GCGGTCAGC TCGTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep  
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN \*VIRQFAAVF  
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI  
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRALYR  
 151 VLRLYRRIIX FAATAXQQA AQYKXXXQH STXLMVSKCR LKRGRRRFRGR  
 201 HRVHFNGRMP TASGTLNNNS RASLRAFAAP ACKISSICEG SAVSSL\*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 204 shows 82.0% identity over a 250 aa overlap with a predicted ORF (ORF 204.ng) from *N. gonorrhoeae*:

m204/g204

	10	20	30	40	50	60
m204 . pep	<b>MAAAEIKRPFAVDFQHIASVLHGGIAAFACLIGLQGGMRNXVI R Q F AAVFGDIAHQF G K Q</b>					
	:					
g204	<b>MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIGLQGGM RNQVISQFAAVFGDIAHQF G K Q</b>					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204 . pep	<b>GMAHAVFCPTCRTVLI IGFHTFAADG F VAGMLADQSDNILFRQA FNRI TDLFFAVVGFA</b>					
	:     :                 :     :     :					
g204	<b>GMAHAVFRPARRRVLSVGFHTFADDG F VVGMLS GPDPGV L FRQA FNRI TD L FF AV VG FA</b>					
	70	80	90	100	110	120
	130	140	150	160	170	180
m204 . pep	<b>FAALSQTGTGNRRIVDIYDFENRFRRAL Y RVLRLY RR IX GF AA TA X QQ AAA QYGKXXXQH</b>					
	:                    : :                 :       :         :					
g204	<b>FATLSQS QTGNRRIVDVFD F EN RFRR AL CR IL RL FR RI FGFA AG GKQQAAAQHGRYFH</b>					
	130	140	150	160	170	180
	190	200	210	220	230	
m204 . pep	<b>STXLMVSKCRLK----RGRRRFGRHRVFHN GRM PT AS GT LS NN S RA SLRAFAAPACKISS</b>					
	:                         :					
g204	<b>SALLMVSKCRLLKCRLKRGRRRFGRHWVYFN GRM PT AS RT LS NN S RA SLRAFCA P ACK ISS</b>					
	190	200	210	220	230	240
	240					
m204 . pep	<b>ICEGS AVSSLX</b>					
	: :					
g204	<b>ICGLEVNAL</b>					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

a204.seq

```
1 ATGGCGGCGG CGGAAATAAA ACGCCCCCTC GCTGTCGATT TCCAGCACAT
51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCCTG CTGATAGGGT
101 TGCAGGGCGG AATGCGAAAT CAGGTAATCC GTCAGTTTGC CGCCGTCCTC
151 GCGCATATTG CCCACAGATT TGGCAAAACA GGTATGGCAC AGCCCGTTTG
201 CCGCCAGCCG CGAAGGCGCG CCCTTTCCGT CGGTTTCCAT ACATTGCGG
251 ACGACGGCTT CCAAGTCGTT GGGATGCTTG CCGTCAGCC GGACGACGTT
301 TTGTTCCGGC AAGCCTTT. . . . .
351 . . . . .
401 . . . . .
451 . . . . .
501 . . . . .
551 . . . . . AAGAG GTTCGGACGG
601 CATTTGGTTT ATTTCAACGG GCGGATACCG ATCCGCATCA GTACTTTGCC
651 CAATAATTCT CGTGCTCTTT TACGCGCTTT TCGCGCCCT GCGTCAAAA
701 TCTCTTCGAG TTGCGAAGGG TCGGCGGTCA GCTCGTTGTA G
```

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

a204.pep

1	MAAAEIKRPL	AVDFQHIASV	LHGIIAFAFC	LIGLQGGMRN	QVIRQFAAVF
51	GDIAHQFGKQ	GMHAVCRPA	RRRLSVGFH	TFADDGFQVV	GMLAGQDDV
101	LFRQAF....	.....	.....	.....	.....
151	.....	.....	.....	.....	.....KRFRGR
201	HWVYFNGRIP	TASRTLPNNS	RASLRAFCAP	ACKISSICEG	SAVSSL*

**m204/a204 54.5% identity in 246 aa overlap**

	10	20	30	40	50	60
m204.pep	MAAAEIKRFFAVDFQHIASVLHGGIAAFACLIQLQGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLQGGMRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFGVAGMLADQSDNILFRQAENRITDLFFAVVGFA					
a204	GMAHAVCRFARRRALSFGHTFADDGFGVAGMLAQPDVLFQAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQGNRRIVDIYDFENRFRRLYRVLRLYRRXGFAATAXQQAAYGKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKGRRRRFGHRVHFNGRMPTASGTLNNRSLRAFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLPNNSRASLRAFCAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

g205.seq

```

1 atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgettgcgcg
51 ctgcggcaaa tccgaaaata cggcggaaca gccgcaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgcgcgtc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaagga cgcgccttcg ggctgggagg aaaacggcgt
351 gtgccatacc ttgtttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaaaactgac tgattacctg atttcgcatt ccgccttgca accctatcag
451 gcaggcaaaa gcggctatgc cgcctgacg aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

g205.pep

```

1 MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51 AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNTA EDGGKLTGYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

m205.seq

```

1 ATGCTGAAwA CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51 tCGGGCAAAT CCGwAAATAC GCGGTACAG CCGCAAACG CGGTACAAAG
101 CGCGCCGAAA CCGTTTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGGA TTTGGGACAA AGCAGCGAAG GCAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGGA AGCCGTCAGC GGCAAATGTA
301 TGGAAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTGCGATGC CGCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

```
m205.pep
1  MLXTXFAVLG  GCLLXCRCGK  SXNTAVQPQN  AVQSAPKPVF  KVIYIDNTAI
51  AGLDLGQSSE  GKTNDGKKQI  SYPIKGLPEQ  NVIRLIGKHP  GDLEAVSGKC
101 METDDKDSPA  GWAENGVCHT  LFAKLVGNIA  EDGGKLTDDL  VSHAALQPYQ
151 AGKSGYAAVQ  NGRYVLEIDS  EGAFYFRRRH  Y*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

```
m205/g205

      10      20      30      40      50      60
m205.pep  MLXTXFAVLGGCLLXCRCGKSXNTAVQPQNNAVQSAPKPVFKVIYIDNTAIAGLDLGQSSE
          |||||
g205       MLKIPFAVLGGCLLLAACGKSENTAEQPQNAAQSAPKPVFKVKYIDNTAIAGLALGQSSE
          |||||

      10      20      30      40      50      60
m205.pep  GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSPAGWAENGVC
          |||||
g205       GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVC
          |||||

      70      80      90     100     110     120
m205.pep  GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSPAGWAENGVC
          |||||
g205       GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVC
          |||||

      70      80      90     100     110     120
m205.pep  LFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFRRRH
          |||||
g205       LFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFRRRH
          |||||

      130     140     150     160     170     180
m205.pep  LFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFRRRH
          |||||
g205       LFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFRRRH
          |||||

      130     140     150     160     170     180

m205.pep  YX
          |
g205      Y
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

```
a205.seq (partial)
1  TCCGAACCTC  TTAAGGCTT  GCCGGAACAA  AACGTCGTCC  GGCTGACCGG
51  CAAGCATCCC  AACGACTTGG  AAGCCGTCGT  CGGCAATGT  ATGGAACCGG
101 ACGGAAAGGG  CGCGCCTTCG  GGCTGGGCGG  CAAACGGCGT  GTGCCATACC
151 TTGTTTGCCA  AACTGGTGGG  CAATATCGCC  GAAGACGGCG  GCAAACCTGAC
201 GGATTACCTG  ATTTTCGATT  CCGCCCTGCA  ACCCTATCAG  GCAGGCAAAA
251 GCGGCTATGC  CGCCGTGCAG  AACGACGCT  ATGTGCTGGA  AATCGACAGC
301 GAGGGGCGT  TTTATTCCG  CCGCCGCCAT  TATTGA
```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

```
a205.pep (partial)
1  SEPLKGLPEQ  NVVRLTGKHP  NDLEAVVGKC  METDGKGAPS  GWAANGVCHT
51  LFAKLVGNIA  EDGGKLTDDL  ISHSALQPYQ  AGKSGYAAVQ  NGRYVLEIDS
101 EGAFYFRRRH  Y*
```

**m205/a205** 88.3% identity in 111 aa overlap

```
      50      60      70      80      90     100
m205.pep  KVIYIDNTAIAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC
          | :|||
a205       SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC
          10      20      30

      110     120     130     140     150     160
m205.pep  METDDKDSPAGWAENGVCHTLFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQ
```

```

||||| :||:|| ||||| ||||| ||||| ||||| ||||| ||||| :||: ||||| ||||| |||||
a205      METDGKGAPSGWAANGVCHTLFAKLVGNI AEDGGKLT DYLISHSALQPYQAGKSGYAAVQ
              40          50          60          70          80          90

               170       180
m205.pep     NGRYVLEIDSEGAFYFRRRHYX
             ||||||| |||||||
a205         NGRYVLEIDSEGAFYFRRRHYX
              100        110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 709>:

g205-1.seq (partial)

1	ATGCTGAAAA	TAcCTTTTGC	CGTGTGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAAAAT	CGGCGGAAAT	GCCGCAAAAT	GCGGCACAAA
101	GCGCGCGCAA	ACCGGTTTTC	AAAGTCAAAT	ACATCGACAA	TACGGCGATT
151	GCGGGTTTGG	CTTTGGGACA	AAGTAGCGAA	GCGCAAAACCA	ACGACGGCAA
201	AAAACAAATC	AGTTATCCGA	TTAAGGCTT	GCCGGAACAA	AACGCCGTCC
251	GGCTGACCGG	AAAGCATCCC	AACGACTTCG	AAGCGCTCGT	CGGCAAAATG
301	ATGGAACCCG	ACGGAAGAGA	CGCGCTTTGG	GGCTGGGCGT	AAAACGGCGT
351	TGCGCATACC	TGTGTTGGCA	AACTGGTGGG	CAATATCGCC	GAAAGACGGC
401	GCAAACTGAC	TGATTACCTG	ATTTCGCATT	CCGCCCTGCA	ACCCTATCAG
451	GACGGCAAAA	GCGGCTATGC	CGCGGTGAG	AACGGACGCT	ATGTGCTGGA
501	ATATCGACAGC	GAGGGGGCGT	TTTA		

This corresponds to the amino acid sequence <SEQ ID 710; ORF 205-1.ng>:

g205-1.pep (partial).

```

1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51 AGLALGQSSE GKTNDGKKQI SYPTKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGDKAPS GAEWGVCHT LFAKLVGNIA EDGGKLT DYL ISHSALQPYQ
151 ASGSGYAAVO NGRVYLETDS EGAFAF

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 711>:

**m205-1.seq..**

1	ATGCTGAAAA	CATCTTTTGC	CGTATTGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAAAAT	CGGCGGAAAT	GCCGCAAAAC	GCGGTACAAA
101	GCGCGCCGAA	ACCGGTTTTC	AAGCTCAAAT	ATATCGACAA	TACGGCGATT
151	GCCGGTTTGG	ATTTGGGACA	AAAGCTGCAA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAATC	AGTTATCCGA	TAAAGGCTT	GCCGGAACAA	AATGTTATCC
251	GACTGATCGG	CAAGCATCCC	GGCAGCTTGG	AGGCGCTCAG	CGGCAAATGT
301	ATGGAACACG	ATGATAAGGA	CAGTCCGCGA	TGTTGGGCAG	AAACCGCGGT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACTGAC	GGATTACCTA	GTTTCCGATC	CCGCGCTCAG	ACCCTATCAG
451	GCAAGCAAAA	GCGGCTATGC	GCGCCGTCAG	ACAGGACGCT	ATGTGCTGGA
501	AATCGACAGC	GAAGGGGGCGT	TTTATTTCGG	CCGCGCCCAT	TATTGA

This corresponds to the amino acid sequence <SEQ ID 712; ORF 205-1>:

m205-1.pgp

1 MLKTSFAVLG GCLLLAACGK SENTAEQPQN AVQSAPKPVF KVKYIDNTAI  
51 AGLDLGGSSE GKTNDGKKQI SYPIKGLNEQ NVIRLIGHPI GDLEAVSGKC  
101 METDDKDSPA GAENGVCVTH FLAKLVLPQIA EDGKKLTDPY VSHAALQPYQ  
151 AEGSGYAAOV NGRVYLEIDS EGAFYFRRRH Y\*

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAAGCKSENTAEQPNAAQSAPKPVFKVKYIDNTAIAGLALGQSSE					
m205-1	MLKTSFAVLGGCLLLAAGCKSENTAEQPNNAVQSAPKPVFKVKYIDNTAIAGLDLGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT					
m205-1	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSPGAWAENGVCHT					



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```

              70      80      90      100      110      120
          130      140      150      160      170
g205-1.pep  LFAKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m205-1      LFAKLVGNI AEDGGKLT DYLV SHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          130      140      150      160      170      180

m205-1      YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
1  CCTCTTAAAG GCTTGCCGGA ACAAACGTC GTCCGGCTGA CCGGCAAGCA
51  TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
101 AGGGCGCGCC TTCGGGCTGG GCGGCAACG GCGTGTGCCA TACCTGTGTT
151 GCCAAACTGG TGGGCAATAT CGCCGAAGAC GCGGCAAAAC TGACGGATTA
201 CCTGATTTCG CATTCGCGCC TGCAACCCTA TCAGGCAGGC AAAAGCGGCT
251 ATGCCGCGCT GCAGAACGGA CGCTATGTGC TGGAAATCGA CAGCGAGGGG
301 GCGTTTTATT TCCGCCGCGC CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
1  PLKGLPEQNV VRLTGKHPND LEAVVGKME TDGKGAPSGW AANGVCHTLF
51  AKLVGNIAED GKLTDYLI SHSALQPYQAG KSGYAAVQNG RYVLEIDSEG
101 AFYFRRRHY*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

          50      60      70      80      90      100
m205-1.pep KYIDNTAIAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKME
          |||:|||||:|||||:|||||:|||||:|||||
a205-1      PLKGLPEQNVVRLTGKHPNDLEAVVGKME
          10      20      30

          110      120      130      140      150      160
m205-1.pep TDDKDSPAGWAENGVCHTLFAKLVGNI AEDGGKLT DYLV SHAALQPYQAGKSGYAAVQNG
          |||:|||||:|||||:|||||:|||||:|||||
a205-1      TDGKGAPSGWAANGVCHTLFAKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNG
          40      50      60      70      80      90

          170      180
m205-1.pep RYVLEIDSEGAFYFRRRHYX
          |||:|||||:|||||:|||||
a205-1      RYVLEIDSEGAFYFRRRHYX
          100      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
1  atgttttccc ccgacaaaac ccttttcctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct ccggcaaaca ccgccaaccg aaacccaaac
101 agacagtccg gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctcggactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgcctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atcccgcaca gccgcctcaa
351 ggccggcgac atcgatttct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcatccatgc ccccggcagc
451 ggcaaaaacca tcaaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttga ggcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```

51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPRT  
101 ARDMAAASRK IPDSRLKAGD IVFNTGGAH RYSHVGLYIG NGEFIHAPGS  
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

```
m206.beq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCCTCCGCA TCAGCCACAT CGACCCGACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCAGCCG
201 CTACAAATGG GCGCGGACGA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAR AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCAGCA TGGCGGCGGC AAGCCGAAA ATCCCCGACA GCCGyTCAA
351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTAC
401 ACGTCGGACT CTACATCGCG AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GCGAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

```
m206.pep..
  1  MFPPDKTLFL  CLSALLLASC  GTTSGKHRQP  KPKQTVRQIQ  AVRISHIDRT
51  QGSQELMLHS  LGLIGTPYKW  GGSSTATGFD  CSGMIQFVYK  NALNVKLPRT
101 ARDMAAASRK  IPDSRXKAGD  LVFFNTGGAH  RYSHVGLYIG  NGEFIHAPSS
151 GKTIKTEKLS  TPFYAKNYLG  AHTFTE*
```

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng)

from *N. gonorrhoeae*:

```

m206/g206

                10         20         30         40         50         60
m206.pep  MFPPDKTLFLCLSLALLASCGETTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g206      MFSPDKTLFLCLGALLASCGETTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS
           10         20         30         40         50         60

                70         80         90        100        110        120
m206.pep  LGLIGTPYKWGGSSTATGFDCSGMIQFVYKNALNVKLPRRTARDMAAASRKIPDSRXKAGD
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g206      LGLIGTPYKWGGSSTATGFDCSGMIQLVYKNALNVKLPRRTARDMAAASRKIPDSRLKAGD
           70         80         90        100        110        120

                130        140        150        160        170
m206.pep  LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPPFYAKNYLGAHTFFTEX
           :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g206      IVFFNTGGAHRYSHVGLYIGNGEFIHAPSGKTIKTEKLSTPPFYAKNYLGAHTFFTE
           130        140        150        160        170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq

```
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGCTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCCGACA
151 CAAGGCTCGG AGGAACTCAT GTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGC GCGCGCAGCA GCACCGCAAC CGGCTTCGAT TGACGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCGCGGACA TGGCGCGCGC AAGCCGCAAA ATCCCGGACA GCCGCCTTAA
351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTACAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD LVFENTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFDCSGMIQFVYKNALNVKLPRTARDMAAASRKIPDSRXKAGD					
a206	LGLIGTPYKWGGSSTATGFDCSGMIQFVYKNALNVKLPRTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFENTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
a206	LVFENTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
1  atgctgcggc atttaggaaa cgacttcgcc ttgggcgcggt tgtttttcga
51  tgctgcggtt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcgggttcag ataggtttgg gcgaacatcg ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgcccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 gtcgtcgcgg tatttttctt tgatggtctg cagttcgggt gcggcggcac
501 gcattttcgc catcgaaagg taggagcggt tggtaaatgg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagcccc agttgccgat
601 aatgttggtc agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgctcgg gatgtttcgg
701 ataacggatg tggtttcggg accggcatac aggttgaccg ccattttcgg
751 ttttgcccc cggttggtga tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
1  MLRHLGNDFE LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGDVVGVG AAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQRQTAA QRVDFLVFEK LHHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEPE ERRCEPVYFT VFQCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
1  ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
51  GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTGAGGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGGGT CGGTCGGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCAGCCAA
```

```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTGTGCA GTTGTTTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTCGGCG ATGTTTGCAG
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGGTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGAGAAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTCGGGG TTTTGGCGAT GTATTGCGCC
951 TCGGATTTCG CGGATTGGC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDFALGALFFDAADVPLLGDGQEVVDYPVQYQTGREEEHHDGE
51 NQRHDFHHFRLHRVGRRRVQISLGEHRCRHNDDGQDVVGVAEEVGNPTQP
101 RCLAQFYGGEQCPIQSDDEGLDQHRQAAAQRVDFLVCVKLHHRLLLRHT
151 VVAVFLFDGLQFGCGGTHFRHRAVRGVGQW IQYGFDDDG*NDNRPAPVAD
201 DVVQLVQEPERGGEPVYFAVVFQQLQVVG DVCDGCGCLRAGVEVDGGFG
251 FAPFWMAAKGTLTLVLYSLSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW
301 CSIMPSQPVGLRMYASDLPLASSSKSEKLTFWKLPSPG V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng) from *N. gonorrhoeae*:

m209/g209

m209.pep	10	20	30	40	50	60
	MLRHLGNDFALGALFFDAADVPLLGDGQEVVDYPVQYQTGREEEHHDGENQRHDFHHFR					
g209	MLRHLGNDFALGALFFDAADVPLLGDGQEVVDHPVENQTGREEEHHDGENQRHDFHHFR					
	10	20	30	40	50	60
m209.pep	70	80	90	100	110	120
	LHRVGRRRVQISLGEHRCRHNDDGQDVVGVAEEVGNPTQPRCLAQFYGGEQCPIQSDDEG					
g209	LHRVGRRRVQISLGEHRCRHNDDGQDVVGVAEEVGNPAQPRCLAQFYGGEQCQPVQADEG					
	70	80	90	100	110	120
m209.pep	130	140	150	160	170	180
	DLQHRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW					
g209	DLQHRQTAAQRVDFLVFEKLRHHRLLLRHTVVAVFFDGLQFGCGGTHFRHRTVGGVGQW					
	130	140	150	160	170	180
m209.pep	190	200	210	220	230	240
	IQYGFDDDGXNDNRPAPVADDVVQLVQEPERGGEPVYFAVVFQQLQVVG DVCDGCGCLR					
g209	IQYGFDDDGQNDDCPAPVADNVVQLVQEPERRCEPVYFTVVFCQLQVVG DVCDGCGCLR					
	190	200	210	220	230	240
m209.pep	250	260	270	280	290	299
	AGVEVDGGGFGF-APFWMAAKGTLTLVLYSLSLRRLMSMLHSPAAQTLCLPLGWRIQVDMK					
g209	TGIQVDRHFRFWPPGWDGSG					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTTAGGAAA CCACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

```

51  TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201 GCGGGTTTCA ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301 AGGTGCCTGG CGCAATTCTA CCGAGGCGAA CAATGCCCAA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAG CTGCATCATG GCTTGTGCT GCGCCATACG
451 GTCGTCGCGG TATTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601 GATGTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCAGT
651 GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTGCGGC GATGTTGCG
701 ATAACGGATG TGGTCTGTGG GCGGCGTAG AGGTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGGTGACGC TGGTGCTGTA
801 CAGCTTGTGC TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851 AAACGCTTTG TCCGCCTTTG GGTGGAGGA TCCAGGTGGA CATGAAGTGG
901 TGTTCATCA TGCCGAGCCA GCCGGTCGGG GTTTGCGGA TGTATTGCGC
951 CTCGGATTG CCGGATTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```

a209.pep
1  MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGE
51  NQRHDFHHER LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQQRQAAA QRVDFLVCVK LHHGLLRHT
151 VVAVFLFDGL QFGRGGTHER HRTVRGVGQW IQYGFDDDG* NDNREAPVAD
201 DVVQLVQPKP EGGGEPVYFA VVFGQLQVVG DVCNCGGLW AGVEVDGGFG
251 FAPFWIAAKG TLTVLVLSL LRRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*

```

m209/a209 95.6% identity in 341 aa overlap

	10	20	30	40	50	60
m209.pep	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR					
a209	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR					
	10	20	30	40	50	60
m209.pep	LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG					
a209	LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG					
	70	80	90	100	110	120
m209.pep	DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW					
a209	DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRTVRGVGQW					
	130	140	150	160	170	180
m209.pep	IQYGFDDDGXNDNRPAVADDVVQLVQEPKEGGGEPVYFAVVFGQLQVVGDVCDGCGGLR					
a209	IQYGFDDDGXNDNRPAVADDVVQLVQEPKEGGGEPVYFAVVFGQLQVVGDVCDGCGGLR					
	190	200	210	220	230	240
m209.pep	AGVEVDGGFGFAPFWMAAKGTLTLVLVLSLRLRLMSMLHSPAAQTLCLPLGWRIQVDMKW					
a209	AGVEVDGGFGFAPFWIAAKGTLTLVLVLSLRLRLMSIRQSPAAQTLCPPLGWRIQVDMKW					
	250	260	270	280	290	300
m209.pep	CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX					
a209	CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX					
	310	320	330	340		
m209.pep						
a209						

```

|||||
a209      CSIMPSQPVGVLRMYSASDLPLASSKSEKLTFWKLP SGVX
              310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```

g211.seq
1  atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atggtgcggc
51  ggtgggaaac ggggtcgata agtttgggcg tgggtctgat aatcaggttg
101 agtttttgga aggaaacctg attgtagtcg gcgcgtccgg gcgtgccgct
151 gtaacggtag ccgtggcgca attcgagcgt gcgtttgttg tccttcagcg
201 agaagttacc ttctttggcg aagatgatgt tgtcgccgcc gtttttgtcc
251 tgttcgcgca ggaacaggtt tttcatgatg ccggtattcg tgatcaagggt
301 ttcgacgaaa taaacctcgc cgttgcgctt gcccaggtta ttgaactcgc
351 cggcttccac caaagacaat tcctgcttct gcttcaaaat ttcggcatat
401 tcgcggtcgc gcagctctgc ccacgggtat acccaaagct gcatgacggc
451 aatcaggatg gcaaacggca cggcaaaact catgacgggg cgtatccact
501 gtttcaacgc caatccgcag gatag

```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

```

g211.pep
1  MLRIAAANQL GGRNGAAVGN GVDFKFRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVQREVTF FGEDDVVAA VFVLFQEQV FHDAGFGVKG
101 FDEINPAVAL AQVIELAGFH QRQFLLLQLQ FGFIAAALC PRYHPKLHDL
151 NQDGKRHGKL HDGAYPLFQR QSAG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```

m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGTACGGC
51  GGTGGGAAAC GGGGTCTGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTGGA AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGCGGCA ATTTCGAGCGT GCGTTTGTG TCCTTCAGCG
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTGCGCGCC GTTTTGTGCC
251 TGTTGCGGCA GGAACAGGTT TTTTCATGATG CCGGATTTCG TATCGAAGGT
301 TTCGACAAAA TAAACCTGCG CGTTGCGCTT GCCCAAAGT TTGAACGCG
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGGTAT ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAAAACGCA CGGCAAAGT CATCACGGG CGTATCCATT
501 GTTCAATGC CAATCCGCag GATAG

```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

```

m211.pep
1  MLRVAAANQL GGRNGTAVGN GVDFEGRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVQREVTF FGEDDVVAA VFVLFQEQV FHDAGFGIEG
101 FDKINPAVAL AQTVELACLH QRQFLLLQLD FSVFAAAXLC PRYHPKLHDL
151 NQNGKRHGKL HHRAYPLFQC QSAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

```

m211/g211

      10      20      30      40      50      60
m211.pep  MLRVAAANQLGGRNGTAVGNQVEFLEGNLIVVGASGRAAVTVAVAQFER
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g211      MLRIAAANQLGGRNGAAVGNQVEFLEGNLIVVGASGRAAVTVAVAQFER
          10      20      30      40      50      60

      70      80      90     100     110     120
m211.pep  AFVVQREVTFFGEDDVVAAVFVLFQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH

```

	:   :   :               :       :
g211	A F V V L Q R E V T F F G E D D V V A A V F V L F A Q E Q V F H D A G F G V K G F D E I N P A V A L A Q V I E L A G F H
	70                80                90                100                110                120
	130                140                150                160                170
m211.pep	Q R Q F L L L L Q D F S V F A A X L C P R Y H P K L H D G N Q N G K R H G K L H H R A Y P L F Q C Q S A G X
	:   :                               :
g211	Q R Q F L L L L Q N F G I F A A A Q L C P R Y H P K L H D G N Q D G K R H G K L H D G A Y P L F Q R Q S A G
	130                140                150                160                170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 731>:

```
a211.seq
  1  ATGTTGCGGG  TTGCTGCTGC  CAATCAGTTG  GCGGTCGGA  ATGGTACGGC
51  GGTGGGAAAC  GGGGTCGATG  AGTTTGGGCG  TGGTGCTGAT  AATCAGGTTG
101 AGTTTTTGGa  AGGAAACCTG  ATTGTAGTCG  GCGCGTCCGG  GCGTGCCGCT
151 GTAACGGTAG  CCGTGGCGCA  ATTCGACGCT  GCGTTTGTG  TCGTTCAGCG
201 AGAAGTTACT  TTTCTTGGCG  AAGATGATGT  TGTCGCGCGC  PTTTTGTCC
251 TGTTCCGCGC  GGAACAGGTT  TTTTCATGAT  CCGGATTCGG  TATCGAAGGT
301 TTCGACAAAA  TAAACCTGCG  CGTTGCGCTT  GCCCAAAGTG  TTGAACCCGC
351 CTGCCTCCAC  CAAAGACAAT  TCCTGCTTCT  GCTTCAGGAT  TTCAGCGTAT
401 TCGCGGCTGC  TAGGCTCTGC  CCACGGTATC  ACCCAAAGCT  GCATGACGGC
451 AACCAAAACG  GTAAACGGCA  CGGCAAAGTG  CATCACCGGG  CGTATCCATT
501 GTTTCATATC  CAATCCGCAG  GATAG
```

This corresponds to the amino acid sequence <SEQ ID 732; ORF 211.a>:

```
a211.pep
  1  MLRVAAANQL  GGRNGTAVGN  GVDEFGRGAD  NQVEFLEGNL  IVVGASGRAA
51  VTVAVAQFER  AFTVVQREV  FFGEDDVVAA  VFVLF AQEQV  FHDAGFGIEG
101 FDKINPAVAL  AQTVEPACLH  QRQFLLLLQD  FSVFAAA*LC  PRYHPKLHDG
151 NQNGKRHGKL  HHRAYPLFC  QSAG*
```

**m211/a211 99.4% identity in 174 aa overlap**

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
a211	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVVAAVFVLFAQEQQVFHDAGFGIEGFDKINPAVALAQTVELACLH					
a211	AFVVVQREVTFFGEDDVVAAVFVLFAQEQQVFHDAGFGIEGFDKINPAVALAQTVEPACLH					
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFSVFAAAXLCPRYHHPKLHDGNQNGKRHGKLGHHRAYPLFQCQSAGX					
a211	QRQFLLLLQDFSVFAAAXLCPRYHHPKLHDGNQNGKRHGKLGHHRAYPLFQCQSAGX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 733>:

g212.seq (partial)

```
1  atggacaatc tcgtatggga cggcattccc gacatccgca cactcgacca
51  aaccatccgc aaacacgcac acccgctcaa cctgattgtc tgcctccccg
101 ataatcagat tcccgatttt caaaccgcac aagatgcttc ggactcggaa
151 tgccgtctga agcaccgttt ggatcaggca acccagtgcc tccagttcga
201 cagcatcaac ctcatcgaac acatcctgcc cgatgtccgc ttctgggttc
251 tcccccttc acgcacccgc cgctctgcag aacatctcca ccacatttcc
301 tggcagacgc aagcatcccc gcgaaccgaa agcaagtcgc acaaacctcg
351 gtttgcaact ccacaaacat ccgaacggaa aaaaccggaa cacgtcctcg
```

```

401 tcatcgggtgc aggcattgcc ggcgcatcga ccgcccacgc cttagcatca
451 cacggcattt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaatctcgc ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctccgacaca tctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccc aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcaccctcct cagccatccg ctgatcgaac tatatgaaaa cacaacgtta
901 accggcattt ccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcatctactg caccggcgcg cacagcccct
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacggcc tcacaccgtc caccctgtt tccgaacaac tgcgttgccg
1101 cgtttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgcactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgcga agcattggca caccttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRDLQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSABE
251 EKIAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 BEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCGCTCAA CCTGATTATC TGCCTCCCGG
101 ATAATCAGAT TCCCGATTT CAAACCGCAC AAGATGCTTC GGACCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ATGCAGTGCC TCCAGTTTCA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGCGCG GGCATATACC GCGCGCGCAA CCGCCACGCG CTTAGCATCA
451 CACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTTGCCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTTCGTC
851 GCACCTCCTT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATTT CCCACGACGG GGAAGAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTATAC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCCTTGCCT
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCAGGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCCGACCACC TTCCCTAGT CGGCGCACTC
1351 GGCGACATTG CCGCCATGCG GCAGACCTAC ACCAACTCG CGCTGGACAA
1401 AAATACCGC ATCGACACCC CATGCCATA CCTGCCAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GACTCGCCA CCGCCCCCAT CTGCGCCGCG

```



1501 GmCAwTGCAG CCCAAATCtT AGGCyTGCCC CATCCCTTTT yAcAAcGCCT  
 1551 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA  
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep  
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE  
 51 CRLKHLRDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS  
 101 WQTEAIPQTE SKPDKPWFAL PQTSEKQKPE HILVIGAGIS GAATAHALAS  
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL  
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA  
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL  
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG  
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA  
 401 EEASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCDP PDHPLVLGAL  
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA  
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng) from *N. gonorrhoeae*:

m212/g212

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLIIICLPDNQIPDFQTAQDASDAECRLKHLRDQA					
	:     :     :     :     :					
g212	MDNLVWDGIPDIRTLDQTIKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRLKHLRDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPDKPWFAL					
	:     :     :     :     :					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRLHEHFHHISWQTEAIPQTESKSDKPWFAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m212.pep	PQTSEKQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	:     :     :     :     :					
g212	PQTSEKQKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHNNH					
	:     :     :     :     :					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHNNH					
	190	200	210	220	230	240
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL					
	:     :     :     :     :					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPYLPETNL AALPLRQIRGQTGLTPSTPF					
	:     :     :     :     :					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAEASNRQALAHLPALSES					

490

g212  
SEQLRCAVSGESYISPSWHGLHCYGFSPINSSNTGWNEAEASNRQALAHLPALAESL  
370 380 390 400 410 420  
430 440 450 460 470 480  
m212.pep  
FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN  
|  
q212  
F

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 737>:

```

a212.seq
1 ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AAATCATCCG AAACACGCAC ACCCGCTCAA CCGTATTGTC TGCCTCCCCG
101 AATCATCAGT TCCCAATTTT CAAACCCGCA AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACC GTTT GGATCAGGCA ACCCAGTGCC TCCAGTTCTGA
201 CAGCATCAAC CTGATTGAAC ACATCTGTCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCGC CGCCTGCACG AACCATTTCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAAACGAA AGTAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCTCTG
401 TTATCGGAGC GGGCATATCC GGGCGGGCAA CCGCCCACGC CTTAGCATCA
451 TACGGCATTT CCGTTACCGT ATTGGAAGCC CGAAAGCCGC CCCAAGCCGC
501 CAGCGGCAAT GCCCAAGGGC TGCTCTACGC CAAATCTCTG CCGCACGACA
551 CCGAACAAC CGAACTGCTG CTTGCCGGCT ACGGCTACAC CAACCGCCTG
601 CTCGGACATA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCCGCA CCGAACAACA ACGCAATCAC GAATTTGGTT
701 TGCAAAAAACA CCATAACCAC CTCTACCGCA GCATCAGCCA GGCAGAAGCC
751 GAAAAAATCG CCGGCATCCC TCTGAACACG CCCTACGCGC AACCATTATG
801 CGGACTGTTT TGGCAGTACG GCGTATGGCT CAATCCTCCC ACATTCTGTC
851 GCGCCCTCCT CAGGCATCCG CTCATTGGAG TACACGAAGA CACACGGTTA
901 ACCGACATTT CCCACGACGG GGAAGAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACACGCCCT
1001 ACCTACCCGA AACCAACCTC GCCACCTGCG CCCTCAGCCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCCTTGGCG
1101 CGTTTCAGCG GAAAGCTACA TCAGCCCGTC GTGGCAGCGA CTGCAGTGCT
1151 ACGGCGCGAG TTTTATTTCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAGGAAGCCT CAAACCGCCA AGCATTTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCACG
1301 CGGCCATACG CTGCGACAGC CCCGACACC TTTCCCTAGT CGGCGGACTC
1351 GGGCAGATTG CGCCTATGCA ACAAACTTAC GCTAAACTCG CGCTGGACAA
1401 AAACATATCG ATCGATGCCC CCTGCCCGTA CCTGCCAAT GCCTACGCCA
1451 ACACCGCCCA CGGCACACGC GGGCTTGCCA CCGCCCCCAT CTGCGCGGCC
1501 GCCGTTGCA CCGAAATCCT AGGCTTGCCC CATCCCTCT CAAAACGCCT
1551 CGGCCACGCC CTCACCCCA ACCGCGCCAT CATCCGCGC ATCGTCAGAA
1601 GGAAGGATCT AACCCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 738; ORF 212.a>:

a212.pep

1	MDNLAWNGIP	DIRTLDQTIK	KHAHPLNLIV	CLPDNQIPNF	QTAQDASDAE
51	CRLKHRLDQA	TQCLQFDSIN	LIEHILPDVR	FWLVPPSRTR	RLHEHFHHIS
101	WQTEAIPQTE	SKPKPKWFLA	PQTSEKQKPE	HILVIGAGIS	GAATAHALAS
151	YGISVTVLEA	RKAAQAASGN	ROGLLYAKIS	PHDTEQTELL	LAGYGYTKRL
201	LGHILPESET	WGGNGIIHLN	YSRTEQQRNH	ELGLQKHNNH	LYRSITQAEA
251	EKIAGIPLNT	PYAEPLCGLF	WQYGVWLNPP	TFVRALLSHP	LIGLHEDTPL
301	TDISHDGEKW	IASTPNGTFT	ATHIIYCTGA	NSPYLPETNL	ATLPLRQIRG
351	QTGLTPSTPF	SEQLRCAVSG	ESYISPSWHG	LHCYGASFIP	NSSHTGWNEA
401	EEASNRQALA	HLNPALESYL	FAANPNPQKH	QGHAAIRCDR	PDHLPLVGAL
451	GDIAAMQQTY	AKALDKNSYR	IDAPCFYLPN	AYANTAHGTR	<u>GLATAPICAA</u>
501	AVAAEILGLP	HPLSKRLRHA	LHPNRAITRA	IVRRKDLTP*	

**m212/a212** 93.7% identity in 539 aa overlap

m212.pep MDNLVWDGIPDIRTLDAQIRKHAPPLNLIICLPDNIQIPDFQTQAQDASDAECRLKHLRDLQA  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
a212 MDNLAWNGIPDIRTLDQTRKHAPHPLNLIVCLPDNQIPIPFQTQAQDASDAECRLKHLRDLQA

	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1  atgatacaaa agatatgtaa gctatttgtt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagcctc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaagcgcgcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gcttcagcca aacgttggac gggggcaaa ggcggtgctg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccggcaa tgccaaagtg cagcgcgcg ggcaggttgc cgaaggtgctg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgcga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

1	MIQKICKLFV	LIVIFATSPA	FALQSDSRRP	IQIEADQGSL	DQANQRTTFS
51	GNVIIIRGTL	NISASCNVNT	RGRQRRRIRE	GGRFARPLQP	NVGRGQRDGA
101	RS GKQRYLFL	RRKHCRSDRQ	CQSAARRRRC	RRCGHYLQHQ	NRSLYHQRQH
151	ETGCEIRFQN	RQGQRHPAF	KHTKNRITPM	PSETETQFRR	HLPTMPRRD
201	Y				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```
m214.seq (partial)
1 ATGATACAAA AGATATGTAA GCTATTGTGT TTAATAGCAT TTTTTTCGGC
51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGTTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTTCAGC
151 GGAACAGCTCG TCGTACAGACA GGTACGCTC AATATTCCGC CCGCCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTCAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...
```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```
m214.pep (partial)
  1  MIQKICKLFV LIAFFSASPFA FALQSDSRQP IQIEADQGSL DQANQSTTFS
 51  GNVVIRQGTI NISAARVNVV RGRQRRRIRE GGRFASPLQP DIGRRQRHGA
101  RTGKQRCLFI CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQRQH
151  KI...
```

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

m214/g214

	10	20	30	40	50	60
m214.pep	MIQKICKLVLI	AFFSASPAFALQSDSR	QPIQIEADQGSLDQAN	QSTTFSGNVVIR	QGT	L
		:   :	:		:	
g214	MIQKICKLVLI	VIVIFATSPAFALQSDSR	RRIPIQIEADQGSLDQAN	QRTTTFSGNVI	I	RQGT
	10	20	30	40	50	60
	70	80	90	100	110	120
m214.pep	NISAARVNVT	RGRQRRIREGGRFASPL	QPDIGRRQRH	GARTGKORCLFICR	QHRSLN	RNRX
	:		:	:	:     :	:
g214	NISASCNVN	TGRQRRRIREGGRFAR	PLQPNVGRGQ	RDGARSGKQRYL	FLLRKHKCR	SDDRQ
	70	80	90	100	110	120
	130	140	150			
m214.pep	CQSTARRRRC	RRRCGDYIQHQNRSLY	HQRQHKI			
	:	:	:			
g214	CQSAARRRC	RRRCGHYLQHQNRSLY	HQRQHEIGCEIR	FQNRRQGQR	RHPAFKH	TKNRITPM
	130	140	150	160	170	180
g214	PSETETQFR	RHLPTMP	PRDY			
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```
a214.seq
1  ATGATACAAA  AGATATGTAA  GCTATTGTGT  TTAATAGCAT  TTTTTTCGGC
51  GTCCCCCGCT  TTTGCCCTTC  AAAGCGACAG  CAGGCAGCCT  ATTCAGATTG
101 AGGCCGACCA  AGGTTGCTCT  GATCAGGCCA  ACCAAGACAC  CACATTACAG
151 GGAACGTCG  TCATCAGACA  GGGTACGCTC  AATATTTCCG  CCGCCCGCGT
201 CAATGTTACA  CGCGGC . GGC  AAAGCGGGCG  AATCCGTGAG  GGCGBAAGGT
251 TCGCCAGTCC  GCTTCAGCCA  GACATTGGAC  TGCGGCAAAG  GCACGGTGGC
301 CGGACAGGCA  AACACCGTTG  CTTATTTCAT  GCGCGCGAGC  ACCGTAGTCT
```

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAATCCG CTTCCTCAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNV T RGXQRRRI R GGRFASPLQ P DIGRRQRHGA
101 RTGKQRCLF I CRQHRSLNR* CQSTARRRC R RRCGDIYQH Q NRSLYHQ RQH
151 KIRRKIRFQ I RQGQRRYP A F EYAKIRIIP M PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m214.pep	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGS	L DQANQSTTFS	GNVVIRQGT
a214	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGS	L DQANQSTTFS	GNVVIRQGT
	70	80	90	100	110	120
m214.pep	NISAARVNV	TRGRQRRRI	REGGRFASPL	QPDIGRRQR	HGARTGKQR	CLFICRQHR
a214	NISAARVNV	TRGXQRRRI	REGGRFASPL	QPDIGRRQR	HGARTGKQR	CLFICRQHR
	130	140	150			
m214.pep	CQSTARRRC	RRCGDIYQH	QNRSLYHQ	RQH K I		
a214	CQSTARRRC	RRCGDIYQH	QNRSLYHQ	RQH K I R R K I R F Q I R Q G Q R R Y P A F E Y A K I R I I P M		
	130	140	150	160	170	180
a214	PSETXTWFG	RHLPT	EILKRYLX			
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTGC AAC
51  TTGCTCCGCT TTTGCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGTAC CACATTTAGC
151 GGCAATGTCA TCATCAGACA GGTACGCTC AACATTCCG CCTCGCGCGT
201 CAACGTCACA CGCGGCGGCA AAGCGGCGCA ATCCGTGAGG GCGGAAGGTT
251 CGCCCGTCCG CTTGAGCCAA ACGTTGGACG GGGGCAAGG GACGGTGC GC
301 GGTGAGGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGGCGGCG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAAGTCT ATACCATCAA CGGCAGCAGC
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQSTTFS
51  GNVIIIRQGT L NISASRVNV T RGGKGGESV R AEGSPVRF S Q TLDGGKGTVR
101 GQANNVTYSS AGSTVVLTG N AKVQRGGDVA EGAVITYNT K TEVYTINGST
151 KSGAKSASKT GRVSVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAACGTCG TCATCAGACA GGTACGCTC AATATTCCG CCGCCGCGT

```

201 CAATGTTACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT  
 251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC  
 301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT  
 351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG  
 401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA  
 451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT  
 501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS  
 51 GNVVIRQGT L NISAARVNV T RGGKGGESV R AEGSPVRF S Q TLDGGKGT V R  
 101 GQANNVAY S S AGSTVVL T GN AKVQRGGD V A EGAVITYN T K TEVYTISG S T  
 151 KSGAKSAS K S GRVSVVIQ P S STQKSE\*

m214-1/g214-1 93.8% identity in 176 aa overlap

	10	20	30	40	50	60
m214-1.pep	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGS L	DQANQSTTFS	GNVVIRQGT L
g214-1	MIQKICKLFV	LIVIFATSP	AFALQSDSR	RP IQIEADQGS L	DQANQSTTFS	GNVVIIRQGT L
	10	20	30	40	50	60
m214-1.pep	NISAARVNV	TRGGKGGES	VR AEGSPVRF	S Q TLDGGKGT	VR GQANNVAY	SSAGSTVVL T GN
g214-1	NISASRVNV	TRGGKGGES	VR AEGSPVRF	S Q TLDGGKGT	VR GQANNVY	SSAGSTVVL T GN
	70	80	90	100	110	120
m214-1.pep	AKVQRGGD	VAEGAVITYN	TKTEVYTISG	STKSGAKSAS	KSGRVSVVIQ	PSSTQKSEX
g214-1	AKVQRGGD	VAEGAVITYN	TKTEVYTING	STKSGAKSAS	KTRVSVVIQ	PSSTQKTEX
	130	140	150	160	170	

g214-1/p38685

sp|P38685|YHBN\_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)  
 >gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF\_0185 [Escherichia coli]  
 >gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185  
 Score = 97.1 bits (238), Expect = 6e-20  
 Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

Query: 19 PAFALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L NISAARVNV TR--GGKGG 76  
 PAF A+ D+ QPI IE+DQ SLD TF+GNV++ QGT+ I+A +V VTR G +G  
 Sbjct: 24 PAFAVTGD TDQPIHIESDQQSLDMQGNVVTFTGNVIVTQGT IKINADKVVVTRPGGEQ GK 83

Query: 77 ESVAEAGSPVRF S Q TLDGGKGT VR GQANNVAY SSAGSTVVL T GN AKVQRGGD VAEGAVIT 136  
 E + G P F Q D GK V G A+ + Y A VVLTGNA +Q+ +G IT  
 Sbjct: 84 EVIDGYGKPATFYQM DNGK-PVEGHASQMHYELAKDFVVL T GNAYLQQVDSNIKGDKIT 142

Query: 137 YNTKTE 142  
 Y K +  
 Sbjct: 143 YLVKEQ 148

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC  
 51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG  
 101 AGGCCGACCA AGGTTCCGTC GATCAAGCCA ACCAAAGCAC CACATTCAGC  
 151 GGAACGTCG TCATCAGACA GGGTACGCTC AATATTTCG CCGCCCGCGT  
 201 CAATGTTACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT  
 251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC  
 301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT  
 351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG  
 401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA  
 451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT  
 501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

51 GNVVIRQGTI NISAARVNV T RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR  
 101 GQANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTISGST  
 151 KSGAKSASKS GRVSVVIQPS STQKSE\*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFVLI	AFFSASP	FALQSDSRQPI	QIEADQGS	LDQANQSTTF	SGNVVIRQGTI
m214-1	MIQKICKLFVLI	AFFSASP	FALQSDSRQPI	QIEADQGS	LDQANQSTTF	SGNVVIRQGTI
	10	20	30	40	50	60
	70	80	90	100	110	120
a214-1.pep	NISAARVNVTR	RGGKGGESV	RAEGSPVRF	SQTLDGGKGT	VRGQANNVAY	SSAGSTVVLTGN
m214-1	NISAARVNVTR	RGGKGGESV	RAEGSPVRF	SQTLDGGKGT	VRGQANNVAY	SSAGSTVVLTGN
	70	80	90	100	110	120
	130	140	150	160	170	
a214-1.pep	AKVQRGGDVA	EGAVITYNTK	TEVYTISGST	TKSGAKSASK	SGRVSIVIQPS	STQKSEX
m214-1	AKVQRGGDVA	EGAVITYNTK	TEVYTISGST	TKSGAKSASK	SGRVSIVIQPS	STQKSEX
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq  
 1 atgaaagtaa gatggcggta cggaaattgcg ttcccattga tattggcgggt  
 51 tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa  
 101 tcgaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc  
 151 ttggacggaa ggcggtttga cgaacaggga tacttgaaag aacatttgag  
 201 cgcgaaaggt gcgaaacagt ttcccgaata cagcgacatc cattttgatt  
 251 cgccgcatct cgtgttcttc caagaaggca ggctgttgta cgaagtcggc  
 301 agcgatgaag ccgtttacca taccgaaaac aaacagggtc tttttaaaaa  
 351 caacgttggtg ctgacaaaaa ccgcccacgg caggcggcag gcgggtaaaag  
 401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaaccc  
 451 gatacgccctg tcagtttcca atatggcgcg tcgcacggtc aggcgggccc  
 501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga  
 551 aagccgcgat ttatgatata aaagatatgt aa

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep  
 1 MKVRWRYGIA FPLILAVLALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS  
 51 LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPHLVFF QEGRLLYEVG  
 101 SDEAVYHTEN KQVLFKNNVV LTKTADGRRQ AGKVETEKLH VDTESQYAQT  
 151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAIIYDT KDM\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)  
 1 ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT  
 51 CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA  
 101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG CGCGAAGGGC  
 151 GCGAAACAGT TTCCGAAAG CAGCGACATC CATTGATTGATT CGCCGCATCT  
 201 CGTGTCTTTC CAAGAAGGCA GGTGTTGTA CGAAGTCGGC AGCGACGAAG  
 251 CCGTTTACCA TACCGAAAAC AAACAGGTTT TTTTAAAAA CAACGTTGTG  
 301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA  
 351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAAAC GATACGCTG  
 401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG CATGACTTAC  
 451 GACCACAWWA CAGGCATGTT GAATTCTCA TCTAAAGTGA AAGCCACGAT  
 501 TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)  
 1 ..SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG  
 51 AKQFPENSDI HFDSPHLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNNVV  
 101 LTKTADGKRQ AGKVEAEKLH VDTESQYAQT DTPVSFQYGA SHGQAGGMTY

151 DHXTGMLNFS SKVKATIYDT KDM\*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVR	LNPDEPQYTMDSLDGRRFDEQG		
g215	MKVRWRYGIAPFLILAVALGSLSAWLGRISEVEIEEVR	LNPDEPQYTMDSLDGLDGRRFDEQG			
	10	20	30	40	50
					60
	50	60	70	80	90
m215.pep	YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV				
	:         :				
g215	YLKEHLSAKGAKQFPENS DIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV				
	70	80	90	100	110
					120
	110	120	130	140	150
m215.pep	LTKTADGKRQAGKV EAEKLHVDTESQAQTDPVS FQYGASHGQAGGMTYDHXTGMLNFS				
	:         :				
g215	LTKTADGRRQAGKVET EKLHVDTESQAQTDPVS FQYGASHGQAGGMTYNHKTGMLNFS				
	130	140	150	160	170
					180
	170				
m215.pep	SKVKATIYDTKDMX				
	:				
g215	SKVKA AIYDTKDM				
	190				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq	1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCCATTTGA	TATTGGCGGT
	51	TGCTTGGGG	AGCCTGTGCG	CATGGTTGGG	AGCAGTCAGC	GAAGTCGAGA
101		TTGAAGAAGT	CAGGCTCAAT	CCGACGAAAC	CGCAATACAC	AATGGACGGA
151		TTGGATGGCA	GGCGGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTGAG
201		TTCGAAGGGC	GCGAAACAGT	TTCCGAAAG	CAGCGACATT	CATTTGACT
251		CACCGCATCT	CGTGTCTTC	CAAGAAGGCA	GGTTGTGTA	CGAAGTCGGC
301		AGCAGTAGA	CCGTTTACCA	TACCGAAAC	AAACAGGTTT	TTTTTAAAAA
351		CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAACCGGCAG	CGCGGTAAAG
401		TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCCAAAC
451		GATACGCCCTG	TCAGTTTCCA	ATATGGTGCA	TGCGACGGTC	AGGCGGGCGG
501		CATGACTTTAC	GACCACAAAA	CAGGCATGTT	GAACTTCTCA	TCTAAAGTGA
551		AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pap

1	<u>MKVWR</u> RYGIA	<u>FPLILA</u> VALG	<u>SLSA</u> WLGRIS	EVEIEEVRLN	PDEPQYTM
51	LDGRRFDEQ	YLKEHLSSK	AKQFP	ESSDI	HFDSPHLV
101	SDEAVYHTN	KQVLFKN	NV	LTKTADG	GRKQ
151	DTPVSFOY	GASGAG	MTY	DHKTGML	NFS
				SKVKAT	IYDT
				KDM*	

**m215/a215 98.3% identity in 173 aa overlap**

				10	20	30	40
m215.pep				SLSAWLGR	ISEVEIEE	VRLNPDEP	QYTMDSL
							DGRRFDEQ
a215	MKVRWRY	GIAFPLI	ALVALGS	SLSAWLGR	ISEVEIEE	VRLNPDEP	QYTMDSL
							DGRRFDEQ
	10	20		30	40	50	60
	50	60		70	80	90	100
m215.pep	YLKEHLS	AKGAKQ	FPESSDI	HFDSPHL	VVFFOEGR	LLYEVGS	DEAVYHT
							ENKOVLF
							KNNNV



```

|||||:|||||
a215      YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
              70      80      90      100      110      120

              110      120      130      140      150      160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHKTGMLNFS
              130      140      150      160      170      180

              170
m215.pep  SKVKATIIDTKDMX
              |||||
a215      SKVKATIIDTKDMX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcgagctc ggtaccacgc gacgaaatca ccgccatcat
51  ccccgcactc aaacgcaaag acattaccct cgtctgcatc accgcccgcc
101 ccgattcaac catggcgcgc catgccgata tccacatcac cgcacggtt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttggcggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcggc
301 aaacgcctgc ttttgcgcgt tgccgacatt atgcacaaag gcggcgccct
351 gcccgcgctc cgactcggca cgcccttgaa aggagccatc gtcagcatga
401 gcgagaaaag tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKDITLVC I TARPDSTMAR HADIIHTASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVVLL RARAFTPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGA I VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51  GCACGCCGAA GCGGAAGGCT TGC CGGAAAT TGCAGCGGAA TTGgACAAAA
101 ACTTCGTCCT TCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGCGA TTTGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTCT TCCTGCTGCG CgcACGCGCG TTCACGCCCG
551 ACGATTTCGC CTTGAGCCAT CTGCGCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GCGCGCCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTACCGG
801 TCTTTGATA GACGAAGTCA TGCATACGCA TCCTAAACC ATCTCCGCCG
851 AACGTCTGCG CACCGAAGCC CTGAAAGTCA TGAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALLHCKGRVV

```

```

51  ITGMVKS GHI GRKMAATMAS TGTPAFFVHP AEAHGD LGM IVDXDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAP TTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHK G GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGR LKGVF
251 TDGDLRRL FQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN
301 GLLVTDADGV LIGALNMHDL LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

m216/g216

```

              70      80      90      100     110     120
m216.pep      TMASTGTPAFFVHPAEAAHGD LGMIVDXDVVVAISNSGESDEIAAIIPALKRKDITLVCI
              ::|||:| ||||:|||||
g216           MISISSVPSDEITAIIPALKRKDITLVCI
              10      20      30

              130     140     150     160     170     180
m216.pep      TARPDMSTARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
|||
g216           TARPDMSTARHADIHITASVSQEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
              40      50      60      70      80      90

              190     200     210     220     230     240
m216.pep      ALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGR
||
g216           ALIHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKGAIVSMSEKGLGMWAGTDGQRLS
              100     110     120     130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

a216.seq

```

1  ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGTT
51  GCACACCGAA GCGGAAGGCT TGCGCGAAAT TGCGGCGGAT TTGGACGAAA
101 ACTTCGCCCT TGCGGCGGAC GCGTTGTTGC ACTGCAAAGG CAGGGTCGTT
151 ATCACGGGCA TGGGCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 CATGGCCTCG ACCGGCACGC CCGCGTTTTT CGTCCACCTT GCGGAAGCGG
251 CACACGGCGA TTTGGGCATG ATTGTGGACA ACGACGTGGT CGTCGCGATT
301 TCCAATTCGG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351 ACGCAAAGAT ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGCG TTATGGCTTT
501 GGGCGATGCG TTGGCGGTTG TCCTGCTGCG CGCCCGCGCG TTCACGCCCG
551 ACGACTTCGC CTTGAGCCAC CCTGCCGCGA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCTGCT CTGCCGTCCT
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCGG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTT TTGGCGGCGC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

a216.pep

```

1  MAMAGNEKYL DWAREVLHTE AEGLEIAAD LDENFALAAD ALLHCKGRVV
51  ITGMGKSGHI GRKMAATMAS TGTPAFFVHP AEAHGD LGM IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAP TTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHK G GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGR LKGVF
251 TDGDLRRL FQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN

```

301 GLLVTDADGV LIGALNMHDL LAARIV\*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENKYLWAREVLHAEAEGLREIAAELXKNFVLAADALLHCKGRVITGMVKSCHI					
a216	MAMAGNEKYLWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVITGMGKSGHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIIPALKRKD					
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDNDVVVAISNSGESDEIAAIIIPALKRKD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLRARA					
a216	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLRARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALSHPAGSLGKRLRLRVADIMHKGGLPAVRLGTPLEAIVSMSEKGLMLAVT					
a216	FTPDDFALSHPAGSLGKRLRLRVADIMHKGGLPAVRLGTPLEAIVSMSEKGLMLAVT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRKLGVTGDLRLRFQECNFTGLSIDEVMHTHPKTI SAERLATEALKVMQANHVN					
a216	DGQGRKLGVTGDLRLRFQECNFTGLSIDEVMHTHPKTI SAERLATEALKVMQANHVN					
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADGVLIGALNMHDLAARIVX					
a216	GLLVTDADGVLIGALNMHDLAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggtatg acggtttgtt gcggcaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttctcaggtt ttggactgcc
101 ttttgggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgagg ttgccccat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggcaa aacgtccgaa catggcggtt
251 tgattcacgt cggcatacca cgcgctgaca tcttgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttc
351 aggtaaacag ctgatccgtg ccgcccgcga tttctccgtc caatcccaaa
401 tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcgc aaacggcgca acacggcgcc ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttccagca agtcggacac gcaactcaac
551 gcataaaaaa acggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgtata gggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence &lt;SEQ ID 764; ORF 217.ng&gt;:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPYPGNIRQ GFEEGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAQQQVGH ALQRIKKRLP AADFHVRNGI

```

201 RQCLRAGLRL SEHGFKRRI GFDIRG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

```

1  ATGGCGGATG ACGGTGTGCG GCGGCAACTG TCCGAAAAT TGCGCCAATT
51  CGGTTTCCGC CTCCATTG ACCCATTCGT TTCAAGGTT TTGGAAGTAC
101 TTTTGGTCAT CGGCTTCAGC TTGAACAAT GTTCAAGCA AATCCCGGCA
151 ACGCGCCACC CATTGCGCGA CCGTTGCGGG CTGCCGCCAT ATCCGTACAA
201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CATGGCGGTT
251 TGATTACAGT CGGCATACCA CGCGCTGACA TCCTGCCACA TCGGATTGCC
301 GCCTTTGGGC AGCATCCAGC CCAATATCAT GCGTCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTCTCCGTC CAAACCCAG
401 TGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGTA AATCGTCCTC
451 AGTCAGTCCG AAACGGCGCA ACACGGGCGC GGTTTCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGGCG GCGGCTGATT TTCACGCTG ACACGGAATA
601 CGGCAATGCC TCGCACCGG GctGCGCTG TCCGAACAG GCTTCGATA
651 AAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVRRL SGKLRQFGR LFPDPFVKV LDXLLVIGFS LEQCFKQIPA
51  TRHPFADRCG LPPYPYNIRO GFEEGGKTSE HGGLIHVGIP RADILPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPVDVQIGN HVVQKRXLV
151 SQSETAQHGR GFXXKHKHFID FKSAFQVQEQ AXQSMKQRLA AADFHVXHGI
201 RQCLRTGLRL SEHGFDKRII GFDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVRRLSGKLRQFGFRLFPDPFVKVLDXLLVIGFSLEQCFKQIPATRHFPADRCG					
g217	MADDGLLRQLSEKPSQSALFLPDPFVFEVLDCLLVIGPGLKQCFKQIPATRHFPADRRR					
	10	20	30	40	50	60
m217.pep	LPPYPYNIROGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVA AFGQHPAQYHTVCRLLPKGQ					
	70	80	90	100	110	120
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXLVLSQSETAQHGRGFXXKHKHFIDFKSAFQVQEQ					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKRQIVPGQSETAQHGRGFQKREHFADFKTAFQOVGH					
	130	140	150	160	170	180
m217.pep	AXQSMKQRLAAADFHVXHGI RQCLRTGLRLSEHGFDKRIIGFDIRGX					
g217	ALQRIKKRLPAADFHVRNGIRQCLRAGLRLSEHGFKRRIIGFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

```

1  GTGGCGGATG ACGGTGTGCA GCGGCAACTG TCCGAAAAT TGCGCCAATT
51  CGGTTTCCGC CTGCCATTG ACCCATTCGT TTTCGAGGCT TTGGAAGTAC
101 TTTTGGTCAT CGCCTTCGAC TTGAACAAT GTTCAAGCA AATCCCGGCA
151 ACGCGCCACC CATTGCTCAA CCGTCGAGG TTGCCGCCAT ATCCGTACAA

```